```
OM protein - protein search, using sw model

          GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:   February 14, 2004, 22:43:11 ; Search time 27 Seconds
                         (without alignments)
                         1919.386 Million cell updates/sec

Title:    US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0:5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters:    127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5785	99.9	1102	1	P11G_PIG	O02697 sus scrofa.
2	5523.5	95.4	1101	1	P11G_HUMAN	P48736 homo sapien
3	5506	95.1	1102	1	P11G_MOUSE	Q9jhg7 mus musculu
4	1465.5	25.3	1068	1	P11A_BOVIN	P32871 bos taurus
5	1460.5	25.2	1068	1	P11A_HUMAN	P42336 homo sapien
6	1450.5	25.1	1068	1	P11A_MOUSE	P42337 mus musculu
7	1362	23.5	1070	1	P11B_RAT	Q9zl0 rattus norv
8	1354.5	23.4	1070	1	P11B_HUMAN	P42338 homo sapien
9	1349.5	23.3	1044	1	P11D_HUMAN	O00329 homo sapien
10	1319	22.8	1043	1	P11D_HUMAN	O35904 mus musculu
11	1297	22.4	1570	1	P3K1_DICDI	P54673 dictyosteli
12	1233	21.3	1858	1	P3K2_DICDI	P54674 dictyosteli
13	1136.5	19.6	1585	1	P3K3_DICDI	P54675 dictyosteli
14	1041	18.0	1146	1	AGE1_CAEEL	Q94125 caenorhabdi
15	1021	17.6	1634	1	PK3B_HUMAN	O00750 homo sapien
16	922	15.9	1505	1	PK3G_RAT	O70173 rattus norv
17	881	15.2	1506	1	PK3G_MOUSE	O70167 mus musculu
18	856.5	14.8	1448	1	PK3G_HUMAN	P75747 homo sapien
19	720.5	12.4	816	1	P3K4_DICDI	P54676 dictyosteli
20	714.5	12.3	801	1	VP34_SCHPO	P50520 schizosacch
21	672	11.6	814	1	P3K1_SOYBN	P42347 glycine max
22	669	11.6	812	1	P3K2_SOYBN	P42348 glycine max
23	657.5	11.4	814	1	PI3K_ARATH	P42339 arabidopsis
24	649.5	11.2	875	1	VP34_YEAST	P22543 saccharomyc
25	562	9.7	1020	1	VP34_CANAL	Q92213 candida alb
26	402	6.9	854	1	P14K_HUMAN	P42356 homo sapien
27	380	6.6	1900	1	STT4_YEAST	P37297 saccharomyc
28	314.5	5.4	1093	1	PI4K_DICDI	P54677 dictyosteli
29	277	4.8	1066	1	PIK1_YEAST	P39104 saccharomyc
30	248	4.3	851	1	YDBG_SCHPO	Q10366 schizosacch
31	239	4.1	4128	1	PRKD_HUMAN	P78527 homo sapien
32	232	4.0	4128	1	PRKD_MOUSE	P97313 mus musculu
33	225	3.9	2787	1	TEL1_YEAST	P38110 saccharomyc
34	215.5	3.7	2337	1	TOR2_SCHPO	Q9y7k2 schizosacch
35	215.5	3.7	2470	1	TOR2_YEAST	P35169 saccharomyc
36	210.5	3.6	2368	1	ESR1_YEAST	P38111 saccharomyc
37	200.5	3.5	2386	1	RAD3_SCHPO	Q02099 schizosacch
38	191	3.3	2473	1	TOR2_YEAST	P32600 saccharomyc
39	191	3.3	3056	1	ATM_HUMAN	Q13315 homo sapien
40	178.5	3.1	2549	1	FRAP_MOUSE	Q9jln9 mus musculu
41	178	3.1	3066	1	ATM_MOUSE	Q62388 mus musculu
42	177.5	3.1	2549	1	FRAP_HUMAN	P42345 homo sapien
43	174.5	3.0	2549	1	FRAP_RAT	P42346 rattus norv
44	172	3.0	2335	1	TOR1_SCHPO	O14356 schizosacch
45	143	2.5	6885	1	SNE2_HUMAN	Q8wxh0 homo sapien

ALIGNMENTS

```
RESULT 1
P11G_PIG
ID   P11G_PIG     STANDARD;     PRT;   1102 AA.
AC   O02697;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (p110) (PI3-kinase p110 subunit gamma) (PtdIns-
DE   3-kinase p110) (PI3K) (P120-PI3K).
GN   PI3CG.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Neutrophils;
RX   MEDLINE=97248491; PubMed=9094719;
RA   Stephens L.R., Eguinoa A., Erdjument-Bromage H., Lui M., Cooke F.,
RA   Coadwell J., Smrcka A.S., Thelen M., Cadwallader K., Tempst P.,
RA   Hawkins P.T.;
RT   "The G beta gamma sensitivity of a PI3K is dependent upon a tightly
RT   associated adaptor,p101.";           [porcine]
RL   Cell 89:105-114(1997).
RN   [2]
RP   REVISIONS.
RA   Stephens L.R.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC       COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC       PROTEINS.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------------
DR   EMBL; Y10743; CAA71731.1; -.
DR   PDB; 1B7U; 01-DEC-00.
DR   PDB; 1B8X; 01-OCT-02.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
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DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS00290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN     17     22     POLY-ARG.
FT   DOMAIN    828   1073     PI3K/PI4K.
SQ   SEQUENCE 1102 AA;  126657 MW;  9E7D4211FD626DFC CRC64;

Query Match      99.9%;  Score 5785;  DB 1;  Length 1102;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1101;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  0;

Qy      1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60

Qy     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120

Qy    121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy    181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy    241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy    301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIIHGKDHESVFTVSLWDCDRK 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIIHGKDHESVFTVSLWDCDRK 360

Qy    361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420

Qy    421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480

Qy    481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKRPTPDPEG 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKRPTPDPEG 540

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy    661 LQLVQAVKPEPYHDSALARPLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 LQLVQAVKPEPYHDSALARPLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy    721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy    841 DMLIQILRIMBSIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 DMLIQILRIMBSIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy    901 AFKDEVLSHWLKEKCPIEEKFQAAVERRVYSCAGYCVATFVLGIDRHNDNIMISETGNL 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AFKDEVLSHWLKEKCPIEEKFQAAVERRVYSCAGYCVATFVLGIDRHNDNIMISETGNL 960

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy   1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
            ||||||||||||||||||||||
Db   1081 TVQFNWFLHLVLGIKQGEKHSA 1102


RESULT 2
P11G_HUMAN
ID   P11G_HUMAN    STANDARD;    PRT;   1101 AA.
AC   P48736;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ...phosphate 3-kinase catalytic subunit, ...(PI3-kinase-
```

OM protein - protein search, using sw model

```
                    GenCore version 5.1.6
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DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (PtdIns-
DE   3-kinase p110) (PI3K) (P120-PI3K).
GN   PIK3CG.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Neutrophils;
RX   MEDLINE=97248491; PubMed=9094719;
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CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
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CC       COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; Y10743; CAA71731.1; -.
DR   PDB; 1ETU; 01-DEC-00.
DR   PDB; 1E8X; 01-OCT-02.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
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Porcine

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DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN     17     22    POLY-ARG.
FT   DOMAIN    828   1073    PI3K/PI4K.
SQ   SEQUENCE  1102 AA;  126657 MW;  9E7D4211FD626DFC CRC64;

Query Match             99.9%;  Score 5785;  DB 1;  Length 1102;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1101;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    0;

Qy     1  MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60

Qy    61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120

Qy   121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240

Qy   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy   301  EEIHLVLDTPPDPALDEVRKEEMPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  EEIHLVLDTPPDPALDEVRKEEMPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420

Qy   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGSKGAQLLYYVNLLLIDHRPLLRHGEY  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGSKGAQLLYYVNLLLIDHRPLLRHGEY  480

Qy   481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPGKRPTPDPEG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  VLHMWQLSGKGEDQGSFNADKLTSRTNPDKENSMSISILLDNYCHPIALPGKRPTPDPEG  540

Qy   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKPLWLEFKCADPTALSNETGIIFKHGDDLRQ  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKPLWLEFKCADPTALSNETGIIFKHGDDLRQ  840

Qy   841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900

Qy   901  AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021  RHHTNLLILIFFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  RHHTNLLILIFFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA 1102
          ||||||||||||||||||||||
Db  1081  TVQFNWFLHLVLGIKQGEKHSA 1102
```

RESULT 2

P11G_HUMAN

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ID   P11G_HUMAN     STANDARD;      PRT;   1101 AA.
AC   P48736;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (PtdIns-
DE   3-kinase p110) (PI3K) (PI3Kgamma).
GN   PIK3CG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95350661; PubMed=7624799;
RA   Stoyanov B., Volinia S., Hanck T., Rubio I., Loubtchenkov M.,
RA   Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nuernberg B.,
RA   Gierschik P., Seedorf K., Hsuan J.J., Waterfield M.D., Wetzker R.;
RT   "Cloning and characterization of a G protein-activated human
RT   phosphoinositide-3 kinase.";
RL   Science 269:690-693(1995).
RN   [2]
RP   REVISIONS.
RA   Waterfield M.D.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC       G PROTEINS.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

```
CC
DR   EMBL; X83368; CAA58284.1; -.
DR   PDB; 1E8Y; 17-NOV-00.
DR   PDB; 1E8Z; 17-NOV-00.
DR   Genew; HGNC:8978; PIK3CG.
DR   MIM; 601232; -.
DR   GO; GO:0004429; F:1-phosphatidylinositol 3-kinase; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR000420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_rbd.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN        18       22       POLY-ARG.
FT   DOMAIN       827     1072       PI3K/PI4K.
SQ   SEQUENCE   1101 AA;  126410 MW;  266BAA6495C8AE9E CRC64;

Query Match             95.4%;  Score 5523.5;  DB 1;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative  21;  Mismatches  31;  Indels  1;  Gaps  1;

Qy          1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH  60
              ||||||:|||||||||||||||||||||||   :||||||||||||||||:||||||||
Db          1 MELENYKQPVVLREDNCRRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH  59

Qy         61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGGQWYEIYDKYQVVQTLD 120
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db         60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGGQWYEIYDKYQVVQTLD 119

Qy        121 CLRYWKVLHRSPGQIHVVQRHAPSSETLAFQRQLNALIGYVTDVSNVHDDELEFTRRRL 180
              |||||:||||||||||:|||||||:|||||:||||||||||||||||||||||||:|||
Db        120 CLRYWKATHRSPGQIHLVQRHPPSSESQAFQRQLTALIGYVTDVSNVHDDELEFTRRGL 179

Qy        181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
              |||||||||||||||||||||||||||||||:||||||||||||||||:|||||||||:
Db        180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYIWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy        241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
              ||:||||||||||||||||||||||||||:|||||||||||||||||||||:||:|||||
Db        240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYIVGETPIKNFQWVRHCLKNG 299

Qy        301 EEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVPTVSLMWDCDRK 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVPTVSLMWDCDRK 359

Qy        361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
              ||||||||||||||:|||||||||||||:|||||||||||||||||||||||||||||||
Db        360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 419

Qy        421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
              ||||||||||||||||||||||:||||:||:||||||:||||||||||||||||||||||
Db        420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy        481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDDPEG 540
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||:|||||||
Db        480 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDDPEG 539

Qy        541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy        601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYL 660
              |||||||||||||:|||||||||:|||||||||||||||||||||||||:||||||||||
Db        600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYL 659

Qy        661 LQLVQAVKFPPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 LQLVQAVKFPPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy        721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDKSLSAEKYDVSSQVISLQKQKLENLQNLNLP 780
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||:
Db        720 LRGGCGTAMLHDFTQQVQVIEMLQKVTLDKSLSAEKYDVSSQVISLQKQKLENLQNSQLP 779

Qy        781 QSFRVPYDPGLKAGALVIEBCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
              :||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        780 ESFRVPYDPGLKAGALAIEBCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy        841 DMLIQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 DMLIQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy        901 AFKDEVLSIWLKEKCPIEKFQAAVERFYYSCAGYCVATFVLGIGDRHNDNIMITETGNL 960
              |||||||:||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        900 AFKDEVLNHWLKEKSPTEBKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy        961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020
              ||||||||||||||||||||||||:||||||||||||||||||:|||||||||||||||||
Db        960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy       1021 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db       1020 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGNEEDAKKYFLDQIEVCRDKGW 1079

Qy       1081 TVQFNWFLHLVLGIKQGEKHSA 1102
              ||||||||||||||||||||||
Db       1080 TVQFNWFLHLVLGIKQGEKHSA 1101

RESULT 3
ID   P11G_MOUSE      STANDARD;      PRT;   1102 AA.
AC   Q9JHG7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (p110) (PI3K) (PI3-kinase p110 subunit gamma) (Ptdins-
DE   3-kinase p110) (PI3Kgamma).
GN   PIK3CG OR PI3KG1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hirsch E.;
RL   "Murine PI3kgamma: cDNA cloning and gene structure description.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Wymann M.P., Hirsch E.;
RT   "Murine G protein-coupled phosphoinositide 3-kinase gamma cDNA and
RT   genomic organisation.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2) (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC       G PROTEINS (BY SIMILARITY). WORTMANNIN SENSITIVE IN NM RANGE.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

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CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; AJ249411; CAB89851.1; -.
DR   EMBL; AJ249414; CAB89851.1; JOINED.
DR   EMBL; AJ249415; CAB89851.1; JOINED.
DR   EMBL; AJ249416; CAB89851.1; JOINED.
DR   EMBL; AJ249417; CAB89851.1; JOINED.
DR   EMBL; AJ249418; CAB89851.1; JOINED.
DR   EMBL; AJ249419; CAB89851.1; JOINED.
DR   EMBL; AJ249420; CAB89851.1; JOINED.
DR   EMBL; AJ249280; CAB89686.1; -.
DR   MGD; MGI:1353576; Pik3cg.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF06613; PI3Ka.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN       18     22       POLY-ARG.
FT   DOMAIN      828   1073       PI3K/PI4K.
SQ   SEQUENCE   1102 AA;  126361 MW;  B9E94CFDD0C21D57 CRC64;

Query Match          95.1%;
Best Local Similarity 94.3%;
Matches 1039;  Conservative  31;  Mismatches  32;  Indels   0;  Gaps   0;

Qy     1 MELENYEQPVVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKPTETALLH 60
         |||||||||||||||| :||:||||| ::|||||||||||||||||||  :||||||||
Db     1 MELENYEQPVVLREDNLRRRRRMKPRSAAGSLSSMELIPIEFVLPTSQRISKTPETALLH 60

Qy    61 VAGHGNVEQMKACQVWLRALETSVSADFYHRLGPDHPLLLYQKKGGQWYEIYDKYQVVQTLD 120
         ||||||||||||||||||||||| :|:||||||||  |||||||||||||||||:|||||||
Db    61 VAGHGNVEQMKACQVWLRALETSVAAEFYHRLGPDQFLLLYQKKGGQWYEIYDRYQVVQTLD 120

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
         ||:|||:::|:|||||||||||.||||||||:||.:||||||||:|||||||||||||||
Db   121 CLHYWKLMHKSPGQIHVVQRHVPSEETLAFQKQLTSLIGYDVTDISNVHDDELEFTRRRL 180

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVPIVIVIHRSTTSQTIKVSADDT 240
         |||||||||||:|||||||||||||||:||| |||:|||:|:|||||:|||||||||||||
Db   181 VTPRMAEVAGRDAKLYAMHPWVTSKPLPDYLSKKIANNCIFIVIHRGTTSQTIKVSADDT 240

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
         ||||||||||||||||||:||||||.|:|||||||||||||||||||:|||||||||||||
Db   241 PGTILQSFFTKMAKKKSLMNIPESQSEQDFVLRVCGRDEYLVGETPLKNFQWVRQCLKNG 300

Qy   301 EEIHLVLDTPPPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCCDRK 360
         :||||||||||.|||||||||||||||||||||||||||||||||||:.|||||||||||
Db   301 DEIHLVLDTPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVVTVSLWDCCDRK 360

Qy   361 FRVKIRGIDIPVLPRTADLTVPEANIYGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
         |||||||||||||||  :||||||| ::|||||||||||||:..|||||||||| |||
Db   361 FRVKIRGIDIPVLPRNTDLTVPEANIQHGQVLCQRRTSPKPFAAEVLMNVWLEFGIKI 420

Qy   421 KDLPKGALLNLQIYCGKCAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
         |||||||||||||||.|. :| ||  ||:  |.|||||||||||:||||||||||||||: 
Db   421 KDLPKGALLNLQIYCCKTPSLSSKASAETPGSESKGKAQLLYVNLLLIDHRFLLRHGDY 480

Qy   481 VLHMWQLSGKGEDQGSFNADKLTSAATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
         |||||| ||| |:|||||||||||| ||||||||||||||||||||||||||||||||||||
Db   481 VLHMWQISGKAEBQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKPKAYPKLFSSVKWGQ 600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
         |||||||||||| ||:|||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLARREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
         |.|||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db   661 LQlVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSSIAQSRHYQQRFAVILEAY 720

Qy   721 LRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
         |||||||||:|||||| :|::|||||||||||||||||||||||||||||||:|||:.|||
Db   721 LRGCGTAMLQDFTQQVHVIEMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLP 780

Qy   781 QSPRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
         :|||||||||||||:|||||||||||||||||||||||||||.||||||||||||||||||
Db   781 ESFRVPYDPGLKAGTLVIEKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQ 840

Qy   841 DMLILQIIRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db   841 DMILLQIIRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAQIQQSTVGNTG 900

Qy   901 AFKDEVLSHWLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
         ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLNHWLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
         ||||||||||||||||||||||:|||||||||||||||.|||||.||||||||||:|||||
Db   961 FHIDFGHILGNYKSFLGINKEVVPFVLTPDFLFVMGGSGKKTSPHFQKFQDVCVRAYLAL 1020

Qy  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy  1081 TVQPNWFLHLVLGIKQGEKHSA 1102
         ||||||||||||||||||||||
Db  1081 TVQPNWFLHLVLGIKQGEKHSA 1102
```

RESULT 4

```
P11A_BOVIN
ID   P11A_BOVIN     STANDARD;      PRT;  1068 AA.
AC   P32871;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (PtdIns-
DE   3-kinase p110) (PI3K).
GN   PIK3CA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92354059; PubMed=1322797;
RA   Hiles I.D., Otsu M., Volinia S., Fry M.J., Gout I., Dhand R.,
RA   Panayotou G., Ruiz-Larrea F., Thompson A., Totty N.F., Hsuan J.J.,
RA   Courtneidge S.A., Parker P.J., Waterfield M.D.;
RT   "Phosphatidylinositol 3-kinase: structure and expression of the 110
RT   kd catalytic subunit.";
RL   Cell 70:419-429(1992).
```

```
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS(4)P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; M93252; AAA30698.1; -.
DR   PIR; A43322; A43322.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN    319    428    C2_DOMAIN.
FT   DOMAIN    797   1068    PI3K/PI4K.
SQ   SEQUENCE   1068 AA;  124327 MW;  C753DCC2F39FDDF0 CRC64;

Query Match          25.3%;  Score 1465.5;  DB 1;  Length 1068;
Best Local Similarity 33.5%;  Pred. No. 1.5e-89;
Matches  382;  Conservative 204;  Mismatches 405;  Indels 149;  Gaps 39;

Qy    23  MKPRSTAASLSSMELIP------IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
              ||| ::|| |::  ||:         ||   | :|:      :|:    : || :::
Db     1  MPPRPSSGELMWGIIHLMPPRILVECLLPNGMVT------LECLREATLITIKHELFKEA   53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTIDCLRYWKVLHRSPGQIHVV  138
             :| ||  :| :       || |  |  |: ::   |                 ||  |
Db    54  RKYPL----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI  102

Qy   139  QRHAPSEETLAFQRQLNALIGYDVDTVDVSNVHDDELEFTRRRLVTPRMAEVVAGRD----  192
              :| :  | :|  :|  :  :|  ::: :::|:      ::  :|
Db   103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVXDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy   193  PKLYAVHPWVTSKP-LPEYLLKIITNNCVFIVI-----HRSTTSQTIKVSADDTPGTIL  245
              ::|  :|  | :      :|: :  :::::         | :| :|  : :| :
Db   162  RAMYVVPPNVESSPELPKHIYNKLDKGQIIVIWVIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy   246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDBYLVGETPIKNFQWVRQCLKN  299
              ||    ::  ::|::::        :|: :|| || |  |  :| |:  | |  |:::
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDBYFLEKYPLSQYKYIRSCIML  279

Qy   300  GEEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL  354
              : |  |::  :   |:  :  |::  |:| :   | :::           :|:  :|
Db   280  GRMPNLML------MAKESLYSQLPM--DCFTMPSVSRRISTATPYMNGE---TSTKSL  327
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Right column alignment:

```
Qy   355  WDCDRKFRVK-------IRGIDIPVLPRTADLTVFEANIQGQVLCQRRTSPKPF  404
               : :  :|           ||| |||| | |  |: | :| |  |: |    |
Db   328  WVINSALRIKILCATYVNVIRDID-------KIYYRTGIYHGGEFLCDNVNTQRVP  377

Qy   405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPSKQAQLLYYV  464
              |::   :  ::|  :| |:| : :|:|  |                -----KEEHCPLAWG  425
Db   378  CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C-----SVKGRKGA

Qy   465  NLLLIDHRFLRHGEYVLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC  524
              | :: | ::  :|   | :| |  :   |: :      :| ::: :: | ::   ::
Db   426  NINLFDYTDTLVSGKWALNIWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELBFDWFS  481

Qy   525  HPIALPKHRPTPDPEGDRV---------RAEMPNQLR----KOLEAIIATDPLN  565
               :      : : |:  | :               :|  | :|::  ::| :| |
Db   482  SVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQRAICTRDPLS  541

Qy   566  PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQBIVAKTYQLLAKREVWDQSALDVG  625
               : :: :  :   |::|:|       |:|| :| :: | :| | :       :::|:|
Db   542  EITEQEKDPIWSRRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPPIKPE  596

Qy   626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR  684
              | : | |:: |:| |:  |   |:|  || :::: || || | | | : ::|  : :|:
Db   597  QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKK  656

Qy   685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK  744
               |   ||   | |      ::   |:  |   ||  : |  | |  ||   || :| |
Db   657  ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVBAMEKLIN  714

Qy   745  VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVYDPGLKAGALVIEKC  801
              :| | |::  | || ||:: |:|:|:||:     ::| :  |    |   | ::::|
Db   715  LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEBC  769

Qy   802  KVMASKKKPIWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLLQILRIMEGIW  855
               :::||| || :::|  |  |         | | |:|||||  ||| :  :|  |: |
Db   770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMTLQIIRIMENIW  824

Qy   856  ETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE  913
              |||  ||: ||| ||||| |||: |:|||:|||| : || || |     ||||::|||
Db   825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883

Qy   914  KCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNLPFHIDFGHILGNYK  973
              | | ::|:  ::||  |||||||||| : |||||:|:||  : |  | |:|||:|| :|
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFIIGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK  942

Qy   974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLLILLF  1031
               | |  | |||| |||||||| |:|||    :| || :  |  ||: || ::|:|: |
Db   943  KKFGVKREVRVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF  1002

Qy  1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091
              ||| ||| |: | || :: |  :  ::  : :     |::::: :  |||  :| ||| |
Db  1003  SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI  1062
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RESULT 5
P11A_HUMAN

ID   P11A_HUMAN    STANDARD;    PRT;    1068 AA.
AC   P42336; Q99762;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (Ptdins-
DE   3-kinase p110) (PI3K).
GN   PIK3CA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95229146; PubMed=7713498;
RA   Volinia S., Hiles I., Ormondroyd E., Nizetic D., Antonacci R.,
```

```
RA   Rocchi M., Waterfield M.;
RT   "Molecular cloning, cDNA sequence, and chromosomal localization of
RT   the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.";
RL   Genomics 24:472-477(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97196568; PubMed=9043658;
RA   Stirdivant S.M., Ahern J., Conroy R.R., Barnett S.F., Ledder L.M.,
RA   Oliff A., Heimbrook D.C.;
RT   "Cloning and mutagenesis of the p110 alpha subunit of human
RT   phosphoinositide 3'-hydroxykinase.";
RL   Bioorg. Med. Chem. 5:65-74(1997).
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       triphosphate.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- SIMILARITY: Contains 1 C2 domain.
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CC   --------------------------------------------------------------------------
DR   EMBL; Z29090; CAA82333.1; -.
DR   EMBL; U79143; AAB39753.1; -.
DR   PIR; I38110; I38110.
DR   Genew; HGNC:8975; PIK3CA.
DR   MIM; 171834; -.
DR   GO; GO:0007048; P:oncogenesis; TAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN      319    428       C2 DOMAIN.
FT   DOMAIN      797   1068       PI3K/PI4K.
FT   CONFLICT     43     43       V -> I (IN REF. 2).
FT   CONFLICT    170    170       H -> N (IN REF. 2).
FT   CONFLICT    187    187       R -> K (IN REF. 2).
FT   CONFLICT    286    287       KM -> ML (IN REF. 2).
FT   CONFLICT    332    332       R -> S (IN REF. 2).
FT   CONFLICT    346    346       L -> V (IN REF. 2).
FT   CONFLICT    723    723       R -> K (IN REF. 2).
FT   CONFLICT    751    751       L -> F (IN REF. 2).
FT   CONFLICT    767    767       K -> E (IN REF. 2).
SQ   SEQUENCE   1068 AA;  124412 MW;  9E16BA7401A87B57 CRC64;
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Query Match   25.2%;   Score 1460.5;   DB 1;   Length 1068;
Best Local Similarity   33.3%;   Pred. No. 3.3e-89;

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Matches  381;  Conservative  206;  Mismatches  400;  Indels  157;  Gaps  40;

Qy      23  MKPRSTAASLSMSMELIP---IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA  78
                                                          :::::::::::::::::
Db       1  -----------------------------------MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA  53

Qy      79  LETSVSADFYHRLGPDHFLLLYQKKGQWYBIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
                :::                  :|::
Db       54  RKYPL-----HQLLQDESSYIFVSVTQEAEREBFFDETRRLCDLRLFQPF-----LKVI  102

Qy     139  QRHAPSEBTLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD-------  192
                                                                  ::|:::
Db     103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy     193  PKLYAVMHPWTSKP-LPEYLLKKITNNCVFIVI-------HRSTTSQTIKVSADDTPGTIL  245
                    :                    :::::::::::::
Db     162  RAMYVYFPHVESSPELPKIHYNKLDRGQIIVIWIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy     246  QSFFTKMAKKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN  299
                                       ::|::     ::::::::::::::::::::::
Db     222  AEAIRK--KTRSMLLSSEQLKLCVLBYQGKYILKVCCGCDEYFLEKYPLSQYXYIRSCIML  279

Qy     300  GEEIHLVLDTPPPALDEVRKE---EWPLVDDCTGVTGYHEQLT----IHGKDHESVF  350
                                                              ::::
Db     280  GRM----------PNLKWMAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS  323

Qy     351  TVSLWDCDRKFRVK----------IRGIDIPVLPRTADLTVVEANIQYGQQVLCQRRTS  400
                |||:|                  :::|:|
Db     324  TKSLWVINRALRIKILCATYVNLNIRDID---------KIYVRTGIYHGGEPLCDNVNT  373

Qy     401  PKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL  460
                ||||                  :|::::|
Db     374  QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA--------KEEHCP  421

Qy     461  LYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGBDQGSFNADKLTSAATNPDKENSMSISILL  520
                :|::                  :|||:|::
Db     422  LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLEBEF  477

Qy     521  DNYCHPIALPKHRPTPDPEGDRV------------RAEMPNQLR---KQLEAIIAT  561
                :                  ::
Db     478  DWFSSVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR  537

Qy     562  DPLNPLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSA  621
                |||                  |::
Db     538  DPLSEITEQBKDFIWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP  592

Qy     622  LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF  680
                :|||                  :|::
Db     593  IKPEQAMELLDCNYPDMWRGFAVRCLBKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF  652

Qy     681  LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID  740
                :::                  ::::::
Db     653  LLKKALTNQRIGHFFFWELKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME  710

Qy     741  MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALV  797
                :::                  ::::
Db     711  KLINLT-DI--LKOERKDETQKV--QMKFLVBQMRRPDFMDALQGLLSPLNPAHQLGNLR  765

Qy     798  IEKCKVMASKKKPiWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLLIQILRIM  851
                :::                  :::::::
Db     766  LKECRIMSSAKRPiWLNWE---NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM  820

Qy     852  ESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FXDEVLSH  909
                :::                  :::::|
Db     821  ENIKQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQPNSHTIHQ  879

Qy     910  WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL  969
                :::                  ::::
Db     880  WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFL  938

Qy     970  GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL  1027
                :::                  ::|:::
Db     939  DHKKKKFGYKRERVPFVLTQDFLIVISKGAQECKTREFERFQEMCYKAYLAIRQHANLF  998
```

```
Qy    1028  IILFSMLMTGMPQLTSKEDIEYIRDALTVCKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087
                  ||||   |||||:   |:|:| :|||:  || |||:  |   :|::|||  : :|:
Db     999  INLFSMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy    1088  LHLV 1091
                 |:
Db    1059  FHTI 1062
```

```
RESULT 6
P11A_MOUSE
ID    P11A_MOUSE              STANDARD;      PRT;   1068 AA.
AC    P42337;
DT    01-NOV-1995 (Rel. 32, Created)
DT    01-NOV-1995 (Rel. 32, Last sequence update)
DT    28-FEB-2003 (Rel. 41, Last annotation update)
DE    Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE    alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (PtdIns-
DE    3-kinase p110) (PI3K).
GN    PIK3CA.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=BALB/c;
RX    MEDLINE=94187738; PubMed=8139567;
RA    Klippel A., Escobedo J.A., Hirano M., Williams L.T.;
RT    "The interaction of small domains between the subunits of
RT    phosphatidylinositol 3-kinase determines enzyme activity.";
RL    Mol. Cell. Biol. 14:2675-2685(1994).
CC    -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC        PREFERENCE FOR PTDINS(4,5)P2.
CC    -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC        bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC        trisphosphate.
CC    -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC        SUBUNIT.
CC    -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC    -!- SIMILARITY: Contains 1 C2 domain.
CC    --------------------------------------------------------------------------
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CC    or send an email to license@isb-sib.ch).
CC    --------------------------------------------------------------------------
DR    EMBL; U03279; AAA18334.1; -.
DR    MGD; MGI:1206581; Pik3ca.
DR    InterPro; IPR0000008; C2.
DR    InterPro; IPR000403; PI3_PI4_kinase.
DR    InterPro; IPR002420; PI3K_C2_.
DR    InterPro; IPR003113; PI3K_p85B.
DR    InterPro; IPR003341; PI3K_ras_bind.
DR    InterPro; IPR001263; PI3Ka.
DR    Pfam; PF00454; PI3_PI4_kinase; 1.
DR    Pfam; PF00792; PI3K_C2; 1.
DR    Pfam; PF02192; PI3K_p85B; 1.
DR    Pfam; PF00794; PI3K_rbd; 1.
DR    Pfam; PF00613; PI3Ka; 1.
DR    SMART; SM00239; C2; 1.
DR    SMART; SM00142; PI3K_C2; 1.
DR    SMART; SM00143; PI3K_p85B; 1.
DR    SMART; SM00144; PI3K_rbd; 1.
DR    SMART; SM00145; PI3Ka; 1.
DR    SMART; SM00146; PI3Kc; 1.
DR    PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR    PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR    PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR    PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW    Transferase; Kinase; Multigene family.
FT    DOMAIN        319     428       C2 DOMAIN.
FT    DOMAIN        797    1068       PI3K/PI4K.
SQ    SEQUENCE   1068 AA;  124453 MW;  67F54FCF8747F81C CRC64;
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Query Match             25.1%;  Score 1450.5;  DB 1;  Length 1068;
Best Local Similarity   33.4%;  Pred. No. 1.5e-88;
Matches  381;  Conservative 204;  Mismatches 406;  Indels 149;  Gaps 39;

Qy      23  MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
                |||  | |:::  :||:    ::||   ::  :::: :::
Db       1  MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT-------LECLREATLVTIKHELFREA 53

Qy      79  LETSVSADPYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
                 :::|  |:| |||   ||::|:: | | :|: :|:| : |    ||:|    ||||
Db      54  RKYPL------HQLLQDETSYIPVSVTQEAEREEFFDETRRLCDLRLFQPF-------LKVI 102

Qy     139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRLVTPRMAEVAGRD------- 192
                  |    | |:     |  :|:|::|  | :|||:  ||:|:  | : :||
Db     103  EPVGNREEKI-LNREIGFVIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy     193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
                 ||:|  |||:|| |  ||  ||| |||:|:      |:|::|||:|  :||| ||:
Db     162  RAMVYPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy     246  QSFFTKMAKKKSLMDIPES--------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
                || |:||:|::|::|:|:        :||::|:|:|:| |:| || |||: ::|: |::
Db     222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGDEYFLEKYPLSQYKYIRSCIML 279

Qy     300  GEEIHIVLDTPPDALDEVRKEEWPLVDDCTGVTGYHEQLT----IHGKDHESVFTVSL 354
                ||:||:|     ||   |   ||::| |::|   :| :||    : : ||::  |:::
Db     280  GRMENLML--------MAKESLYSQLPI--DSFTMPSYSRRISTATPYMNGE----TSTKSL 327

Qy     355  WDCDRKFRVK------------IRGIDIPVLPRIADLTVFVEANIQYGQGVLCQRRTSPKPF 404
                |     |:             |::|| |:|: ||  |:: : |:     |:::  ||:
Db     328  WVINSALRIKILCATYVNVNIRDID--------------KIYVRTGIYHGGEPLCDNVNTQRVP 377

Qy     405  TEBVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLIYVV 464
                |:|:|:|:|   :||:  |   | :|:|:|:||     |:| :   |: ::|| |: ::
Db     378  CSNPRWNEWLNYDIYIPDLPRLARLCLSI-C----------SVKGRKGA------KEEHCPLAWG 425

Qy     465  NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSAINPDKENSMSISILLDNYC 524
                ||:|:  | ||: |||:|:||:|:||:|:| :|  |::|:  | ||: |:::|: |::|
Db     426  NINLFDYTDTLVSGKMALNLWPVHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS 481

Qy     525  HPIALPKHRPTPDPEGDRV------------------RAEMPNQLR---KQLEAIIATDPLN 565
                |   |||:| ||:|  |:                  :| ::| :   |::| :  ||:|
Db     482  SVKFPDMSVIEEHANWSVSREAGFSYSHTGLSNRLARDNELRENDXEQLRALCTRDPLS 541

Qy     566  PLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG 625
                | : |||:| || ||:|| ||||||: |::||||: | :| | :: |:|::||:|  ||
Db     542  EITEQEKDFLWSRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL----VKDWPPIKPE 596

Qy     626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR 684
                ||::|||||:|:||| |||| :|:| ||||:|::||  ||  |:|:||::| || ||||:
Db     597  QAMELLDCNYPDPMVRSFAVRCLEKYLTDDKLSQYLIQLVQVKYEQYLDNLLVRFLLKK 656

Qy     685  GLRNKRIGHPLFWFLRSEIAQSRHYQORPAVILEAYLRGCGTAMLHDFTQQVVIDMLQK 744
                ||||||||||| || |||:  |||  :|||:| ||:||| | ||:|| ||| ::|:|::
Db     657  ALTNQRIGHFFWFHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN 714

Qy     745  VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC 801
                | ||:|:||:|||||| :||:| ||::||:    ||:|: ::| |::| | ::|::||:
Db     715  LT-DI--LKQEKKDBTQKV--QMKFLVEQMRQPDFMDALQGFLSPLNPAHQLGNLRLEBC 769

Qy     802  KVMASKKKPLWLEPKCADPTALS------NETIGIIFKGDDLRQDMILQILRIMESIW 855
                |: ::|:| || :|  | :| |:       | : ||||| |||| ||:|::|| | ||
Db     770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW 824

Qy     856  ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE 913
                :|| |:|| |||| |:| :|:| |||  | ||| |: | ||:|:|  ::| ::|  ||:
Db     825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI--QCKGGLKGALQFNSHTLHQWLKD 883
```

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KW   Transferase; Kinase; Multigene family.
FT   DOMAIN       800   1050       PI3K/PI4K.
SQ   SEQUENCE   1070 AA;  122607 MW;  4E8EB2333B96E4D5 CRC64;

Query Match             23.5%;  Score 1362;  DB 1;  Length 1070;
Best Local Similarity   32.5%;  Pred. No. 1.2e-82;
Matches  358;  Conservative 196;  Mismatches 397;  Indels 152;  Gaps 36;

Qy     78 ALETSVSADFYHRLG---------PDHFLLLYQKKGQWYEI--YDKYQVVQTLD-----CLR 123
          :                        |  ::     ::   :   :         :    :
Db     25 ASDGSISVDFLLPTGIYIQLEVPREATISYIKQMLWKQVHNYPMFNLLMDIDSYMFACVN 84

Qy    124 YNKVLHRSPGQ----------------IHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHD 170
              ::                       :    ::
Db     85 QTAVYELEDETRRLCDVRPFLPVLKIVTRSCDPAEKL--DSKIGVILGKGLHEFDALKD 142

Qy    171 DEL-EFTR--RRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEY-------LLKKITNNCV 220
          :   : :    :          :       |   ::  :
Db    143 PEVNEFRRKMRKFPSEDKIQSLVG-----LSWIDWLKHTYPPEHEPSVLENLEDKLYGGKL 197

Qy    221 FIVIHRSTTSQ--TIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFRVCGRD 278
          :      :         |:     |        :  ::::     :  ::
Db    198 VVAVHFENSQDVFSFQVSPNLNPIKINE---LAIQKRLTIRGKEBEASPCDYVLQVSGRV 254

Qy    279 EYLVGETPIKNFQWVRQCLKNGEBIHIVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQ 338
          :  :               :                       :
Db    255 EYVFGDHPLIQFQYIRNCVMNRTLPHFIL----------------VECCKIKMYEQ 295

Qy    339 --LTIHGKDHESVFTVSL--------------WDCDRKFR-VKIRGIDIPVLPRTADLTVF 382
            :                            :         : ::
Db    296 EMIAIEAAINRNSSSLPLPLPPKKTRVISHVWGNRNNPFQIVLVKG--NKLNTEETVKVH 352

Qy    383 VEANIQVGQQVLCQRRTSPK-PFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPAL 441
          :        :     :  :          :   : :  :    :         :: :
Db    353 VRAGLFHGTELLCKTTVVSSEISGKNDHIWNEQLEFDINICDLPRMARLCFAVY-AVLDKV 411

Qy    442 SGKTSAEMPSP---ESKGKAQLLYY-----VNLLLIDHRFLRLRHGEVYLHMWQLSGKGEDQ 494
          :  :          :  :             :           :  :    :
Db    412 KTYKKSTKTINPSKYQTIRKAGKVHYPVAWVNTMVFDFKGQLRSGDVILHSW-------KHRPTPDP 462

Qy    495 GSFNADKL-----------TSATNPDKENSMSISILL-DNYCHPIALP----------KHRFTPDP 538
          |                                :  :       :            ||||||
Db    463 SSF-PDELEEMLNPMGTVQTNYAENATALHIKFPENKKQPYYYPPFDKIIEKAABIASG 521

Qy    539 EGDRVRAEMPNQLRKQLBAIIATDPLNPLTAEDKELLMHFRYESLKD-PKAYPKLFSSVK 597
          |           :   :                 :          :     :    :
Db    522 DSANVSSRGGKKFLAVLKEILDRDPLSQLCENEMDLIWTLRQDCRENFPQSLPKLLLSIK 581

Qy    598 WGQOEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVL 657
          |              ::    :                     :  :      :
Db    582 WNKLEDVA--QLQALLQIWPK-LPPREALELLDFNVPDQYVREYAVGCLRQMSDEELS 636

Qy    658 HYLLQLVQVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVIL 717
          |         :  :    |  ||  :    |  | :         :      :
Db    637 QYLLQLVQVLKYEPFLDCALSRFLLERALDNRRIGQFLFWHILRSEV-HTPAVSIQFGVIL 695

Qy    718 EAYLRGCGTAMLHDFTQQVQVIDMLQKVT--IDIKSLSAEKYDVSSQVISQLKQK----- 770
          ||         :   :              :   :    :   :
Db    696 EAYCRG-SVGHMKVLSKQVEALNLKTLNSLIKLNAMKLNRAKGKEAMHTCLKQSAYREA 754

Qy    771 LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKKPLMLEFKCADPTALSNETIGI 830
          ||         :                 :     :
Db    755 LSDLQS---------PLNPCVILSELYVEKCRYMDSRMKPLMLVY---SNRAFGEBDAVGV 802

Qy    831 IFKGDDLRQDMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAK 890
          ||    :||    :   : :   :  :  : |   : :  :   :     :
Db    803 IFKNGDLRQDMLTIQMLRLMDLLWKEAGLDLRMLPYGCLATGDRSGLIEVVSTSETIAD 862

Qy    891 IQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRH 948
          |        |       |    :   :               ||||||||||||||||||
Db    863 IQLNSSNVAATAAFNKDALLNWLKEYNSGDD-LDRAIEFTLSCAGYCVASYVLGIGDRH 921

Qy    914 KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK 973
          ||||||||||||||||||||||||||||||||||| || :|    ||||||||||||||
Db    949 NDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQK 1008

Qy    884 KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK 942
          |:|  |  ||  |||| |||||||||| ||||||||| |||  ||| ||||||| ||  |

Qy    974 SFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILF 1031
          ||||||||||||||||||||||    |||||||||||     :|:::   |    :::
Db    943 KKFGVKRERVPFVLTQDFLVISKGAQEVTKTREFERPQEMCYKAYLAIRQHANLFINLF 1002

Qy   1032 SMMLTMGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
          ||||| ::: |        |||  | |  ||||  ||||:||| |||||||| |||||
Db   1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFTKQMNDAHHGWTTKMDWIFHTI 1062
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RESULT 7
P11B_RAT
ID   P11B_RAT     STANDARD;     PRT;   1070 AA.
AC   Q9ZLL0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
DE   isoform (EC 2.7.1.153) (PI3-kinase p110 subunit beta) (PtdIns-3-kinase
DE   p110) (PI3K) (PI3Kbeta).
GN   PIK3CB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Mulder H., Stenson Holst L., Degerman E.;
RT   "Phosphatidylinositol-3 kinase and activation of phosphodiesterase 3B
RT   in adipocytes.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS(4,5)P2 AND PTDINS4P AND
CC       PREFERENCE FOR PTDINS(4,5)P2 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ012482; CAA10046.1; -.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR003341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
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Db    922   SDNIMVKKTGQLFHIDFGHIIGNFKSKFGIKRERVPFILYDFIHVIQQGKTGNTEKFGR  981
            :||||: .:|| ||||||||| .|| ||.||::||| |||:|| |: ||. .:
Qy   1009   FQDVCVKAYIALRHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYF 1068
            || ||:|: ||:||||||: ||:||.|| :| |||:|.|::|||::||||||||||
Db    982   FRQCCEDAYLILRRHGNLFITLFALMTAGLPELTSVKDIQYLKDSLALGKSEEEALKQF 1041

Qy   1069   LDQIEVCRDKGWTVQFNWFLHLV 1091
            || :| |:||||||:||||||||
Db   1042   KQKFDEALRESWTTKVNWMAHTV 1064
```

```
RESULT 8
P11B_HUMAN
ID   P11B_HUMAN     STANDARD;      PRT;   1070 AA.
AC   P42338;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
DE   isoform (EC 2.7.1.153) (PI3-kinase p110 subunit beta) (PtdIns-3-kinase
DE   p110) (PI3K) (PI3Kbeta).
GN   PIK3CB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94067128; PubMed=8246984;
RA   Hu P., Mondino A., Skolnik E.Y., Schlessinger J.;
RT   "Cloning of a novel, ubiquitously expressed human
RT   phosphatidylinositol 3-kinase and identification of its binding site
RT   on p85.";
RL   Mol. Cell. Biol. 13:7677-7688(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kossila M., Sinkovic M., Karkkainen P., Laukkanen P., Miettinen R.,
RA   Rissanen J., Kekalainen P., Kuusisto J., Yla-Herttuala S., Laakso M.;
RT   "Gene encoding the catalytic subunit p110beta of human
RT   phosphatidylinositol 3-kinase: cloning, genomic structure and
RT   screening for variants in patients with type 2 diabetes.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- TISSUE SPECIFICITY: Expressed ubiquitously.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S67334; AAB29081.1; -.
DR   EMBL; AJ297549; CAC21449.1; -.
DR   EMBL; AJ297550; CAC21449.1; JOINED.
DR   EMBL; AJ297551; CAC21449.1; JOINED.
DR   EMBL; AJ297552; CAC21449.1; JOINED.
DR   EMBL; AJ297553; CAC21449.1; JOINED.
DR   EMBL; AJ297554; CAC21449.1; JOINED.
DR   EMBL; AJ297555; CAC21449.1; JOINED.
DR   EMBL; AJ297556; CAC21449.1; JOINED.
DR   EMBL; AJ297557; CAC21449.1; JOINED.
DR   EMBL; AJ297558; CAC21449.1; JOINED.
DR   EMBL; AJ297559; CAC21449.1; JOINED.
DR   EMBL; AJ297560; CAC21449.1; JOINED.
DR   PIR; A54600; A54600.
DR   Genew; HGNC:8976; PIK3CB.
DR   MIM; 602925; -.
DR   GO; GO:0004429; F:1-phosphatidylinositol 3-kinase; TAS.
DR   GO; GO:0000187; P:activation of MAPK; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR   GO; GO:0000074; P:regulation of cell cycle; TAS.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN      800   1050     PI3K/PI4K.
SQ   SEQUENCE   1070 AA;  122762 MW;  81135FE93452C00E CRC64;
```

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Query Match             23.4%;  Score 1354.5;  DB 1;  Length 1070;
Best Local Similarity   31.8%;  Pred. No. 3.8e-82;
Matches   361; Conservative  202; Mismatches 407; Indels 165; Gaps   37;

Qy     30  ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH    89
           .| :.:: :|| ||: |.:::| ||
Db     22  SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM------    68

Qy     90  RLGPDHFLLLYQKKGQWYEIYDXYQVVQTLD-----LRYWKVLHRS--PQGIH       136
           :| |::||::.:|.:|:|:: ::| | : :|      |.:.: :|::  | :|
Db     69  ------FNLLMDIDSYMFACVNQTAVYELEDETRRLCDVRPFLPVLKLVTRSCDPGE-- 120

Qy    137  VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
                 :.| .|  |::| .|:    :||.| |::      |.:|    ..:  .: |.:
Db    121  ------------KLDSKIGVLIGKGLHFPDSLKDPEVNEFRRKRMRKFSEEKILSLVGLSW 168

Qy    193  -PKLYAMHPWVISKPLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249
            || : |.|::  ::| || ::: |::  .| |: : :::   :||::||:|. .|.|
Db    169  MDWLKQTYPPEHBPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE--- 225

Qy    250  TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEBIHLVLDT 309
           .|: |.: :|:  |.:::::||:| :| |:| ||.:  :|.| |:|.  ::|| :::|:|
Db    226  LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVFGDHPLIQFQYIRNCVMNRALPHFIL-- 283

Qy    310  PDDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------- 354
            :|.| ::  | | || .| :| :|: :|   :.:.|:|::|.
Db    284  ---------------VECCKIKKMYEQEMIAIEAAINRNSSNLPLPKKTRIISHV       326

Qy    355  WDCDRKFR-VKIRGIDIPVLCKTIVSSEVSGKNDHIWNE 412
           | :  : :| .: :|:.
Db    327  WENNNPFQIVLVKG---NKLNTEETVKVHVRAGLFHGTELLCKTIVSSEVSGKNDHIWNE 383

Qy    413  WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP---ESKGKAQLLYY----VN 465
           |: ::|::|.|| ::.:::.::  :|:|::|::.|::  :     :.|.|| ::    .|
Db    384  PLEFDINICDLPRMARLCFAVT-AVLDKVKTKKSTKTINPSKYQTIRKAGKVHYPVAWVN 442

Qy    466  LLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKL-------TSATNPDXENSMSIS 517
           :|::| ||::| |:| :|:| ||.|::|.::|.|:.|        ||:||| :|||: |:
Db    443  TMVFDFKGQLRTGDIILHSW----------------SSF-PDELEEMLNPMGIVQTNPYTENATALH 492

Qy    518  ILL-DNYCHPIALP------KHRPTDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA 569
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DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF06613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase.
FT   DOMAIN       851   1127       PI3K/PI4K
FT   VARIANT      826    826       S -> N (IN AGE1 (MG109)).
FT   CONFLICT    1010   1010       F -> V (IN REF. 1).
SQ   SEQUENCE   1146 AA;  132961 MW;  0D362E419407253A CRC64;

Query Match             18.0%;  Score 1041;  DB 1;  Length 1146;
Best Local Similarity   27.3%;  Pred. No. 3.1e-61;
Matches  314;  Conservative  227;  Mismatches  399;  Indels  210;  Gaps  44;

Qy    78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
                :||| :  |||  |||| :        :       :  |:  ||:|     :|      
Db    68 SLEIKLS-DFKGHQL---FELIAPMKWGTYSVKPQDYVFRQLNNFGEISVIFNDDQPLSK 122

Qy   138 VQRHAPSEETLAFQ---------RQLNALIGYDVTDVSNVHDDEL-EF--------TRR 178
            :       |::         ||||| |  |   |  | || :|         :|:
Db   123 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTK 182

Qy   179 RLVT------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI-------AEI 215
          :|:                         :|           :           :||
Db   183 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK-------AEI 235

Qy   216 TNNCVFIVIHRSTTSQTIKVSADDTPGTIIQSFFTKMAKKKSLMDIPESQNERD--FVLR 273
             |:    :         |: :                    :          :   :|
Db   236 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK----LDVYDTDDPADBGWFLQ 285

Qy   274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH---LVLD--TPPDPALDE--VRKE 321
           |    :   :              : |     ||:|   ||||      | |:   |: 
Db   286 LAGRTTFVTNPDVKLTSYDGVRSELESYRCPGFVVRRQSLVLKDYCRPKPLYEPHYVRAH 345

Qy   322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT---------VSLWDCDRKFRVK--IRGI 368
                                               ||:|| |:|  |    :||:
Db   346 ERKLALDVLGVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 403

Qy   369 DIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWL-EFSIKIKDLPKGA 427
          |  :      |  |  :  | |  :|      :  :::        ||::|:| : | 
Db   404 DFPA--DVDMYVRIEFSVVYGTLTLASKSTT-KVNAQFAKWNKEMYTFDLYMKDMPPSA 459

Qy   428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVLHWWQL 487
                 | |                        |:  : :|  : | :      |: :
Db   460 VLSIRVLYGK-------------VKLKSEFE----VGWVNMSLTDWRDELRQGQFLFHLW-- 503

Qy   488 SGKGEDQGSFNADKLTSATNPDKEN------SMSISILLDNYCHPIALP----------KH 532
            |  :                         |:||::  | : |    :         |:|
Db   504 --------APEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMPSQGGQTYLVKH 552

Qy   533 R----PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
          |     :  :     : | |       :|      |  :  :||     |||:||::|:|
Db   553 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEEQRHVMWMR-RYIQKQE 611

Qy   586 PKAYPKLFS-SVKWGGQEIVAKTYQLLAKREVWDQSALDVGLIMQLLDCNFSDENVRAIA 644
          |   :    :  |    :   : :  ::|  |       |:    ||:| :   :  : |
Db   612 PDLLIVLSELAFVWTDRENFSELIYMLEK---WKPPSVAAALT--LIGKRCTDRVIRKFA 666

Qy   645 VQKLBSLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLENKRIGHFLFWFLRSEI 703
          |:||  |         | | : |:|:||| :    |:|| :|  :|||| || |||:|
Db   667 VEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMLLTRALCDYRIGHRLFWLLRAEI 726

Qy   704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSABKY 757
          |:           :  |::|||||||| ||||||| || ::|||||| ||:|:|: :|
Db   727 ARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDELTRISTLVKGMPK--- 782

Qy   758 DVSS----QVISQLKQLENLQNLNLPQSFRVPYDPGLKAGALVIEBCKVMASKKKPLWL 813
          ||:     |:::| |:|:|:  :     |  :  || |   :::|||:: || |:|:|
Db   783 DVATMKLRDELRSISHKMENMDS------------PLDPVYKLGEMIDKAIVLGSAKRPLML 833

Qy   814 EFKCADPTA-LSNETIGIIFKHGDLRQDMLIIQILRIMESIWETESLDLCLLPYGCIST 872
           :|  :|:  |:|:||| :||:||| |||| :|:| :|::||  ::|:| |||| |:|:
Db   834 HWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 893

Qy   873 GDKIGMIBIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIBE-------- 919
          | :||::|: |: || : ||||   |: |   ::|:|  :|::|:||:|
Db   894 GEMIGIIEVVPNCKTIFEIQVGTGFMNKWIRKQCGIEDEKRKCSKKDST 953

Qy   920 ---------------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                         |::  :::||||||:|| |||::||||||:|||:|: ||| ||||
Db   954 KNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYFHID 1013

Qy   965 FGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
          |||||| :::||||::|:: |:|| :|: :   |:| :::  :|||| :|||:|| :: :
Db  1014 FGHILGHGKTKLGIQRDRQPFILTEHFMVIRSGKSVDGNSHELQKFKTLCVBAYEVMWN 1073

Qy  1023 HTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
           :::: |||:::|:||:| |:||:|::  :  |   | ||| |:::| ::|:|    :|:
Db  1074 NRDLFVSLFTLMLGMELPLSTKADLDHLKKTLFCNGSKEEARKFFAGIYEEAFNGSWS 1133

Qy  1082 VQFNWFLHLV 1091
          ::::|| | |
Db  1134 TKTNWLFHAV 1143


RESULT 15
PK3B_HUMAN
ID   PK3B_HUMAN     STANDARD;     PRT;    1634 AA.
AC   O00750; O95666;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta
DE   polypeptide (EC 2.7.1.154) (Phosphoinositide 3-kinase-C2-beta)
DE   (Ptdins-3-Kinase C2 beta) (PI3K-C2beta) (C2-PI3K).
GN   PIK3C2B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Breast;
RX   MEDLINE=97289668; PubMed=9144573;
RA   Brown R.A., Ho L.K.F., Weber-Hall S.J., Shipley J.M., Fry M.J.;
RT   "Identification and cDNA cloning of a novel mammalian C2 domain-
RT   containing phosphoinositide 3-kinase, HsC2-PI3K.";
RL   Biochem. Biophys. Res. Commun. 233:537-544(1997).
RN   [2]
RP   SEQUENCE OF 26-1634 FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Monocytes;
RX   MEDLINE=99047700; PubMed=9830063;
RA   Arcaro A., Volinia S., Zvelebil M.J., Stein R., Watton S.J.,
RA   Layton M.J., Gout I., Ahmadi K., Downward J., Waterfield M.D.;
RT   "Human phosphoinositide 3-kinase C2beta, the role of calcium and the
RT   C2 domain in enzyme activity.";
RL   J. Biol. Chem. 273:33082-33090(1998).
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS AND PTDINS4P WITH A PREFERENCE FOR
CC       PTDINS. DOES NOT PHOSPHORYLATE PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4-
CC       phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4-bisphosphate.
CC   -!- SUBCELLULAR LOCATION: FOUND MOSTLY IN THE MICROSOME, BUT ALSO IN
CC       THE PLASMA MEMBRANE AND CYTOSOL.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT LEVELS ARE HIGHEST IN
CC       THYMUS AND PLACENTA AND LOWEST IN PERIPHERAL BLOOD, SKELETAL
CC       MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

```
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   -!- SIMILARITY: Contains 1 phox homology (PX) domain.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
CC
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CC       entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC       or send an email to license@isb-sib.ch).
CC
DR   EMBL; Y11312; CAA72168.1; -.
DR   EMBL; Y13892; CAA74194.1; -.
DR   PIR; JC5500; JC5500.
DR   HSSP; P21707; 1RSY.
DR   Genew; HGNC:8972; PIK3C2B.
DR   MIM; 602838; -.
DR   GO; GO:0005792; C:microsome; NAS.
DR   GO; GO:0005886; C:plasma membrane; NAS.
DR   GO; GO:0016305; F:phosphatidylinositol 3-kinase, class II act. .; NAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2_1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00312; PX; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN     1365   1481       PX.
FT   DOMAIN      156    162       PRO-RICH.
FT   DOMAIN      169    174       PRO-RICH.
FT   DOMAIN     1079   1343       PI3K/PI4K.
FT   DOMAIN     1517   1608       C2 DOMAIN.
FT   PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
FT   PROSITE; PS50004; C2_DOMAIN_2; 1.
FT   PROSITE; PS00915; PI3_4_KINASE_1; 1.
FT   PROSITE; PS00916; PI3_4_KINASE_2; 1.
FT   PROSITE; PS50290; PI3_4_KINASE_3; 1.
FT   PROSITE; PS50195; PX; 1.
FT   CONFLICT     63     63       P -> S (IN REF. 2).
FT   CONFLICT     75     75       R -> W (IN REF. 2).
FT   CONFLICT     99     99       Q -> L (IN REF. 2).
FT   CONFLICT    246    246       V -> A (IN REF. 2).
FT   CONFLICT    278    278       K -> S (IN REF. 2).
FT   CONFLICT    567    567       P -> S (IN REF. 2).
FT   CONFLICT    664    665       DM -> EL (IN REF. 2).
SQ   SEQUENCE   1634 AA;  184856 MW;  C0B5DF63C668B824 CRC64;
```

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Query Match             17.6%;  Score 1021;  DB 1;  Length 1634;
Best Local Similarity   28.0%;  Pred. No. 1.2e-59;
Matches   304;  Conservative 178;  Mismatches 391;  Indels 212;  Gaps    29;
```

```
Qy    159 GYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAM--HPWVTSKPLPBYLLKKIT 216
          |:::||||:|| |||   |:|:                        ||||||:| :::  ::
Db    322 GHELFEVSEERDBEVAAFCHMLDILR----SGSDIQDYFPLTGYWSAVTPSPEHLGDEV- 376

Qy    217 NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCG 276
          |: :|    ||     : :|                   : ||   ||  |||||||:| |
Db    377 NLKVTVLCDRLQEALTFTCNCSSTVDLLI--YQTLCYTHDDLRNV---DVGDFVLKPCG 430

Qy    277 RDEYLVGETPIKNFQWVRQCLK-------------------------------------- 298
```

```
Db    431 LEEFLQNKHALGSHEYIQYCRKFDIDIRLQLMEQKVVRSDLARTVNDDQSPSTLNYLVHL 490
          :||:  |    |::| : :::
Qy    299 -------------NGEBIHLVLDT------------------------------------ 309

Db    491 QERPVKQTISRQALSLLFDTYHNEVDAFLLADGDFPLKADRVVQSVXAICNALAAVETPE 550
          :|:|:  :
Qy    310 ------------------PP----DPALDEVRKEEWPLV-----------------DDCT 330

Db    551 ITSALNQLPPCPSRMQPKIQKDPSVLAVRENREKVVEALTAAILDLVELYCNTFNADFQT 610
          |: |
Qy    331 GVTGYHEQLTIHGKDH--ESVFTVSLWDCDRKFPRVKIRGIDIPVLPRTADLTVFVEANI 387

Db    611 AVPGSRKHDLVQBACHFARSLAFTV--YATHR--------IPIIWATSYEDFYLSCSL 658
          |||
Qy    388 QYGGQVLC-----QRRTSPKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYC--GKAPA 440

Db    659 SHGG3DMCSPLQTRRAHFSKYLFHLIVNDDQQICFPVQVNRLPRETLLCATLYALPIPPPG 718
          :|:
Qy    441 LSGKTSAEMPSPESKGAKQLLYVNLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNAD--- 500

Db    719 SSSEANKQRVPEALG------WVTTPLPNFRQVLTCGRKLLGLWPATQE-------NPS 765
          :||||:||||:
Qy    501 KLTSATNPDKENSMSISILLDNVCHPIALPKHRPTPDPEGDRVR-----AEMPNQLRKQL 555

Db    766 ARWSAPNFHQPDSVILQIDFPTSAFDIKF-------TSPPGDKFSPRIEFGSLREEDQRKL 819
          | : |
Qy    556 EAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKRE 615

Db    820 KDIMQKESLYWLTDADKKRLWEKRYCHSEVSSLPLVLASAPSWEWACLPDIYVLLKQ-- 877
          :|| |||
Qy    616 VW---DQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEP 671

Db    878 -WTHMNHQDALG-----LLHATFPDQEVRRMAVQWIGSLSDAELLDYIPQLVQALKYEC 930
          :|  |: ||||
Qy    672 YHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHD 731

Db    931 YLDSPLVRFPLLKRAVSDLRVTHYFYFWLLKDGLKDSQ-FSIRYQYLLAALLCCGKGLREE 989
          |||:||||||
Qy    732 FTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENL-QNLNLPQSFRVPVPDPG 790

Db    990 FNRQCWLVNALAKLAQQVR----EAAPSAROGI--LRTGLEEVKQFFALNGSCRLPLSPS 1043
          :||:||
Qy    791 LKAGALVIEBCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQIIRI 850

Db   1044 LLVKGIVPRDCSYFNSNAVPLKLLSFQNVDPL---GENIRVIFKCGDDLRQDMLTLQMIRI 1100
          ||:| |||||
Qy    851 MESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLSHW 910

Db   1101 MSKIWVQEGLDMRMVIFRCFSTGRGRGNVEMIPNAETLRKIQVBH-GVTGSFKDRPLADW 1159
          ||| :|
Qy    911 LKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILG 970

Db   1160 LQKNPGEDEYEKAVENFYSCAGCCVATYVLGICDRHNDNIMLKTTGHMFHIDFGRFIG 1219
          ||:|||||:||::|:|||||
Qy    971 NYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLALRRHTNLLIIL 1030

Db   1220 HAQMFGNIKRDRAPFVFTSDMAYVI-NGGDKPSSRFHDFVDLCCQAYNLIRKHTHLFNL 1278
          ||:|||
Qy   1031 FSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQPNWFLHL 1090

Db   1279 LGLMLSCGIPELSDLEDLKYVYDALRPQDTEANATTYFTRLIESSLGSVAT-KLNFFIHN 1337
          |||| |
Qy   1091 VLGIK 1095

Db   1338 LAQMK 1342
```

Search completed: February 15, 2004, 02:05:07
Job time : 37 secs

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        February 14, 2004, 17:24:00  ; Search time 77 Seconds
                                  (without alignments)
                                  2271.645 Million cell updates/sec

Title:         US-09-974-573-1
Perfect score: 5790
Sequence:      1 MELENYEQPVVLREDNRRRR........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:     1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    A_Geneseq_19Jun03:*
         1:   /SIDS17/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                             SUMMARIES
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	98.9	1102	19	AAW23948	Porcine phosphoino
2	5726	98.9	1102	20	AAW90083	Porcine G-protein
3	5726	98.9	1102	21	AAY76802	Pig p120 regulator
4	5523.5	95.4	1101	20	AAW90089	Human G-protein re
5	5523.5	95.4	1101	21	AAY76803	Human p120 regulat
6	5500.5	95.0	1101	19	AAU09689	Human p110gamma is
7	5500.5	95.0	1101	19	AAW23947	Human phosphoinosi
8	5222	90.2	1050	17	AAW11577	Human phosphatidyl
9	5093.5	88.0	1049	17	AAW11576	Human phosphatidyl

```
        10   1467.5   25.3   1068   15   AAR46294     PtdIns 3-kinase 11
        11   1465.5   25.3   1068   14   AAR43341     p110. Homo sapien
        12   1460.5   25.2   1068   14   AAR43342     Human p110. Homo
        13   1460.5   25.2   1068   23   AAU09687     Human p110alpha is
        14   1354.5   23.4   1070   21   AAB11124     Human PI3 kinase p
        15   1354.5   23.4   1070   23   ABP65170     Hypoxia-regulated
        16   1354.5   23.4   1070   23   AAU09688     Human p110beta iso
        17   1351.5   23.3   1044   19   AAW58570     Human phosphatidyl
        18   1351.5   23.3   1044   20   AAW97390     p110-delta amino a
        19   1351.5   23.3   1044   21   AAY50179     Human PI 3-kinase-
        20   1349.5   23.3   1044   19   AAW46625     Mammalian novel cl
        21   1349.5   23.3   1044   21   AAY88372     Phosphatidylinosi
        22   1349.5   23.3   1044   23   AAU09685     Human p110delta is
        23   1283     22.2   1088   22   ABB60424     Drosophila melanog
        24   1076.5   18.6   1726   18   AAW38756     Phosphatidylinosi
        25   1074     18.5   1686   19   AAW70991     Human class II PI3
        26   1074     18.5   1686   24   ABJ19811     Androgen-independe
        27   1034     17.9   1157   19   AAW47544     Caenorhabditis ele
        28   1034     17.9   1157   21   AAB06072     Caenorhabditis ele
        29   873.5    15.1   1876   22   ABB61970     Drosophila melanog
        30   873.5    15.1   1876   22   ABB66876     Drosophila melanog
        31   866.5    15.0   1876   18   AAW38757     Phosphatidylinosi
        32   856.5    14.8   1445   23   ABB97312     Novel human protei
        33   856.5    14.8   1450   22   ABG04173     Novel human diagno
        34   856.5    14.8   1450   22   ABG07330     Novel human diagno
        35   855      14.8   1462   22   AAM25582     Human protein sequ
        36   855      14.8   1475   22   ABB11449     Human PI3-kinase h
        37   767.5    13.3   311    22   ABG09801     Novel human diagno
        38   709.5    12.3   887    22   AAM39431     Human polypeptide
        39   709.5    12.3   901    22   AAM41217     Human polypeptide
        40   705.5    12.2   887    24   ABU54626     Human NOVX polypep
        41   705.5    12.2   913    24   ABU54625     Human NOVX polypep
        42   690.5    11.9   803    20   AAW97880     Maize phosphatidyl
        43   645      11.1   1157   22   ABB61471     Drosophila melanog
        44   550.5    9.5    818    24   ABU54627     Human NOVX polypep
        45   478.5    8.3    1146   22   ABG14251     Novel human diagno
```

                                                    ALIGNMENTS

```
RESULT 1
AAW23948
ID   AAW23948 standard; Protein; 1102 AA.
XX
AC   AAW23948;
XX
DT   17-AUG-1998  (first entry)
XX
DE   Porcine phosphoinositide 3OH-kinase p120 subunit.
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
KW   therapy; drug screening.
XX
OS   Sus scrofa.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   40..41
FT                   /note "cryptic thrombin cleavage site"
FT   Domain          310..315
FT                   /note "WW domain, may be involved in interaction
FT                   with p101 subunit"
FT   Domain          173..302
FT                   /note "weak pleckstrin homology domain, may be
FT                   involved in membrane binding and/or
FT                   G-beta,gamma subunit interaction of the
FT                   p101/120 complex"
```

```
XX
PN   WO9749818-A2.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1997;   97WO-US11219.
XX
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1998-077181/07.
DR   N-PSDB; AAV04634.
XX
PT   DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase
PT   p101 and p120 subunits - useful for diagnosis, drug screening,
PT   clinical trial monitoring and treatment of inflammatory disorders
XX
PS   Claim 54; Fig 4; 151pp; English.
XX
CC   This is the deduced amino acid sequence of the p120 catalytic
CC   subunit of pig G-protein regulated phosphatidylinositol-3' kinase
CC   (PI3K), a heterodimeric enzyme which produces the intracellular
CC   messenger phosphatidylinositol (3,4,5)-triphosphate in response to
CC   activation of trimeric G protein-linked receptors. This novel
CC   protein, which also contains a regulatory subunit, p101 (see
CC   AAW23946), is found in cells of haematopoietic origin and is involved
CC   in immune system responses which cause inflammation. p101 cDNA (see
CC   AAV04634) was obtained from a neutrophil cDNA library. The invention
CC   encompasses pig and human p101 and p120 nucleotides (see AAV04633-34),
CC   host cell expression systems, p101 and p120 proteins (see AAW23946-49),
CC   fusion proteins, polypeptides and peptides, antibodies to these
CC   proteins, and transgenic and knockout animals. Compounds which are
CC   useful for treating inflammatory response disorders can be
CC   identified by screening assays using a G protein activated PI3K, or
CC   a cultured host cell that expresses the p101 gene. Antagonists of
CC   G protein stimulated PI3K (acting through the p101 subunit,
CC   especially by disrupting the interaction between the p101 and p120
CC   subunits) can be used to treat arthritis, septic shock, adult
CC   respiratory distress syndrome (ARDS), pneumonia, asthma, allergies,
CC   reperfusion injury, atherosclerosis, cancer and Alzheimer's disease.
CC   The nucleic acids and their products can also be used for diagnosis,
CC   drug screening and clinical trial monitoring of inflammatory
CC   diseases.
XX
SQ   Sequence  1102 AA;

Query Match           98.9%;   Score 5726;   DB 19;   Length 1102;
Best Local Similarity  98.9%;   Pred. No. 0;
Matches 1090;   Conservative  6;   Mismatches  6;   Indels  0;   Gaps  0;

Qy     1  MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKTPETALLH    60
          |||||||||||||||||||||||||||||||||||||||||||:  ::|||||||||
Db     1  MELENYEQPVLREDNRRRRRMKPRSTAASLSMELIPIEFVLATSQRNTKTPETALLH    60

Qy    61  VAGHGNVEOMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD   120
          ||||||||:|||||:||||||||   |||||||||||||:||||:||:||||||||||||
Db    61  VAGHGNVEKKKAQVLRALETSVWDFYRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD   120

Qy   121  CLRYWKVLHRSPGGIHVVQRHAPSEEETLAFQRQLNALIGYDVTDVSNVHDDLEFTRRRL   180
          |||| |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CLRYWEVLHRSPGQIHVVQRHAPSEEETLAFQRQLNALIGYDVTDVSNVHDDLEFTRRRL   180

Qy   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYILKKITNNCVFIVIHRSTTSQTIKVSADDT   240
          |||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT   240

Qy   241  PGTILQSFFTKMACKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG   300
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG   300

Qy   301  EEIHLVLDTPPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  EEIHLVLDTPPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK   360

Qy   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLWNVWLEPFSIKI   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLWNVWLEPFSIKI   420

Qy   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLLRHGEY   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLLRHGEY   480

Qy   481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTDPEG   540
          |||||||||||||||||||||||||| |||||:|||||||||||||||||||||||||||
Db   481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTDPEG   540

Qy   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ   600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ   600

Qy   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL   660

Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLPWFLRSEIAQSRHYQQRFAVILEAY   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLPWFLRSEIAQSRHYQQRFAVILEAY   720

Qy   721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP   780

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ   840

Qy   841  DMLILQIIRIMESIWETESLDICLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  DMLILQIIRIMESIWETESLDICLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG   900

Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL   960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL   960

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020

Qy  1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEDDAKKYFLDQIEVCRDKGW  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEDDAKKYFLDQIEVCRDKGW  1080

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA  1102
          |||||||||||||||||||||
Db  1081  TVQFNWFLHLVLGIKQGEKHPA  1102
```

```
RESULT 2
AAW90083
ID   AAW90083 standard; Protein; 1102 AA.
XX
AC   AAW90083;
XX
DT   09-MAR-1999  (first entry)
XX
DE   Porcine G-protein regulated PI3K p120 adapter subunit protein.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; porcine;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; haematopoietic system;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
```

```
XX
OS   Sus scrofa.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;    97US-0916917.
XX
PR   15-AUG-1997;    97US-0916917.
PR   27-JUN-1996;    96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   N-PSDB; AAV74100.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example IX; Fig 4; 75pp; English.
XX
CC   This sequence represents a novel catalytic subunit, p120, from porcine
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 1102 AA;

Query Match           98.9%;    Score 5726;    DB 20;    Length 1102;
Best Local Similarity 98.9%;    Pred. No. 0;
Matches 1090;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    1 MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKPETALLH 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLATSQRNTKPETALLH 60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
          |||||||||:|||||:|||||||||:||||||:||||||::|||||:|||||||||||||
Db   61 VAGHGNVERMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy  181 VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy  241 PGTILQSFPFTKMAKKGKSLMDIPBSQNERDFVLRVCGRDEYLVGETPIKNFQWVRQLKNG 300
          ||||||||||||||||| ||||||:|||||||||||||||||||||||||||||||||||:
Db  241 PGTILQSFPFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQLKNG 300

Qy  301 EEIHLVLDTPPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EEIHLVLDTPPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
          |||||||||||||||||||||||||:||||||:|||||||||||||||||||||||||||
Db  481 VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKGHRPTPDPEG 540

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
          ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy  721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSABKYDVSSQVISQLKQKLENLQNLNLP 780
          |||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db  721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy  841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
          ||||||||||||||||||||||
Db 1081 TVQFNWFLHLVLGIKQGEKHPA 1102
```

```
RESULT 3
AAY76802
ID   AAY76802    standard; Protein; 1102 AA.
XX
AC   AAY76802;
XX
DT   20-APR-2000   (first entry)
XX
DE   Pig p120 regulatory subunit proteinsequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; pig.
XX
OS   Sus sp.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
```

```
PF
XX   04-JAN-1999;    99US-0225170.
PR   15-AUG-1997;    97US-0916917.
PR   27-JUN-1996;    96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
XX
DR   WPI; 2000-136682/12.
DR   N-PSDB; AA286813.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Example; Fig 4; 75pp; English.
XX
CC   This sequence represents the pig p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders.The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which can affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence  1102 AA;

Query Match     98.9%;   Score 5726;   DB 21;   Length 1102;
Best Local Similarity  98.9%;   Pred. No. 0;
Matches 1090;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;

Qy     1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
           ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH 60

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
           ||||||||:|||||:|||||||||:||||:|||||||:|||||:||||||||||||||||
Db    61 VAGHGNVERMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
           |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy   181 VTPRMAEVAGRDPKLYAMHPWVISKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
           ||||||||||||||||||:|||:||||||||||||||||||||||||||||||||||||
Db   181 VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy   301 EEIHLVLDTTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 EEIHLVLDTTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480

Qy   481 VLHMWQLSGKGEBDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
           ||||||||||||||||||||||||||:||||||:|||||||||||||||||||||||||||
Db   481 VLHMWQLSGKGEBDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG 540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy   721 LRGCGTAMLHDFTQQVVDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRGCGTAMLHDFTQQVVDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPlWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPlWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy   841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
           ||||||||||||||||||||:|
Db  1081 TVQFNWFLHLVLGIKQGEKHPA 1102
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PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   N-PSDB; AAV74104.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Claim 15; Fig 13; 75pp; English.
XX
CC   This sequence represents a novel catalytic subunit, p120, from human
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence  1101 AA;

Query Match   95.4%;   Score 5523.5;   DB 20;   Length 1101;
Best Local Similarity   95.2%;   Pred. No. 0;
Matches 1049;   Conservative  21;   Mismatches  31;   Indels  1;   Gaps  1;

Qy     1 MELENYEQPVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
         |||||:||||||| :|||||||||| ||||||||||||||||||:|||: ::||||||
Db     1 MELENYKQPVLREDNCRKRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH   59

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
         |||||||||||||||||||||||:|||||||||:|||||||||||||||||||||||||||
Db    60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD  119

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
         |||||| ||||||||:|||||:|||||:.||||||:||||||||||||||||||||:||:|
Db   120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELFTRRGL  179

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
         ||||||||:||||||||||||||||||||||:||:|||:|||||||||||||||||::|||
Db   180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT  239

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
         ||.||||||||||||||||||||||:|:|||||||||||||||||||||||||||:|||||
Db   240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG  299

Qy   301 EEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 EEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  359

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKFPTEEVLWNVWLEFSIKI  420
         ||||||||||||||| |||||||||||::||||||||||||||||||||||||||||||||
Db   360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKFPTEEVLWNVWLEFSIKI  419

Qy   421 KDLPKGALNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480
         |||||||||||||||||||||.|:.|:||:||:|||| .||||||||||||||||||:|||
Db   420 KDLPKGALNLQIYCGKAPALSSKSASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY  479

Qy   481 VLHMWQLSGKGEDQGSFNADKLISATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
         ||||||:||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   480 VLHMWQISGKGEDQGSFNADKLISATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG  539

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
         ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ  599

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
         |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  659

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  719

Qy   721 LRGCGTAMLHDFTQQVVIDMQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
         ||||||||||||||||||:||||||:||||||||||||||||||||||||||||:|| :|
Db   720 LRGCGTAMLHDFTQQVVIEMQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP  779

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIPKHGDDLRQ  840
         :|||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   780 ESFRVPYDPGLKAGALAIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIPKHGDDLRQ  839

Qy   841 DMLILQLIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 DMLILQLIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  899

Qy   901 AFKDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
         ||||:||.||||:||:|.:|||||||||||||||||||||||||||||||||:|||||||
Db   900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL  959

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020
         |||||||||||||||||||||||||||||||||||||||||||:||::||:|||||||||
Db   960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL  1019

Qy  1021 RHHTNLLILFSMLMTGMPQLTSKEDIEYIRDALTVGKSEBEDAKKYFLDQIEVCRDKGW  1080
         ||||||| ||||||||||||||||||||||||||||| :::||:|||||||||||||||||
Db  1020 RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW  1079

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA  1102
         ||||||||||||||||||||||
Db  1080 TVQFNWFLHLVLGIKQGEKHSA  1101


RESULT 5
AAY76803
ID   AAY76803 standard; Protein; 1101 AA.
XX
AC   AAY76803;
XX
DT   20-APR-2000  (first entry)
XX
DE   Human p120 regulatory subunit protein sequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; human.
XX
OS   Homo sapiens.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
PF   04-JAN-1999;   99US-0225170.
XX
PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
```

```
XX
DR   WPI; 2000-136682/12.
DR   N-PSDB; AAZ86814.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Disclosure; Fig 13; 75pp; English.
XX
CC   This sequence represents the human p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence   1101 AA;

Query Match             95.4%;  Score 5523.5;  DB 21;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative  21;  Mismatches  31;  Indels  1;  Gaps  1;

Qy      1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
            |||||||||||||||||| |||||||||||||||| ||||||||||| | |||||
Db      1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTID 119

Qy    121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
            ||||| |||||||||||| |||| || |||| ||||||||||||| ||||||||| |||
Db    120 CLRYWKATHRSPGQIHLVQRHPPSSESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy    181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPBYLLKKITNNCVPFIVIHRSTTSQTIKVSADDT 240
            |||||||| ||||||||| |||||||||||| |||| |||||||||| ||||||||  |
Db    180 VTPRMAEVASRDPKLYAMHPWVTSKPLPBYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy    241 PGTILQSFFTKMAKKKSLMDIPESQNBRDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
            ||  ||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db    240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy    301 EEIHLVLDTPPDPALDEVRKSEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy    361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
            |||||||||||| ||| |||||||||||||||||| |||||||||||||||||||||||
Db    360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 419

Qy    421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    420 KDLPKGALLNLQIYCGKAPALSSKASAEBPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy    481 VLHMWQLSGKGEBDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    480 VLHMWQISGKGEBDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 DRVRAEMPNQLRKQLEAIIATDPLNPLTABDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy    721 LRGCGTAMLHDFTQQVVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
            | |||||||||||||| |||||||||||| ||||||||||||||||||||||| |||||
Db    720 LRGGGTAMLHDFTQQVVEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
            :|||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db    780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy    841 DMLILQILRIMESIWETESLDLCLLPYCGISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    840 DMLILQILRIMESIWETESLDLCLLPYCGISTGDKIGMEIVKDATTIAKIQQSTVGNTG 899

Qy    901 AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    900 AFKDEVLNHWLKEKSPTEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy   1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
            ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1020 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
            |||||||||||||||||||||
Db   1080 TVQFNWFLHLVLGIKQGEKHSA 1101


RESULT 6
AAU09689
ID   AAU09689 standard; Protein; 1101 AA.
XX
AC   AAU09689;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human p110gamma isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110gamma isoform;
KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US15065.
XX
PR   10-MAY-2000; 2000US-203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   N-PSDB; AAS14367.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3
PT   domain-containing polypeptides e.g. LASP-1, comprising allowing the
```

```
PT   binding partners to interact in the presence and absence of a test
PT   compound -
XX
PS   Example 1; Page 77-80; 85pp; English.
XX
CC   The present invention relates to identifying a modulator of the
CC   phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC   the catalytic subunit via a SH3 domain-containing polypeptide such as
CC   LASP-1. Also described are methods of assaying the specific binding
CC   affinity of the PI-kinase binding partner. Such modulators are useful
CC   for the treatment of diseases characterised by the undesirable or
CC   excessive activity of PI3kdelta. For example the modulators can be used
CC   for inhibiting the growth or proliferation of cancer cells
CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC   system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC   and Type I diabetes mellitus. The present sequence represents human
CC   p110gamma isoform of PI3k.
XX
SQ   Sequence 1101 AA;

Query Match             95.4%;  Score 5523.5;  DB 23;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative   21;  Mismatches  31;  Indels   1;  Gaps  1;

Qy     1 MELENYEQPVLREDNRRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKPETALLH 60
           ||||||:||||||||:||||||||  ||||||||||||||||||||:|  :||||||
Db     1 MELENYKQPVLREDNCRRRRRMKPRS-AASLSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
           |||||||||||||||||||||||||:|||:||||:||||||||||||||||||||||||||
Db    60 VAGHGNVEQMKAQVWLRALETSVAADFYIRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDLEFTRRRL 180
           ||||||  ||||||||:||||  ||||  ||||||  |||||||||||||||||||| |
Db   120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDLEFTRRGL 179

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPBYLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
           |||||||||:||||||||||||||||||||||  |||:|:||||||||||||||||:||||
Db   180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy   241 PGTILQSFFTKMAKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
           ||:|||||||||||||||||||||  ||  |||||||||||||||||||||||||:||:||
Db   240 PGAILQSFFTKMAKKSLMDIPESQSEQFVLRVCGRDEYLVGETPIKNFQWVRHCLRNG 299

Qy   301 EEIHLVLDTPDPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
           ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 EEIHVVLDTPDPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy   361 FRVKIRGIDIPVLPRTADLITVFVEANIQYGQGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
           ||||||||||||||||  |||||||||||  ||  ||||||||||||||||||||||||||||
Db   360 FRVKIRGIDIPVLPRNTDLITVFVEANIQHGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 419

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLHGEY 480
           ||||||||||||||||||||||| | |||  | |||||  |||:||||||||||||| ||||
Db   420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLIYYVNLLLIDHRFLLRRGEY 479

Qy   481 VLEMWQLSGKGEDQGSFNADKLITSATNPDKENSMSISILLDNYCHPIALPKRPTDPPEG 540
           ||:|||:|||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db   480 VLHMWQISGKGEDQGSFNADKLITSATNPDKENSMSISILLDNYCHPIALPKHQPTDPPEG 539

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKBLLWHFRYESLKDPKAYPKLFSSVKWGQ 600
           |||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db   540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKBLLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy   601 QEIVAKTYQLLAXREVWDQSALDVGLIMQLLDCNFSDENVRAIAVQKLESLEDDVLHYL 660
           |||||||||||| ||||||||||||||:||||||||||||||||||||||||||||:||||
Db   600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy   721 LRGGGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLP 780
           ||||  ||||||||||||||:||||||:||||||||||||||||||:||||||||||| ||
Db   720 LRGGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
           :|||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db   780 BSFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy   841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
           |||||||:|||||| |:|||||||||||||||||||||||||||||||||||||||:|||||
Db   900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
           ||||||||||||||||||||||||||||||||||||||||||||:|||||||:||||||||
Db   960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy  1021 RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
           ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db  1020 RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
           ||||||||||||||||||||||
Db  1080 TVQFNWFLHLVLGIKQGEKHSA 1101

RESULT 7
AAW23947
ID   AAW23947 standard; Protein; 1101 AA.
XX
AC   AAW23947;
XX
DT   17-AUG-1998 (first entry)
XX
DE   Human phosphoinositide 3OH-kinase p120 subunit.
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
KW   therapy; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Cleavage-site  40..41
FT                  /note= "cryptic thrombin cleavage site"
FT   Domain         310..315
FT                  /note= "WW domain, may be involved in interaction
FT                  with p101 subunit"
FT   Domain         173..302
FT                  /note= "weak pleckstrin homology domain, may be
FT                  involved in membrane binding and/or
FT                  G-beta,gamma subunit interaction of the
FT                  p101/120 complex"
XX
PN   WO9749818-A2.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1997; 97WO-US11219.
XX
PR   27-JUN-1996; 96US-0672211.
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Db    420 KDLPKGALLNLQIYCGKAPALSSKASAEBPSPSSESKGKVRLLYYVNLLIDHRFLRRGEY 479
          |||||||||||||||||||||| ||||  ||||||||||||| |||||||||||||||||
Qy    481 VLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKIRPTPDPEG 540
          ||||| ||||||||||||||||||||||||||||||||||||||||||||: ::|||||
Db    480 VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKIQPTPDPEG 539

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db    600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy    721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
          |||||||||||||||||| |||||||:||||||||||||||||||||||||||||| :||
Db    720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy    781 QSFVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          :|| ||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          |||:|||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    840 DMILQILRIMESIWETSLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy    901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
          ||||||| |||||| |:||||||||||||||||||||||||||||||||||||:|||||
Db    900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQPDVCKAYIAL 1020
          |||||||||||||||||||||||||||||||||||||||||||: ||:| |||:|||
Db    960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYIAL 1019

Qy   1021 RHHTNLLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||| ||||:|||||||||||||||||||||||:|||||||||||||||||||||
Db   1020 RHHTNLLLIFSMMILMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
          ||||||||||||||||||||||
Db   1080 TVQFNWFLHLVLGIKQGEKHSA 1101
```

RESULT 8
AAW11577
ID   AAW11577   standard; Protein; 1050 AA.
XX
AC   AAW11577;
XX
DT   25-MAR-1997 (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   742..756
FT   /label= immunogen
FT   /note= "antibodies are pref. raised against this
FT   peptide; location given as 742-746 in the
FT   claims"
XX
PN   DE4445562-C1.

XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1998-077181/07.
XX
PT   DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase,
PT   p101 and p120 subunits - useful for diagnosis, drug screening,
PT   clinical trial monitoring and treatment of inflammatory disorders
XX
PS   Claim 55; Fig 11; 151pp; English.
XX
CC   This is the deduced amino acid sequence of the p120 catalytic
CC   subunit of human G-protein regulated phosphatidylinositol-3' kinase
CC   (PI3K), a heterodimeric enzyme which produces the intracellular
CC   messenger phosphatidylinositol (3,4,5)-triphosphate in response to
CC   activation of trimeric G protein-linked receptors. This novel
CC   protein, which also contains a regulatory subunit, p101 (see
CC   AAW23949), is found in cells of haematopoietic origin and is involved
CC   in immune system responses which cause inflammation. Human p120
CC   cDNA was obtained from a leukocyte cDNA library. The invention
CC   encompasses pig and human p101 and p120 nucleotides (see AAV04633-34),
CC   host cell expression systems, p101 and p120 proteins (see AAW23946-49),
CC   fusion proteins, polypeptides and peptides, antibodies to these
CC   proteins, and transgenic and knockout animals. Compounds which are
CC   useful for treating inflammatory response disorders can be
CC   identified by screening assays using a G protein activated PI3K, or
CC   a cultured host cell that expresses the p101 gene. Antagonists of
CC   G protein stimulated PI3K (acting through the p101 subunit,
CC   especially by disrupting the interaction between the p101 and p120
CC   subunits) can be used to treat arthritis, septic shock, adult
CC   respiratory distress syndrome (ARDS), pneumonia, asthma, allergies,
CC   reperfusion injury, atherosclerosis, cancer and Alzheimer's disease.
CC   The nucleic acids and their products can also be used for diagnosis,
CC   drug screening and clinical trial monitoring of inflammatory
CC   diseases.
XX
SQ   Sequence   1101 AA;

```
Query Match      95.0%;   Score 5500.5;   DB 19;   Length 1101;
Best Local Similarity  94.7%;   Pred. No. 0;
Matches 1044;  Conservative  23;  Mismatches  34;  Indels  1;  Gaps  1;

Qy    1 MELENYEQPVLREDNRRRRRMKPRSTRAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
        ||||||:||| ||||| ||||||||||| :|||||||||||||||||||||  :||||||
Db    1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
        |||||||||||||||||||||||:||||||||||:|||||||||||||||||||||||||
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        ||||||  |||||||| |||||||||: |||||||:|||||||||||||||||||||| |
Db  120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
        |||||||||:|||||||||||||||||||| |||||||| |||||||||||||||||||:|
Db  180 VTPRMAEVASRDPKLYAMHPWTSKPLPEYIWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        ||:|:|||||:||||||||||||||| |:|||||||||||||||||||||||||:||||
Db  240 PGAIIQSFFTQMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
        |||||||||||||||  |||||||||||:|||||||||||||||||||||||||||||||
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 419

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMSPESKGKAQLLYYVNLLIDHRFLRHGEY 480
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XX
PD   04-APR-1996.
XX
PF   20-DEC-1994;   94DE-445562.
PR   13-OCT-1994;   94DE-4436696.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Hanck T, Stoyanov B, Wetzker R;
XX
DR   WPI; 1996-172545/18.
DR   N-PSDB; AAT58546.
XX
PT   New phosphatidyl:inositol 3-kinase protein - useful as immunogen and
PT   for determ. of kinase activity
XX
PS   Claim 1; Page -; 10pp; German.
XX
CC   A 402 bp cDNA fragment was amplified from a human bone marrow
CC   library using PCR primers corresponding to amino acid sequences
CC   KNGDDIR and HIDFG. The amplified fragment was used to probe a human
CC   U937 cell cDNA library and several overlapping clones were isolated.
CC   The largest clone coded for a protein of 1049 residues. The protein
CC   is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its
CC   regulatory mechanism from the known PI3k-alpha and -beta enzymes.
CC   The new enzyme has been designated PI3k-gamma. Another clone, coding
CC   for a PI3k-gamma having the present sequence of 1050 residues, was
CC   then isolated. The enzyme can be used as an immunogen. The enzyme,
CC   antibodies against it or nucleic acid encoding it can be
CC   used for modulating cell proliferation, receptor-mediated signal
CC   transmission, histamine secretion, nerve cell differentiation,
CC   glucose transport and anti-lipolytic activity or for treating
CC   Alzheimer's disease.
CC   N.B. Although the claimed sequences are referred to by SEQ.ID.
CC   Numbers, a sequence listing did not appear in the original printed
CC   patent application.
XX
SQ   Sequence   1050 AA;

Query Match             90.2%;  Score 5222;  DB 17;  Length 1050;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches  990;  Conservative  20;  Mismatches  30;  Indels  0;  Gaps  0;

Qy    35 MELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPD 94
          |||||||||||||||||||:|:||||||||||||||||||||||||||||:||||||||
Db     1 MELIPIEFVLPTSQRKCKSPETALLHVAGHGNVEQMKAQVWLRALETSVAADFYHRLGPH 60

Qy    95 HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQL 154
          ||||||||||||||||||||||||||||||||||:||:||||||||||||| ||||||||
Db    61 HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKATHRSPGQIHLVQRHPFSBESQAFQRQL 120

Qy   155 NALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKK 214
          |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db   121 TALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKK 180

Qy   215 ITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRV 274
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 IANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRV 240

Qy   275 CGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDALDEVRKEEWPLVDDCTGVTG 334
          |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   241 CGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDALDEVRKEEWPLVDDCTGVTG 300

Qy   335 YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFEANIQYGGQVL 394
          |||||:|||||||||||||||||||||||||||||||||||||:|||||:||||||||
Db   301 YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVL 360

Qy   395 CQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQITYCGKAPALSGKTSAEMPSPES 454
          |||||||||||||||||||||||||||||||||||||||||||||||::||||||||||
Db   361 CQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQITYCGKAPALSSKASASABSPSSES 420

Qy   455 KGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSM 514
          |||:|||||||||||||||||||||:||||||||:||||||||||||||||||||||||
Db   421 KGKVRLLYYVNLLLIDHRFLLRRGEYVLHWWQISGKGEDQGSFNADKLTSATNPDKENSM 480

Qy   515 SISILLDNYCHPIALPKGHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL 574
          ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db   481 SISILLDNYCHPIALPKHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL 540

Qy   575 LWHFRYESLKDPKAYPKLFSSVKNGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCN 634
          ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db   541 LWHFRYESLKGPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCN 600

Qy   635 FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF 694
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF 660

Qy   695 LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSA 754
          ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   661 LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVQIEMLQKVTLDIKSLSA 720

Qy   755 EKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLE 814
          ||||||||||||||||||||||:|::|||||||||||||||||||||:|||||||||||
Db   721 EKYDVSSQVISQLKQKLENLQNSQLPESRVPYDPGLKAGALAIEKCKVMASKKKPLWLE 780

Qy   815 FKCADPTALSNETIGIIFKHGDDLRQDMLILQIIRIMESIWETESLDLCLLPYGCISTGD 874
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 FKCADPTALSNETIGIIFKHGDDLRQDMLILQIIRIMESIWETESLDLCLLPYGCISTGD 840

Qy   875 KIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAG 934
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 KIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPIEEKFQAAVERFVYSCAG 900

Qy   935 YCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV 994
          ||||||||||||||||||||:|||||||||||||||||||||||||||||:||||||||
Db   901 YCVATFVLGIGDRHNDNIMITETGNLFHIDFGHILGNYKSFLGINKERVPFFVLTPDFLFV 960

Qy   995 MGTSGKKTSLHFQKFQDVCVKAYLALRHTNLLILFSMLMTGMPQLTSKEDIEYIRDA 1054
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 MGTSGKKTSPHFQKFQDICVKAYLALRHTNLLILFSMLMTGMPQLTSKEDIEYIRDA 1020

Qy  1055 LTVGKSEEDAKKYFLDQIEV 1074
          |||||:||||||||||||||
Db  1021 LTVGKNEBDAKKYFLDQIEV 1040
```

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KW   antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW   platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
XX
OS   Homo sapiens.
XX
PN   WO9321328-A1.
XX
PD   28-OCT-1993.
XX
PF   13-APR-1993;  93WO-GB00761.
XX
PR   13-APR-1992;  92GB-0008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI   Panayotou G, Volinia S, Gout I;
XX
DR   WPI; 1993-351738/44.
DR   N-PSDB; AAQ51155.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 4; Fig 9; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a.  Positive clones were sequenced to give a human
CC   PI3 kinase p110 sequence.  This sequence has 95 percent
CC   homology with the bovine sequence.  The domain encoding residues 19-
CC   100 of human p110 is sufficient to encode the kinase which will
CC   associate with the p85 kinase subunit.  The gene may be used to
CC   provide a protein with PI3 kinase activity, and is useful for
CC   screening for (ant)agonists of PI3 kinase activity which could be
CC   useful for stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy.  Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAR43342 and AAR46552-3.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 1068 AA;

Query Match             25.3%;
Best Local Similarity   33.5%;  Pred. No. 1.3e-113;   Score 1465.5; DB 14; Length 1068;
Matches  382;  Conservative 204; Mismatches 405; Indels 149; Gaps 39;
```

```
Qy   23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
          ||||| ||:: :|  ::    ::| |  |  |||||||||||||||||||
Db    1 MPPRPSSGELWGIHIMPPRILVECLLPNGMIVT------LECLREATLITIKHELFKEA 53

Qy   79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
          |::  :||: :|:| ::|   ::                       :|:
Db   54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFPDETRRLCDLRLFQPF------LKVI 102

Qy  139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------- 192
Db  103 EPVGNREEKI-LNREIGFAIGMPVCEPDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy  193 PKLYAMHPWTSKP-LPEYILKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
          ||  | |:|  :| |:||::||:                 ||:
Db  162 RAMYVYPNVESSPELPKHIYNKLDKGQIIVVIWIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy  246 QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
          :|::      ::|:| |::      |||||:|:||    |||::||| : :::|:
Db  222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy  300 GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL 354
          | :|||:|  |||||| ||:||||:::   | |||::|::    :::|| | ::  |:|
Db  280 GRMPNLML-----MAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TSTKSL 327
```

```
Qy  355 WDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPF 404
Db  328 WVINSALRIKILCATYVNVIRDID--------KIYVRTGIYHGGEPLCDNVNTQRVP 377

Qy  405 TBEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV 464
Db  378 CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C-----SVKGRKGA--------KEEHCPLAWG 425

Qy  465 NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC 524
Db  426 NINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS 481

Qy  525 HPIALPKHRPTPDPEGDRV----------RAEMPNQLR---KQLEAIIATDPLN 565
Db  482 SVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS 541

Qy  566 PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGGQQEIVAKTYQLLAKREVWDQSALDVG 625
Db  542 EITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQWYCL-----VKDWPPIKPE 596

Qy  626 LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR 684
Db  597 QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKK 656

Qy  685 GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK 744
Db  657 ALTNQRIGHFFFWHLKSBM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMBKLIN 714

Qy  745 VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALVIEKC 801
Db  715 LT-DI--LKQEKKDETQKV--QMKFLVEQMRPDFMDALQGFLSPLNPAHQLGNLRLLBEC 769

Qy  802 KVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRIMESIW 855
Db  770 RIMSSAKRPLWLNWE---NPDIMSBLLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW 824

Qy  856 ETEBSLDLCLLPYGCISTGDKIGMEIBIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE 913
Db  825 QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGKLKGALQFNSHTLHQWLKD 883

Qy  914 KCPIEBKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK 973
Db  884 KNK-GEIYDAAIDLFTRSCAGYCVATFIIGIGDRHNSNIMVKDDGQLPHIDFGHFLDHKK 942

Qy  974 SFLGINKSRVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYIALRHTNLLILLF 1031
Db  943 KKFGYKEBRVPFVLTQDFLIVISKGAQBCTKTREFERFQEMCYKAYLAIRQHANLFINLF 1002

Qy 1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db 1003 SMMLGSGMPELQGFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062
```

```
RESULT 12
AAR43342
ID   AAR43342 standard; protein; 1068 AA.
XX
AC   AAR43342;
XX
DT   25-MAR-2003  (updated)
DT   12-APR-1994  (first entry)
XX
DE   Human p110.
XX
KW   Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW   antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW   platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          19..100
```

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FT         /note= "binds with p85 subunit"
XX
PN   WO321328-A1.
XX
PD   28-OCT-1993.
XX
PF   13-APR-1993;  93WO-GB00761.
XX
PR   13-APR-1992;  92GB-0008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI   Panayotou G, Volinia S, Gout I;
XX
DR   WPI; 1993-351738/44.
DR   N-PSDB; AAQ51156.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 24; Fig 16; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a. Positive clones were sequenced to give the human
CC   PI3 kinase p110 sequence. This sequence has 95 percent homology
CC   with the bovine sequence. The domain contg. residues 19-100 of human
CC   p110 is sufficient to associate with the p85 kinase subunit. The
CC   protein with PI3 kinase activity is useful for screening for
CC   (ant)agonists of PI3 kinase activity which could be useful for
CC   stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy. Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAR43341 and AAR46552-3.
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence  1068 AA;

Query Match           25.2%;  Score 1460.5;  DB 14;  Length 1068;
Best Local Similarity 33.3%;  Pred. No. 3.3e-113;
Matches   381;  Conservative 206;  Mismatches 400;  Indels 157;  Gaps  40;

Qy     23  MKPRSTAALSLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
               ||  :  ||    ||:||||||   || :::  |||
Db      1  MPPRPSSGELWGIHLMPPRIIVEC LLPNGMIVT------LECLREATLVTIKHELFKEA   53

Qy     79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
               ||  :  |||     :: || ||| :|:|
Db     54  RKYPL----HQLLQDBSSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI  102

Qy    139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
               :| ||  ||     ||  |:  |  |  :: ::
Db    103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy    193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL  245
               :|:  :||  ::|| |   :|  : ||| :|
Db    162  RAMYVYPPHVESSPELPKHIYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy    246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN  299
                     :::|      :|| :    || |  |  || :  :::::
Db    222  AEAIRK--KTRSMLLSSEQLKJCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy    300  GEEIHLVLDTPPDPALDEVRKE----EWPLVDDCTGVTGYHEQLT----IHGKDHESVF  350
                  :|: |  || |::|            |   :|:  | :  |   :|   :: :||
Db    280  GRM--------PNLKMMAKESLYSQLPM-DCFTMPSYSRRISTATPYMNGE----TS  323

Qy    351  TVSLWDCDRKFRVK----------IRGIDIPVLPRTADLIVFVEANIQYGQQVLCQRRTS  400
               ::: |  ||:|:             :| | |: ||  ||  ::  :| |::  |:  :
Db    324  TKSLWVINRALRIKILCATYVNLNIRDID---------KIYVRTGIYHGGEPLCDNVNT  373
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Qy    401  PKPFTEEVLMNVWLBFSIKIDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL  460
               :   :: ||: |   |    :|||  | |: |  :||| |::
Db    374  QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA-----KEEHCP  421

Qy    461  LYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL  520
               ||   ||  :|: |:|| :  || :|  :||  ::    ::   |:|| ||||||
Db    422  LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF  477

Qy    521  DNYCHPIALPKGHRPTPDPEGDRV----------RAEMPNQLR----KQLEAIIAT  561
               |  |||  | ::| | |||
Db    478  DWFSSVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR  537

Qy    562  DPLNPLTAEDKELLWHFRYESLKDPKAYPKLPSSVKWGQQEIVAKTYQLLAKREWVDQSA  621
               ||:|| | :|| :|| |::| : ::|  ::||  ::|  ::|  ::| : ::
Db    538  DPLSEITEQEKDFLWSRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP  592

Qy    622  LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF  680
               |  :: |  | ::   |   ::|:: ::| ||||  | :| : ::  :::| : |:|
Db    593  IKPEQAMELLDCNYPDMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF  652

Qy    681  LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID  740
               ||: :|:|:|| |    :| | |:::|  : :|  : |||   | : |:|   :|:::
Db    653  LLKKALINQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME  710

Qy    741  MLQKVTIDKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALV  797
               :|   | ::| :|| ::  ||:|| :: |:|:|   : |  : |  |  :|| |
Db    711  KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR  765

Qy    798  IEKCKVMASKKKPLWLEFKCADPTALS------NETIGIIFKGHGDDLRQDMLILQILRIM  851
               :| | ::|:| ||  |:     :      |  ||:  :|:|:|||||||:|:| :||:
Db    766  LKBCRIMSSAKRPLWLNWB--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM  820

Qy    852  ESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH  909
               |:   ||| |||||||||   ||| |:|:|  |: ::|:  ||   |  | :| | |
Db    821  ENTWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ  879

Qy    910  WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL  969
               ||:::|  ::|:   :::|  |||||| | :|:||||:| ||| :::|| |||||||:
Db    880  WLKDKNK-GBIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFL  938

Qy    970  GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL  1027
               |||| |||  ||| |   |  |  : :|   |::|  |::|::  |  ||::| | :| :
Db    939  DHKKKKFGVKRERVFPVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLF  998

Qy   1028  IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF  1087
               | || ::|:|::| ||  |||  |||: ||:|| ::|: ||  |:   |::|:|: | |
Db    999  INLFSMMLGSSGMPELQSFDDIAYIRKTLALDKTKEQEALEYFMKQMNDAHHGGWTTKMDWI  1058

Qy   1088  LHLV  1091
             |::
Db   1059  FHTI  1062
```

```
RESULT 13
AAU09687
ID   AAU09687 standard; protein; 1068 AA.
XX
AC   AAU09687;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human p110alpha isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase;  PI3K; p110alpha isoform;
KW   LASP-1; cancer; inflammatory disease;  ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
CS   Homo sapiens.
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
```

```
XX
PF   10-MAY-2001; 2001WO-US15065.
XX
PR   10-MAY-2000; 2000US-203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   N-PSDB; AAS14365.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3
PT   domain-containing polypeptide e.g. LASP-1, comprising allowing the
PT   binding partners to interact in the presence and absence of a test
PT   compound -
XX
PS   Example 1; Page 60-63; 85pp; English.
XX
CC   The present invention relates to identifying a modulator of the
CC   phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC   the catalytic subunit via a SH3 domain-containing polypeptide such as
CC   LASP-1. Also described are methods of assaying the specific binding
CC   affinity of the PI3-kinase binding partner. Such modulators are useful
CC   for the treatment of diseases characterised by the undesirable or
CC   excessive activity of PI3kdelta. For example the modulators can be used
CC   for inhibiting the growth or proliferation of cancer cells
CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC   system inflammatory disorders (e.g. meningitis; bacterial pneumonia,
CC   and Type I diabetes mellitus. The present sequence represents human
CC   p110alpha isoform of PI3k.
XX
SQ   Sequence 1068 AA;

Query Match             25.2%;  Score 1460.5;  DB 23;  Length 1068;
Best Local Similarity   33.3%;  Pred. No. 3.3e-113;
Matches  381;  Conservative  206;  Mismatches  400;  Indels  157;  Gaps  40;

Qy      23 MKPRSTAASLSSMELIP---IEPVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA  78
            |: ||  |||: ||    :|    || |   : |:| ||||||||:||  |::||||
Db       1 MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT-------LECLREATLVTIKHELFKEA  53

Qy      79 LETSVSADFYHRLGPDHPLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
              :  |  |  | |: ||           |:|  |::  | ||||  ||    || |||
Db      54 RKYPL-----HQLIQDESSYIFVSVTQEAREREFFDETRRLCDLRLFQPF-----LKVI 102

Qy     139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
                |  | |  |  ||  | ||  || ||| |||  ||  | ||:|| |
Db     103 EPVGNREEKI-LNREIGPAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy     193 PKLYAMHPWTSKP-LPEYLLKKITNNCVFIVI------HRSTSQTIKVSADDTPGTIL  245
            ||| | ||: |  |  || |:||      :|        || :| || || |  |:|
Db     162 RAMVYYPPHVESSPELPKHIYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy     246 QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
            |||  ||| | ||     |      |  |  |  |  |   | |      |  |::|  |
Db     222 AEAIRK--KTRSMLLSSEQLKLCVLEYGQGKYILKVCGCDEYFLEKYPLSQYKIRSCIML 279

Qy     300 GEEIHLVLDTPPDPALDEVRKE---EWPLVDDCTGVTGYHEQLT----IHGKDHRSVF 350
            |  ||:| | |   ||       |   |  || | ||: :     ::|
Db     280 GRM-------PNLKMWMAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS 323

Qy     351 TVSLWDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTS 400
            |  |  | |:|  |         ||  |: |   ||||  :|||    || |:| |
Db     324 TKSLWVINRALRIKILCATYVNLNIRDID----------KIYVRTGIYHGGEPLCDNVNT 373

Qy     401 PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
            : ||  |  :|  : |                 :|   |  |  | : |
```

XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowsert LM;
XX
DR   WPI; 2000-686014/67.
DR   N-PSDB; AAC65590.
XX
PT   Antisense compound 8-30 nucleobases in length targeted to a start codon
PT   of the coding region of human PI3 kinase p110beta, useful for
PT   inhibiting the expression of the human polynucleotide -
XX
PS   Example 1; Column 43-50; 34pp; English.
XX
CC   This invention describes a novel antisense compound (I) 8-30 nucleobases
CC   in length targeted to a start codon or nucleobases 4-3174 of the coding
CC   region of human PI3 kinase p110beta (II), in which (I) specifically
CC   hybridizes with and inhibits the expression of (II). The products of the
CC   invention have cytostatic, antiinflammatory and antiinfective activity.
CC   (I) is useful for inhibiting the expression of (II) in human cells or
CC   tissues. The antisense compound can be utilized for diagnostics,
CC   therapeutics, prophylaxis and as research reagents and kits. The
CC   antisense compounds may also be useful prophylactically, e.g. to prevent
CC   or delay infection, inflammation or tumor formation. The antisense
CC   compounds are useful for research and diagnostics, because these
CC   compounds hybridize to nucleic acids encoding (II).
XX
SQ   Sequence   1070 AA;

Query Match   23.4%; Score 1354.5; DB 21; Length 1070;
Best Local Similarity   31.8%; Pred. No. 2.7e-104;
Matches 361; Conservative 202; Mismatches 407; Indels 165; Gaps 37;

Qy   30 ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH 89
              ::::||:|:||||||
Db   22 SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM------- 68

Qy   90 RLGPDHFLLIYQKKGQWYEIYDKYQVVQTLD------C-----LRYWKVLHRS--PGQIH 136
              ||||||
Db   69 ------FNLLMDIDSYMFACVNQTAVYEELEDETRRLCDVRPFLPVLKLVTRSCDPGE-- 120

Qy   137 VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
              ||| :| ::| ||
Db   121 ---------KLDSKIGVLIGKGLHEFDSLKDPEVNEFRRKMRKFSBEKIISLSLVGLSW 168

Qy   193 -PKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249
              :|:: || |
Db   169 MDWLKQTYPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE--- 225

Qy   250 TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDT 309
              : ::| ||:||| :|:::| | |:||| :||
Db   226 LAIQKRLTIHGKSDEVSPYDVYLQVSGRVEYVFGDHPLIQFQYIRNCVMNRALPHFIL-- 283

Qy   310 PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------- 354
              ||| ||||
Db   284 -----VECCKIKKMYEQEMIAIEAAINRNSSNLPLPLPPKKTRIISHV 326

Qy   355 WDCDRKFR-VKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPK-PFTEEVLWNV 412
              |: :| | |:| ||
Db   327 WENNNPFQIVLVKG---NKLNTEETVKVHVRAGLFHGTELLCKTIVSSEVSGKNDHIWNE 383

Qy   413 WLEPSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP---ESKGKAQLLYY----VN 465
              |:| ||| ||||||
Db   384 PLEFDINICDLPRMARLCPAVY-AVLDKVKTKKSTKTINPSKYQTIRRAGKVHYPVAWVN 442

Qy   466 LLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKL--------TSATNPDKENSMSIS 517
              :::::|:|| |:|:|| ::|
Db   443 TMVFDFKGQLRTGDIILHSW--------SSF-PDELEMLNPMGTVQTNPYTENATALH 492

Qy   518 ILL-DNYCHPIALP------KHRPTDPPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA 569
              |: :||||||
Db   493 VKFPENKKQPYYYPPFDKIIEKAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE 552

Qy   570 EDKELLWHFRYESLK-DPKAYPLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM 628
              ::|:||::|:|:   :|: :|||
Db   553 NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA--QLQALLQIWPK--LPPREAL 607

Qy   629 QLIDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEPYHDSALARPLLKRGLRN 688
              ||||||:| |||:::| :|:: |||:||||||
Db   608 EILLDFNYPDQYVREYAVGCLRQMSDEELSQYLLQLVQVLKYEPPLDCALSRFLLERALGN 667

Qy   689 KRIGHFLFWFLRSEIAQSRH--YQQRFAVILEAYLRGCGTAMLHDFTQQVVIDMLQKV 745
              |:||:|:|||| ::||:|:   ::|: :||
Db   668 RRIGQFLFWHLRSEV----HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKKTL 722

Qy   746 T--IDIKSLSAEKYDVSSQVISQLKQK-----LENLQNLNLPQSFRVPYDPGLKAGALVI 798
              | :::|| ::: || :|||:
Db   723 NSLIKLNAVKLNRAKGKEAMTCLKQSAYREALSDLQS--------PLNPCVILSELYV 773

Qy   799 EKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWETE 858
              |||| ||| ||||||: ::: :::|: :|:|
Db   774 EKCKYMDSKMKPLWLVY---NNKVFGEDSVGVIFKNGDDLRQDMLTLQMLRLMDLLWKEA 830

Qy   859 SLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLEKCP 916
              |:|:||||| ||:|| :||:| |:||| ::::|:|||
Db   831 GLDLRMLPYGCLATGDRSGLIEVSTETIADIQLNSSNVAAAAAFNKDALLNWLKEYNS 890

Qy   917 IEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL 976
              ||::| |::::|||::|:|:   ::||| ||||||||| |
Db   891 GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTGQLFHIDFGHILGNFKSKF 949

Qy   977 GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLM 1036
              |:||:| ::| | : : | :|:::| :|
Db   950 GIKRERVPFILYDFIHVIQQGKTGNTEKFGRFRQCCEDAYLILRHGNLFTTLFALMLT 1009

Qy   1037 TGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
              || |:   :|:|::   :| | |::|:||:||||
Db   1010 AGLPELTSVKDIQYLKDSLALGKSEEEALKQFKQKPEALRESWTTKVNWMAHTV 1064

RESULT 15
ABP65170
ID   ABP65170 standard; Protein; 1070 AA.
XX
AC   ABP65170;
XX
DT   12-NOV-2002 (first entry)
XX
DE   Hypoxia-regulated protein #44.
XX
KW   Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW   antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
KW   hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
KW   ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW   preeclapmsia; atherosclerosis; inflammatory condition; wound healing;
KW   inflammation; erythropoiesis; hair loss; human.
XX
OS   Homo sapiens.
XX
PN   WO200246465-A2.
XX
PD   13-JUN-2002.
XX
PF   10-DEC-2001; 2001WO-GB05458.
XX
PR   08-DEC-2000; 2000GB-0030076.
PR   08-FEB-2001; 2001GB-0003156.
PR   25-OCT-2001; 2001GB-0025666.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI   Rayner WN;
XX
DR   WPI; 2002-627238/67.
XX

```
PT   Identifying a gene involved in disease for treating hypoxia-regulated
PT   conditions, comprises comparing the transcriptome/proteome of two cell
PT   types under different conditions and identifying a differentially
PT   regulated gene -
XX
PS   Claim 35; Page 363; 538pp; English.
XX
CC   The present invention relates to methods for identifying genes and
CC   proteins that are implicated in a specific disease or physiological
CC   condition. The method comprises comparing the transcriptome/proteome of a
CC   specialised cell type implicated in a disease or condition with that of a
CC   second specialised cell type, under two experimental conditions, and
CC   identifying a gene that is differentially regulated in the two
CC   specialised cell types under experimental conditions. ABV77873-ABV78116
CC   and ABP65061-ABP65257 were identified using the methods of the invention.
CC   The coding sequences and proteins are useful for treating a disease in a
CC   patient, for manufacture of a medicament for treating hypoxia-regulated
CC   conditions, and for regulating tumourigenesis, angiogenesis, apoptosis,
CC   biological response to hypoxia conditions, or hypoxi-associated
CC   pathology in a patient. The coding sequences and proteins are also useful
CC   for monitoring the therapeutic treatment of a disease or physiological
CC   condition, such as cancer, ischaenic conditions, reperfusion injury,
CC   retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory
CC   conditions, wound healing, inflammation, erythropoiesis or hair loss.
XX
SQ   Sequence 1070 AA;

Query Match             23.4%;    Score 1354.5;  DB 23;   Length 1070;
Best Local Similarity   31.8%;    Pred. No. 2.7e-104;
Matches   361;  Conservative 202;  Mismatches 407;  Indels 165;  Gaps 37;

Qy    30 ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH 89
Db    22 SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM------ 68

Qy    90 RLGPDHPLLILYQKGQWYEIYDKYQVVQTLD------C----LRYWKVLHRS--PGQIH 136
Db    69 -----FNLLMDIDSYMFACVNQTAVYEELEDETRRLCDVRPFLPVLKJVTRSCDPGE-- 120

Qy   137 VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
Db   121 ---------KLDSKIGVLIGKGLHEFDSLKDPEVNEFRRKRKFSEEKILSLVGLSW 168

Qy   193 -PKLYAMHPVTSKRLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249
Db   169 MDWLKQTYPPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE-- 225

Qy   250 TKMAKKKSLMDIPESQNERDPVLRVCGRDEYLVGETPIKNFQWRQCLKNGEEIHLVLDT 309
Db   226 LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVFGDHPLIQFQYIRNCVMNRALPHFIL-- 283

Qy   310 PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------- 354
Db   284 ------------VECCKIKMYEQEMIAIEAAINRNSSNLPLPLPPKTRIISHV 326

Qy   355 WDCDRKFPR-VKIRGIDIPVLPRTADLTVFVBEANIQYGQQVLCQRRTSPK-PFTEEVLMNV 412
Db   327 WENNNPFQIVLVKG---NKLNTEETVKVHVRAGLFHGTELLCKTIVSSEVSGKNDHIWNE 383

Qy   413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP--ESKGKAQLLYY----VN 465
Db   384 PLEFDINICDLPRMARLCFAVY-AVLDKVKTKKSKTINPSKYQTIRKAGKVHYPVAWVN 442

Qy   466 LLLIDHRFLLRHGEVVLHMWQLSGKGEDQGSFNADKL-------TSATNPDKENSMSIS 517
Db   443 TMVFPDFKGQLRTGDIILHSW--------SSF-PDELEEMLNPMGTVQTNPYTENATALH 492

Qy   518 ILL-DNYCHPIALP-------KHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA 569
Db   493 VKFPENKKQPYYYPPFDKIIEKAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE 552

Qy   570 EDKELLWHFRYESLK-DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM 628
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```
Db   553 NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA---QLQALLQIWPK--LPPREAL 607

Db   629 QLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRN 688
Db   608 ELLDFNYPDQYVREYAVGCLRQMSDEELSQYILQLVQVLKYEPFLDCALSRFLLERALGN 667

Qy   689 KRIGHFLFWFLRSEIAQSRH---YQQRFAVILEAYLRGCGTAMLHDFTQQYQVIDMLQKV 745
Db   668 RRIIGQFLFWHLRSEV----HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKLKTL 722

Qy   746 T--IDIKSLSABKYDVSSQVISQLKQK----LENLQNLNLPQSFRVPYDPGLKAGALVI 798
Db   723 NSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQS-------PLNPCVILSELYV 773

Qy   799 EKCKVMASKKKPLMLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWETE 858
Db   774 EKCKYMDSKMKPLWLVY---NNKVFGEDSVGVIFKNGDDLRQDMLTLQMLRLMDLLWKEA 830

Qy   859 SLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCP 916
Db   831 GLDLRMLPYGCLATGDRSGLIEVVSTSETIADIQLNSSNVAAAAAFNKDALLNWLKEYNS 890

Qy   917 IEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL 976
Db   891 GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTCQLFHIDFGHILGNFKSKF 949

Qy   977 GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILLFSMMLM 1036
Db   950 GIKRERVPFILYDFIHVIQQGKTGNTEKFGRFRQCCEDAYLILRHGNLFTTLFALMLT 1009

Qy  1037 TGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGWTVQPNWFLHLV 1091
Db  1010 AGLPELTSVKDIQYLKDSLALGKSEEEALKQFKQKFDEALRSWTTKVNWMAHTV 1064
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Search completed: February 15, 2004, 02:02:56
Job time : 86 secs

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OM protein - protein search, using sw model

Run on: February 15, 2004, 02:03:09 ; Search time 28 Seconds
    (without alignments)
    1665.234 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR..........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	98.9	1102	2	US-08-916-917-4	Sequence 4, Appli
2	5726	98.9	1102	2	US-08-972-631-4	Sequence 4, Appli
3	5726	98.9	1102	2	US-08-972-629-4	Sequence 4, Appli
4	5726	98.9	1102	2	US-08-972-630-4	Sequence 4, Appli
5	5726	98.9	1102	2	US-08-672-211-4	Sequence 4, Appli
6	5726	98.9	1102	3	US-09-225-170-4	Sequence 4, Appli
7	5523.5	95.4	1101	2	US-08-916-917-14	Sequence 14, Appl
8	5523.5	95.4	1101	3	US-09-225-170-14	Sequence 14, Appl
9	5222	90.2	1050	2	US-08-817-090B-4	Sequence 2, Appli
10	5093.5	88.0	1049	2	US-08-817-090B-2	Sequence 2, Appli
11	1465.5	25.3	1069	2	US-08-162-081B-37	Sequence 37, Appl
12	1465.5	25.3	1069	2	US-08-780-872-37	Sequence 37, Appl
13	1465.5	25.3	1069	3	US-09-085-957-37	Sequence 37, Appl
14	1463.5	25.3	1080	2	US-08-162-081B-36	Sequence 36, Appl
15	1463.5	25.3	1080	2	US-08-780-872-36	Sequence 36, Appl
16	1463.5	25.3	1080	3	US-09-085-957-36	Sequence 36, Appl
17	1450.5	25.1	1068	4	US-08-390-874C-11	Sequence 11, Appl
18	1450.5	25.1	1068	4	US-09-265-772-11	Sequence 11, Appl
19	1351.5	23.3	1044	2	US-08-777-405A-2	Sequence 2, Appli
20	1351.5	23.3	1044	2	US-08-977-871A-2	Sequence 2, Appli
21	1351.5	23.3	1044	2	US-09-225-951-2	Sequence 2, Appli
22	1351.5	23.3	1044	2	US-09-841-341-2	Sequence 2, Appli
23	1349.5	23.3	1044	4	US-08-194-640A-1	Sequence 1, Appli
24	1076.5	18.6	1726	3	US-08-609-049A-30	Sequence 30, Appl
25	1076.5	18.6	1726	3	US-09-170-996-30	Sequence 30, Appl
26	1075.5	18.6	1658	2	US-08-609-049A-13	Sequence 13, Appl
27	1075.5	18.6	1658	3	US-09-170-996-13	Sequence 13, Appl
28	1074	18.5	1686	4	US-09-355-160D-2	Sequence 2, Appli
29	1034	17.9	1167	3	US-08-857-076-48	Sequence 48, Appl
30	874	15.1	1876	2	US-08-609-049A-28	Sequence 28, Appl
31	874	15.1	1876	3	US-09-170-996-28	Sequence 28, Appl
32	873.5	15.1	1876	2	US-08-609-049A-12	Sequence 12, Appl
33	873.5	15.1	1876	3	US-09-170-996-12	Sequence 12, Appl
34	851.5	14.7	171	3	US-08-609-049A-23	Sequence 23, Appl
35	851.5	14.7	171	3	US-09-170-996-23	Sequence 23, Appl
36	690.5	11.9	803	3	US-09-118-442-2	Sequence 2, Appli
37	690.5	11.9	803	3	US-09-677-064-2	Sequence 2, Appli
38	649.5	11.2	868	2	US-08-162-081B-33	Sequence 33, Appl
39	649.5	11.2	868	2	US-08-780-872-33	Sequence 33, Appl
40	649.5	11.2	868	3	US-09-085-957-33	Sequence 33, Appl
41	499.5	8.6	171	2	US-08-609-049A-22	Sequence 22, Appl
42	499.5	8.6	171	3	US-09-170-996-22	Sequence 22, Appl
43	486.5	8.4	171	2	US-08-609-049A-21	Sequence 21, Appl
44	486.5	8.4	171	3	US-09-170-996-21	Sequence 21, Appl
45	464	8.0	171	3	US-08-609-049A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-916-917-4
; Sequent 4, Application US/08916917
; Patent No. 5855132
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5856132e
US-08-916-917-4

Query Match   98.9%; Score 5726; DB 2; Length 1102;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
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Db    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH 60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
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Db   61 VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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Db  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
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Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
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Db  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAY 720
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Db  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAY 720

Qy  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy  781 QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGHDDLRQ 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGHDDLRQ 840

Qy  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
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Db  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
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Db 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
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Db 1081 TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 2
US-08-972-631-4
; Sequence 4, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/972,631
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-972-631-4

Query Match   98.9%; Score 5726; DB 2; Length 1102;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
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Db    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH 60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
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Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
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Db  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
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Db  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
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                                    COUNTRY: USA
                                    ZIP: 94025
                               COMPUTER READABLE FORM:
                                    MEDIUM TYPE: Floppy disk
                                    COMPUTER: IBM PC compatible
                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                               CURRENT APPLICATION DATA:
                                    APPLICATION NUMBER: US/08/972,629
                                    FILING DATE:
                                    CLASSIFICATION:
                               PRIOR APPLICATION DATA:
                                    APPLICATION NUMBER: US 08/672,211
                                    FILING DATE: 27-JUN-1996
                               ATTORNEY/AGENT INFORMATION:
                                    NAME: Halluin, Albert P.
                                    REGISTRATION NUMBER: 25,277
                                    REFERENCE/DOCKET NUMBER: 8549-0005-999
                               TELECOMMUNICATION INFORMATION:
                                    TELEPHONE: (415)854-3660
                                    TELEFAX: (415)854-3694
                               INFORMATION FOR SEQ ID NO: 4:
                                    SEQUENCE CHARACTERISTICS:
                                    LENGTH: 1102 amino acids
                                    TYPE: amino acid
                                    STRANDEDNESS:
                                    TOPOLOGY: unknown
                                    MOLECULE TYPE: peptide
                               US-08-972-629-4

Query Match             98.9%;  Score 5726;  DB 2;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches 1090;  Conservative 6;  Mismatches 6;  Indels 0;  Gaps 0;

Qy    1  MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTTSQRNTKTPETALLH  60
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Qy   61  VAGHGNVEQMKAQVVLRALETSVSADFYHRLGPDHFLLYQKKGQWYEIYDKYQVVCTLD  120
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Db   61  VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy  121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
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Db  121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy  181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
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Qy  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
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Db  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

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Db  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
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Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY  480
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Db  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY  480

Qy  481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
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Db  481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG 540

Qy  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
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Db  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
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Db  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy  721  LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy  781  QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
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Db  781  QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy  841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
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Db  841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900

Qy  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
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Db  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy  961  FHIDFGHILGNYKSPLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020
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Db  961  FHIDFGHILGNYKSPLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020

Qy 1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
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Db 1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081  TVQFNWFLHLVLGIKQGEKHSA 1102
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Db 1081  TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 3
US-08-972-629-4
; Sequence 4, Application US/08972629
; Patent No. 5859201
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California

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;
;  TELEFAX:  (415) 854-3694
; INFORMATION FOR SEQ ID NO: 4:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH:  1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-972-630-4

Query Match             98.9%;  Score 5726;  DB 2;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches 1090;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;

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Db   61 VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWEIYDKYQVVQTLD  120

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
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Db  121 CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNCVFIVIHRSTTSQIKVSADDT  240
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Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
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Db  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy  301 EEIHLVLDTPPPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
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Db  301 EEIHLVLDTPPPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEVLMNVWLEFSIKI  420
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Db  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEVLMNVWLEFSIKI  420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480
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Qy  481 VLHMWQLSGKEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG  540
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Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLMHFPRYESLKDPKAYPKLFSSVKWGQ  600
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Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLMHFPRYESLKDPKAYPKLFSSVKWGQ  600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
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Db  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy  721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
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Db  721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy  841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy  961 FHIDPGHILGNYKSFIGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 FHIDPGHILGNYKSFIGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021 RHHTNLLILFSMMLMTGNMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 RHHTNLLILFSMMLMTGNMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
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Db 1081 TVQFNWFLHLVLGIKQGEKHPA 1102


RESULT 4
US-08-972-630-4
; Sequence 4, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Pennie & Edmonds
;    STREET: 2730 Sand Hill Road
;    CITY: Menlo Park
;    STATE: California
;    COUNTRY: USA
;    ZIP: 94025
;   COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/972,630
;    FILING DATE:
;    CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/672,211
;    FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;    NAME: Halluin, Albert P.
;    REGISTRATION NUMBER: 25,277
;    REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (415)854-3660
```

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Qy   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
         |||||||||||||||||||| |
Db  1081 TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 5
US-08-672-211-4
; Sequence 4, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/672,211
;   FILING DATE: 27-JUN-1996
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-672-211-4

Query Match   98.9%; Score 5726; DB 2; Length 1102;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy     1 MELENYEQPVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
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Db     1 MELENYEQPVLREDNRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH   60

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
         ||||||||:|||||  |||||||||:||||||:|||||  :||||:|||||||||||||||
Db    61 VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD  120

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy   181 VTPRMAEVAGRDPKLYAMHPWTTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   181 VTPRMAEVAGRDPKLYANHPWTTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy   301 EEIHLVLDTPPDALEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 EEIHLVLDTPPDALEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK   360

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRTSPKPFTEEVLWNVWLEFSIKI   420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRTSPKPFTEEVLWNVWLEFSIKI   420

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY   480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY   480

Qy   481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
         ||||||||||||||||||||||||:|||||:||||||||||||||||||||||||||||||
Db   481 VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG  540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900

Qy   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
         |||||||||||||||||||| |
Db  1081 TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 6
US-09-225-170-4
; Sequence 4, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:

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Qy   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEY  480
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Db   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEY  480

Qy   481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
          ||||||||||||||||||||||||:||||||:|||||||||||||||||||||||||||
Db   481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG  540

Qy   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy   841  DMLILQIIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVDATTIAKIQQSTVGNTG  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  DMLILQIIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVDATTIAKIQQSTVGNTG  900

Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020

Qy  1021  RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA  1102
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Db  1081  TVQFNWFLHLVLGIKQGEKHPA  1102
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RESULT 7
US-08-916-917-14
; Sequence 14, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b

;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/225,170
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/916,917
;   FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Abrams, Samuel B
;   REGISTRATION NUMBER: 30,605
;   REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-493-4935
;   TELEFAX: 650-493-5556
;   TELEX: 66141 PENNIE
US-09-225-170-4
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: No. 6017763e
US-09-225-170-4

Query Match   98.9%; Score 5726; DB 3; Length 1102;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy     1  MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH  60
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Db     1  MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH  60

Qy    61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
          |||||||:||||||:||||||||||:||||:|||||||::||||:|||||||||||||||
Db    61  VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD  120

Qy   121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
          |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy   181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240

Qy   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy   301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy   361  FRVKIRGIDIPVLPRTADLITVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  FRVKIRGIDIPVLPRTADLITVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
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CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/916,917
  FILING DATE: 15-AUG-1997
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/672,211
  FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Abrams, Samuel B
  REGISTRATION NUMBER: 30,605
  REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-493-4935
  TELEFAX: 650-493-5556
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1101 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: No. 5856132e
US-08-916-917-14

Query Match      95.4%;   Score 5523.5;  DB 2;   Length 1101;
Best Local Similarity 95.2%;  Pred. No. 0;
Matches 1049;  Conservative 21;  Mismatches 31;  Indels 1;  Gaps 1;

Qy     1 MELENYEQPVVLREDNRRRRRMKPRSTRAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
           |||||| ||||||||| ||||||||||| ||||||||||||||||||||||  :  ||||||
Db     1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
           |||||||||||||||||||||||:|||||||||| |||||||||||||||||||||||||
Db    60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAPQRQLNALIGYDVTDVSNVHDDELFTRRRL 180
           ||||||  :|||||||:|||| |||| |||:||||: |||||||||||||||||||:|||
Db   120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELFTRRGL 179

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
           ||||||||.|||||||||||||||||||||| |||:|||:||||||||||||||||.|||
Db   180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy   241 PGTIIQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
           ||:|||||||||||||||||||||||:|:|||||||||||||||||||||||||:|||||
Db   240 PGAIIQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy   301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
           ||||.|||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGDHESVFTVSLWDCDRK 359

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
           ||||||||||||||||.|||||||||||:||||||||||||||||||||||||||||||||
Db   360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 419

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
           |||||||||||||||||||||| || :|  | |:|:|:|.||||||||||||||||:|||
Db   420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSEESKGKVRLLYVNLLLIDHRFLLRRGEY 479

Qy   481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGRPTDPPEG 540
           ||||||:|.|||||||||||||||||||||||||||||||||||||||||||:|:||||||
Db   480 VLHMWQISCKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTDPPEG 539

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy   601 QEIVAKTYQLLAXREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLEWFLRSEIAQSRHYQQRFAVILEAY 720
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy   721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
           |||||||||||||||||||:|||||||:||||||||||||||||||||||||||||||: |
Db   720 LRGGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
           :||||||||||||||||.|||||||||||||||||||||||||||||||||||||||||||
Db   780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy   841 DMLLQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 DMLLQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 899

Qy   901 AFKDEVLSHWLKEKCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
           ||||||| ||||||.| :|||||||| |||||||||||||||||||||||||||:|||||
Db   900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFKFQDVCVKAYALAL 1020
           ||||||||||||||||||||||||||||||||||||||||||| ||:|||:|||||||||
Db   960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYALAL 1019

Qy  1021 RHHTNLLIILFSVMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
           |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db  1020 RHHTNLLIILFSVMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
           ||||||||||||||||||||||
Db  1080 TVQFNWFLHLVLGIKQGEKHSA 1101
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```
;   FILING DATE: 13 April 1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pasqualini, Patricia A.
;     REGISTRATION NUMBER: 34,894
;     REFERENCE/DOCKET NUMBER: LUD 5256
;   TELECOMUNICATION INFORMATION:
;     TELEPHONE: (212) 688-9200
;     TELEFAX:   (212) 838-3884
; INFORMATION FOR SEQ ID NO: 37:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1069 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-162-081B-37

Query Match              25.3%;  Score 1465.5;  DB 2;  Length 1069;
Best Local Similarity    33.5%;  Pred. No. 1.6e-133;
Matches   382;  Conservative 204;  Mismatches 405;  Indels 149;  Gaps 39;

Qy   23 MKPRSTAASLSSMELIP---IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQWLRA  78
         : :.:  :  .:  ::    ::::
Db    1 MPPRPSSGELWGIHLMPPRILVBCLLPNGMIVT-------LECLREATLITIKHELFKEA  53

Qy   79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
              :.:                                              -LKVI
Db   54 RKYIPL-----HQLLQDESSYIFVSVTQEAEREFFDETRRLCDLRLFQPF------LKVI 102

Qy  139 QRHAPSEETLAFQRQLNALIGYDTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
Db  103 EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy  193 PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIV------HRSTTSQTIKVSADDTPGTIL 245
Db  162 RAMYVYPPNVESSPELPKHIYNKLDKGQIIVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy  246 QSFFTKMAKKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
         :.:::                  :.::          :::          ::::
Db  222 ABAIRK--KTRSMLLSSEQLKLCVLEYQGKYIIKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy  300 GEBIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFFVSL 354
          :::                                 :::
Db  280 GRMENLML------MAKESLYSQLPM-DCFTMPSYSRSIRISTATPYMNGE----TSTKSL 327

Qy  355 WDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKF 404
          :.:                ::  :
Db  328 WVINSALRIKILCATYVNVNIRDID-------KIYVRTGIYHGGEPLCDNVNTQRVP 377

Qy  405 TEEVLWNVWLEFSKIKIDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV 464
Db  378 CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA-------KEEHCPLAWG 425

Qy  465 NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC 524
Db  426 NINLPFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS 481

Qy  525 HPIALPKHRPTPDPEGDRV----------RAEMPNQLR---KQLEAIIATDPLN 565
Db  482 SVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS 541

Qy  566 PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG 625
Db  542 EITEQEKDFLWSRHYCVTIPBILPKLLLSVKNSRDEVAQMYCL-----VKDWPIKPB 596

Qy  626 LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR 684
Db  597 QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKK 656

Qy  685 GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVIDMLQK 744
Db  657 ALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYIKH-LNRQVEAMEKLIN 714

Qy  745 VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC 801
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Db  417 SESKGKVRLLYYVNLLLIDHRFLLRRGEYVLHMWQISGKGEDQGSFNADKLTSATNPDKE 476
                          ::::::::: ::::::::::  ::::::::::::::::::::::
Qy  512 NSMSISILLDNYCHPIALPKGHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAED 571
        :::::::::::::::::::::: :::::::::::::::::::::::::::::::::::::::::
Db  477 NSMSISILLDNYCHPIALPKGHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAED 536

Qy  572 KELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL 631
        :::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::::::
Db  537 KELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLL 596

Qy  632 DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRI 691
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  597 DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRI 656

Qy  692 GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVIDMLQKVTIDIKS 751
        ::::::::::::::::::::::::::::::::::::::::::::::::: :::::::: :::
Db  657 GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVIEMLQKVTLDIKS 716

Qy  752 LSAEKYDVSSQVISQLKQKLENLQNINLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPL 811
        :::::::::::::::::::::::::::  :::::::::::::::::: :::::::::::::::
Db  717 LSAEKYDVSSQVISQLKQKLENLQNSQLPESFRVPYDPGLKAGALAIEKCKVMASKKKPL 776

Qy  812 WLEFKCADFTALSNETIGIIFKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCIS 871
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db  777 WLEFKCADFTALSNETIGIIFKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCIS 836

Qy  872 TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYS 931
        ::::::::::::::::::::::::::::::::::::::: ::::: : :::::::::::::::
Db  837 TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPTEEKFQAAVERFVYS 896

Qy  932 CAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSPLGINKERVPFVLTPDF 991
        :::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::::
Db  897 CAGYCVATFVLGIGDRHNDNIMITETGNLFHIDFGHILGNYKSPLGINKERVPFVLTPDF 956

Qy  992 LFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYI 1051
        ::::::::::: :::::::: :::::::::::::::::::::::::::::::::::::::::
Db  957 LFVMGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYI 1016

Qy 1052 RDALTVGKSEEDAKKYFLDQIEV 1074
        :::::::: ::::::::::::::
Db 1017 RDALTVGKNEEBDAKKYFLDQIEV 1039
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Best Local Similarity   33.5%;  Pred. No. 1.6e-133;
Matches  382;  Conservative  204;  Mismatches  405;  Indels  149;  Gaps  39;

Qy   23  MKPRSTAASLSSMELIP---IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
             :  : :||: | :     :  | :  |:  ||:|  ::  |: :  :   : |:::  :::
Db    1  MPRPPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLIITKHELFKBA   53

Qy   79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
             | |:|:|  | |     |   :    |:    :|:  :|:||:||:  :  :  | | :|
Db   54  RKYPL-----HQLLQDESSYIFVSVTQEAEREFFDETRRLCDLRLFQPF------LKVI  102

Qy  139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
Db  103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDPRRNILNVCKEAVDLRDLNSPHS  161

Qy  193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL  245
Db  162  RAMYVYPPNVESSPELPKGHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy  246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEVLVGETPIKNFQWVRQCLKN  299
Db  222  AEAIRK-KTRSMLLSSEQLKLCVLEYGKYLKVCGGDEYPLEKYPLSQYKYIRSCIML     279

Qy  300  GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT---IHGKDHESVFTVSL    354
Db  280  GRMPNLML------MAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE---TSTKSL   327

Qy  355  WDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPF   404
Db  328  WVINSALRIKILCATYVNVNIRDID--------KIYVRTGIYHGGEPLCDNVNTQRVP   377

Qy  405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
Db  378  CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCPLAWG  425

Qy  465  NLLLIDHRFLLRHGEYLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC   524
Db  426  NINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEPDWFS  481

Qy  525  HPIALPKGHRPTPDPEGDRV--------------RAEMPNQLR----KQLBAIIATDPLN  565
Db  482  SVVKFPDMSVIEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS   541

Qy  566  PLTAEDKELLWHPRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG  625
Db  542  EITEQEKDFLWSHRHYCVTIPEILPKLLSVKWNSRDEVAQMYCL----VKDWPIKPE    596

Qy  626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEYHDSALARFLLKR   684
Db  597  QAMELLDCNYPDMVRGFAVRCLEKYITDDKLSQYILQVLQVLKYQYLDNLLVRFLLKK    656

Qy  685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK  744
Db  657  ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN  714

Qy  745  VTIDIKSLSAEKYDVSSQVISQLQKLENLQN--LNLPQSFRVPVDPGLKAGALVIEKC   801
Db  715  LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEEC  769

Qy  802  KVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIMESIW   855
Db  770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW  824

Qy  856  ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE   913
Db  825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883

Qy  914  KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK  973
Db  884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGGQLFHIDFGHFLDHKK 942

Qy  974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHTNLLILF   1031
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Db  715  LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEEC  769
Qy  802  KVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIMESIW   855
Db  770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW  824
Qy  856  ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE   913
Db  825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883
Qy  914  KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK  973
Db  884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGGQLFHIDFGHFLDHKK 942
Qy  974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLAIRQHANLFINLF  1031
Db  943  KKFGYKRERVPFVFVLTQDFLLVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF 1002
Qy 1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVVCRDKGWTVQFNWPLHLV 1091
Db 1003  SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI  1062
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Db   943 KKFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF 1002
Qy   1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db   1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062

RESULT 13
US-09-085-957-37
; Sequence 37, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
;   APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;   APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
;   APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
;   APPLICANT: Stefano; Gout, Ivan Tarasovitch
;   TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
;   TITLE OF INVENTION: THEIR PREPARATION AND USE
;   NUMBER OF SEQUENCES: 50
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Felfe & Lynch
;   STREET: 805 Third Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: USA
;   ZIP: 10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/085,957
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/780,872
;   FILING DATE: 09-JAN-1997
;   APPLICATION NUMBER: 08/162,081
;   FILING DATE: February 7, 1994
;   APPLICATION NUMBER: PCT/GB93/00761
;   FILING DATE: 13 April 1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Pasqualini, Patricia A.
;   REGISTRATION NUMBER: 34,894
;   REFERENCE/DOCKET NUMBER: LUD 5256
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 37:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1069 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-085-957-37

  Query Match   25.3%; Score 1465.5; DB 3; Length 1069;
  Best Local Similarity   33.5%; Pred. No. 1.6e-133;
  Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

Qy   23 MKPRSTAASLSSMELIP-----IEFVLPTSQRNTKTPETALLHVACHGNVEQMKAQVWLRA 78
                :|| :| : :::| || || :: :| | :| :||: ::|
Db   1 MPPRPSSGELWGIHLMPPRILVECLLPNGMVT------LECLREATLITIKHELFKEA 53

Qy   79 LETSVSSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
                 :: : : ||: ||| :| | : ::| :| :|| :| |: ||
Db   54 RKYPL-----HQLLQDESSYIFVSVTQEABREEFFDETRRLCDLRLFQPF-----LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------- 192
               :| :: | :|| | : ::| :: :::|| :| :::|
Db   103 EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

RESULT 14
US-08-162-081B-36
; Sequence 36, Application US/08162081B
; Patent No. 582492
; GENERAL INFORMATION:
;   APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;   APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
;   APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,

Qy   193 PKLYAMHPWTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
                 |::|:| | :|::::| : |:: |::|::|:| | ::
Db   162 RAMYVYPPNVESSPELPKGIYNKLDKGQIIVVWIVSPNNDKQXYTLKINHDCVPEQVI 221

Qy   246 QSFFTKMAKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
               ::: |::|:   ::: :: ||:| :::|:|:::|
Db   222 ABAIRK--KTRSMLLSSEQLKLCVLEYQGKYLKVCGCDEYFLEKYPLSQYYIRSCIML 279

Qy   300 GEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLT----IHGKDHESVFTVSL 354
               :| :   :|:| |:|:| | | | | |: ||| ||:| :|:|
Db   280 GRMPNLML------MAKESLYSQLPM-DCFTMPSYSRRISTATPYMNGE----TSTKSL 327

Qy   355 WDCDRKFRVK--------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPF 404
               | :| : | :| :::| :: :||| :|| |:| ::| |::|::|
Db   328 WVINSALRIKILCATYVNVNIRDID------KIYVRGIYHGGEPLCDNVNTQRVP 377

Qy   405 TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV 464
               |::| ::|::|| |:| ||| | :| || |:|| : ::|:: | ::| ::|||| :
Db   378 CSNPRWNEWLNYDIYIPDLPRAAARLCLSI-C----SVKGRKGA------KEEHCPLAWG 425

Qy   465 NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC 524
               ::|::| :: :||||:|: :::: || : ||: | :|:: :|||:||:| :||:|:
Db   426 NINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS 481

Qy   525 HPIALPKHRPTPDPEGDRV----------RAEMPNQLR---KQLEAIIATDPLN 565
               | :| | | |:| | |: ||:| :| : :: :|
Db   482 SVVKFPDMSVIEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS 541

Qy   566 PLTAEDKELLWHFRYESLKDPAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG 625
               ||| ||:||||||:|||||||:|||||||| :| :||| | | ::::| |::|| |
Db   542 EITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL----VKDWPPIKPE 596

Qy   626 LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR 684
               || :|| :| | || | :| ||| :::| :| |:: :: ||:|||:|||
Db   597 QAMELLDCNYPDMVRGFAVRCLEKVLTDDKLSQYILQLVQLVKYEQYLDNLLVRFLLKK 656

Qy   685 GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVLEAYLRGCGTAMLHDFTQQVQVIDMLQK 744
               || ||||||||||:|| ::|:||| ||||| ||| | || |||||:|||::|:||:|
Db   657 ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN 714

Qy   745 VTIDIKSLSAEKYDVSSQVISOLQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC 801
               :| || : | || ||: ::::||:|:   :|||: |: | |||:||| :|||
Db   715 LT-DI--LKQEKKDETQRV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRIEEC 769

Qy   802 KVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRMESIW 855
               |: |::||| | | | :| | | :|:| :| || ||||| |||:|:|:|
Db   770 RIMSSAKRPLWLNWE--NPDIMEBLLFQNNE--IIFKNGDDLRQDMLTLQIIRIMENIW 824

Qy   856 ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE 913
               :| :||: |||| |:| ||| :|| :|::|| : :|||:|||: |::|::|:|
Db   825 QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD 883

Qy   914 KCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISBTGNLFHIDFGHILGNYK 973
               | ||:|:   :|| |||||||||| |||||||:||| |::|:|| ||||||| |:|
Db   884 KNK-GEIYDAAIDLFTRSCAGYCVATFLGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK 942

Qy   974 SFLGINKERVPFVLTPDFLFVWGTSGKK--TSLHFQKFQDVCVKAYLALRHTNLLILLF 1031
               | |:|:|||||| || ||::|::|:| ||: |||: ||||| :|| ||:|:||
Db   943 KKFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF 1002

Qy   1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
               |||| |||:||| ||| ||| | : ::| | | | |:| | |||| : |: |
Db   1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062

APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Felfe & Lynch
    STREET: 805 Third Avenue
    CITY: New York
    STATE: New York
    COUNTRY: USA
    ZIP: 10022
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
    COMPUTER: IBM PS/2
    OPERATING SYSTEM: PC-DOS
    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/162,081B
    FILING DATE: February 7, 1994
    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/GB93/00761
    FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
    NAME: Pasqualini, Patricia A.
    REGISTRATION NUMBER: 34,894
    REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212) 688-9200
    TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
    LENGTH: 1080 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-08-162-081B-36

Query Match   25.3%;   Score 1463.5; DB 2;   Length 1080;
Best Local Similarity 33.3%;   Pred. No. 2.5e-133;
Matches 386; Conservative 206; Mismatches 406; Indels 161; Gaps 41;

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Qy    23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA  78
             || :|| :||    | ||:|||:|| ||:|: |::    :||
Db     1 MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA  53

Qy    79 LETSVSADFVHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
            || :|| ||   | :||:| |::||||||: :: ::||||
Db    54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRLVTPRMABVAGRD------- 192
             || :::: |      ::|: |:   || ::| ||:
Db   103 EPVGNREEKI-LNRBIGFAIGMPVCBFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193 PKLIYAMHPWTSKP-LPEYLLKKITNNCVFIVI-------HRSTTSQTIKVSADDTPGTIL 245
             ||::| ||: ||| :|| ||:||:|      || ::|: :||||
Db   162 RAMYVVPPHVESSPELPKHIYNKLDRGQIIVVIWVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246 QSFFTKMAKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWRQCLKN 299
             :| :|: :||| | :||    || ||||||:|||||||:: ||||
Db   222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy   300 GEEIHLVLDTPPDPALDEVRKE-----EWPLVDDCTGVTGYHEQLT-----IHGKDHESVF 350
             :|||:|:||: || ||||||:   :|: ||:: :::  :||:
Db   280 GRM--------FNLKMWAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS 323

Qy   351 TVSLWDCCDRKFRVK-------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS 400
            | ||:|||:::|||        :|::|:|    ::||| ||||:|||||::| ||
Db   324 TKSLWVINRALRIKILCATYVNLNIRDID--------KIYVRTGIYHGGEPLCDNVNT 373

Qy   401 PKPFTEEVLNNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKRTSAEMPSPESKGKAQL 460
             |:  ::|:|:|    :: ::|: |    : |  ::|::| ::
Db   374 QRVPCSNPRNNEWLNVDIYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCP 421
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Qy   461 LYYVNLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSAATNPDKENSMSISILL 520
             |:::||| |: :|::  :: | :   ::
Db   422 LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477

Qy   521 DNYCHPIALPKHRPTPDPEGDRV-------------------RAEMPNQLR----KQLEAIIAT 561
            |:| :  :::|| |::             ||          ::
Db   478 DWFSSVVKFPDMSVIEBIANWSVREAGFSYSHAGLSNRLARDNELRENDKSQLKAISTR 537

Qy   562 DPLNPLTAEDKELLWHFRYESLKDPKAYPKLPSSVKWGQQEIVAKYQLLAKREVWDQSA 621
             ||| ||||:|||::|||||:||:|:   |: ::|:|||||:||||
Db   538 DPLSEITEQEKDFLWSRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy   622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LBDDDVLHYLLQLVQAVKFEPYHDSALARF 680
             :::|||:|:  :|  :: : :|::| ||||  | |:
Db   593 IKPEQAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF 652

Qy   681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFPAVILEAYLRGCGTAMLHDFTQQVQID 740
             ||| ::|:||||:| |:|| :|| || : :::|| |||| |:|| | ||:||:|||||
Db   653 LLKKALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME 710

Qy   741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALV 797
             :||:|||::|:     |:|: :: ::| :||   :|:| |  : :|  :|||:||||
Db   711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGGNLR 765

Qy   798 IEBCKVMASKKKPLWLBFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIM 851
             ||  |:|:::|| | |:|     || |:|||||| :|||::||||||:| |::|||||
Db   766 LKECRIMSSAKRPLWLNWB---NPDIMSLLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy   852 ESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
             ::||| |||: |||||| |||||:|||||:|||:: ||||| ||||||
Db   821 ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879

Qy   910 WLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
             ||:|| ||:|||:|:||| ||||| |||||| ||||||:|||:|| |||||||||:|||
Db   880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFL 938

Qy   970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYIALRHHTNLL 1027
             ||:|| |::|:||||||:|  :|::|||:|   ||||:|||::|||:|||::|||:|||
Db   939 DHKKKKFGVKRERVPFVJTQDFLVISKGAQECTKTREFERFQEMCKKAYLAIRQHANLF 998

Qy  1028 IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087
             |:|||::||||||||| |  |::|||   ||| |:   |:::|  :|| :|||||||||
Db   999 INLFSMMLGSGMPELQSFDDIAVIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy  1088 LHLV----LGIKQGEKHSA 1102
             |:|:    ::||:||:::|
Db  1059 FHTIKQHALNXKTEKMKA 1077
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;  SOFTWARE: Wordperfect
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/780,872
;    FILING DATE: 09-JAN-1997
;    CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: 08/162,081
;    FILING DATE: February 7, 1994
;    APPLICATION NUMBER: PCT/GB93/00761
;    FILING DATE: 13 April 1993
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Pasqualini, Patricia A.
;    REGISTRATION NUMBER: 34,894
;    REFERENCE/DOCKET NUMBER: LUD 5256
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (212) 688-9200
;    TELEFAX: (212) 838-3884
;  INFORMATION FOR SEQ ID NO: 36:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 1080 amino acids
;    TYPE: amino acid
;    STRANDEDNESS: single
;    TOPOLOGY: linear
US-08-780-872-36

Query Match       25.3%;   Score 1463.5;   DB 2;   Length 1080;
Best Local Similarity   33.3%;   Pred. No. 2.5e-133;
Matches  386;   Conservative 206;   Mismatches 406;   Indels 161;   Gaps  41;

Qy  23 MKPRSTAASLSSMELIP----IBFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
        ||     :    |||   :::  ||
Db   1 MPPRPSSGELWGIHHLMPPRIIVECLLPNGMIVT------LECLREATLVTIIKHELFKEA 53

Qy  79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
                 :|:   |||:
Db  54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPP------LKVI 102

Qy 139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
Db 103 EPVGNREEKI-LNRBIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy 193 PKLYAVHPWVTSKP-LPEYLLKKITNNCVFVI------HRSTTSQTIKVSADDTPGTIL 245
                  : |   |      :          :  ::
Db 162 RAMYVYPFHVSSSPELJPKHIVNKLDRGQIIVWIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy 246 QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKQN 299
Db 222 AEAIRK--KTRSMLLSSEQLKLCVLBYQGKYILKVCGCDEYFLEKYPLSQXKYIRSCIML 279

Qy 300 GEEIHLVLDTPDPALDEVRKE----EWPLVDDCTGVTGYHEQLI------IHGKDHESVF 350
                           :|:
Db 280 GRM--------PNLKMMAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS 323

Qy 351 TVSLWDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTS 400
                ||||    |:   :
Db 324 TKSLWVINRALRIKILCATYVNLIRDID---------KIYVRTGIYHGGEPLCDNVNT 373

Qy 401 PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
                                       : :|:
Db 374 QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C------SVKGRKGA------KEEHCP 421

Qy 461 LYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520
                    :  |::|
Db 422 LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477

Qy 521 DNYCHPIALPKHRPTPDPEGDRV----------RAEMPNQLR----KQLEAIIAT 561
             : |::|
Db 478 DWFSSVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR 537

Qy 562 DPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVNDQSA 621
        |||:: :|  ::  |||:    :||  ::     :::  ||
Db 538 DPLSEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy 622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF 680
         :         |||:     |||:      |:|  ||:|||:|||:||::|:|||
Db 593 IKPEQAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF 652

Qy 681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGGTAMLHDFTQQVQVID 740
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Db 653 LLKKALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME 710

Qy 741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALV 797
         ||:|| |:   ::|  :    ::| |  :|  |:|    ::|::   |||:||:
Db 711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765

Qy 798 IEKCKVNASKKKPLWLEPKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRIM 851
        :|   ::::|:|||||:       |   :   ::||:||:|:|||||||||| |||:|||
Db 766 LKECRIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy 852 ESTWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
        |  |: :.||| :||||| ||| :||:|:||:.:|::  : |  ::  :   |::||
Db 821 ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879

Qy 910 WLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
        ||::|    ::|   | ||| ||||||||||:||||||||:|||: : |:|||||:||:|
Db 880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFLLGIGDRHNSNIMVKDDGQLFHIDPGHFL 938

Qy 970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL 1027
            :.:|| ||:||||||| |||::|.: :|:  || ||:| |:::|||||||:|:|: |:
Db 939 DHKKCKFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLF 998

Qy 1028 IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087
         |:||||| ..|||:|  :|:|||::|:| |:|:: |:|||::|||  :::|||| ::||
Db  999 INLFSMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy 1088 LHLV---LGIKQQEKHSA 1102
              : ||::|||:|
Db 1059 FHTIKQHALNXKITEKMKA 1077

Search completed: February 15, 2004, 02:08:29
Job time : 35 secs
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2004, 02:05:12 ; Search time 80 Seconds
                                        (without alignments)
                                        2884.241 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   Published_Applications_AA:*
   1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
   2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
   3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
   4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
   5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
   6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
   7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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   9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
  10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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  18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	5790	100.0	1102	11	US-09-974-573-1	Sequence 1, Appli
2	5538	95.6	1103	12	US-10-334-143-4	Sequence 4, Appli
3	5523.5	95.4	1110	12	US-10-101-235A-4	Sequence 4, Appli
4	5298.5	91.5	1076	12	US-10-101-235A-6	Sequence 6, Appli
5	1460.5	25.2	1068	12	US-10-101-235A-8	Sequence 8, Appli
6	1351.5	23.3	1044	12	US-10-337-192-2	Sequence 2, Appli
7	1351.5	23.3	1044	14	US-10-027-591-2	Sequence 2, Appli
8	1349.5	23.3	1044	15	US-10-162-160-1	Sequence 1, Appli
9	1074	18.5	1686	14	US-10-092-219-2	Sequence 2, Appli
10	1034	17.9	1167	9	US-09-205-658-48	Sequence 48, Appli
11	1034	17.9	1167	9	US-09-844-353A-48	Sequence 48, Appl
12	1034	17.9	1167	12	US-09-963-693-48	Sequence 48, Appli
13	980	16.9	204	12	US-10-101-235A-2	Sequence 2, Appli
14	979	16.9	195	12	US-10-101-235A-9	Sequence 9, Appli
15	698.5	12.1	887	10	US-09-771-161A-192	Sequence 192, App
16	698.5	12.1	887	10	US-09-771-161A-193	Sequence 193, App
17	690.5	11.9	803	10	US-09-921-232-2	Sequence 2, Appli
18	690.5	11.9	803	10	US-09-921-330-2	Sequence 2, Appli
19	690.5	11.9	803	10	US-09-921-329-2	Sequence 2, Appli
20	679.5	11.7	928	12	US-10-369-493-3211	Sequence 3211, Ap
21	649.5	11.2	875	12	US-10-369-493-1795	Sequence 1795, Ap
22	646	11.2	873	12	US-10-369-493-5060	Sequence 5060, Ap
23	562.5	9.7	756	10	US-09-771-161A-101	Sequence 101, App
24	380	6.6	1900	10	US-09-801-368-390	Sequence 390, App
25	351.5	6.1	150	9	US-09-205-658-17	Sequence 17, Appl
26	351.5	6.1	150	12	US-09-844-353A-17	Sequence 17, Appl
27	351.5	6.1	150	12	US-09-963-693-17	Sequence 17, Appl
28	345.5	6.0	816	12	US-10-205-219-3	Sequence 3, Appl
29	321	5.5	817	10	US-09-976-165-28	Sequence 28, Appl
30	321	5.5	817	12	US-10-342-276-28	Sequence 28, Appl
31	321	5.5	829	10	US-09-976-165-31	Sequence 31, Appl
32	321	5.5	829	12	US-10-342-276-31	Sequence 31, Appl
33	282	4.9	508	10	US-09-771-161A-102	Sequence 102, App
34	277	4.8	1066	12	US-10-369-493-1948	Sequence 1948, Ap
35	274.5	4.7	604	12	US-10-369-493-6700	Sequence 6700, Ap
36	272	4.7	997	12	US-10-369-493-3593	Sequence 3593, Ap
37	255.5	4.4	113	9	US-09-205-658-18	Sequence 18, Appl
38	255.5	4.4	113	12	US-09-844-353A-18	Sequence 18, Appl
39	255.5	4.4	113	12	US-09-963-693-18	Sequence 18, Appl
40	252	4.4	51	9	US-09-86-761-48478	Sequence 48478, A
41	248	4.0	925	12	US-10-369-493-2281	Sequence 2281, Ap
42	232	4.0	4128	12	US-10-205-194-1	Sequence 1, Appli
43	215.5	3.7	1973	12	US-10-369-493-2380	Sequence 2380, Ap
44	215.5	3.7	2470	12	US-10-369-493-22191	Sequence 22191, A
45	210.5	3.6	2368	12	US-10-369-493-1468	Sequence 1468, Ap

ALIGNMENTS

RESULT 1
US-09-974-573-1
; Sequence 1, Application US/09974573
; Publication No. US2003002344A1
; GENERAL INFORMATION:
;   APPLICANT: Williams, Roger
;   APPLICANT: Ried, Christian
;   APPLICANT: Walker, Edward H
;   APPLICANT: Stephens, Len
;   TITLE OF INVENTION: PHOSPHOINOSITIDE 3-KINASES
;   FILE REFERENCE: ONYX1048-US
;   CURRENT APPLICATION NUMBER: US/09/974,573
;   CURRENT FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: US 60/242,801
;   PRIOR FILING DATE: 2000-10-23
;   NUMBER OF SEQ ID NOS: 1
;   SOFTWARE: PatentIn version 3.1
;
;   SEQ ID NO 1
;   LENGTH: 1102
;   TYPE: PRT
;   ORGANISM: Porcine PI3K
US-09-974-573-1

Query Match   100.0%; Score 5790; DB 11; Length 1102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MELENYEQPVVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MELENYEQPVVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLYQKKGQWYEIYDKYQVVQTLD 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLYQKKGQWYEIYDKYQVVQTLD 120

Qy 121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQLNALIGYDVTDVSNVHDDELEFTRRRL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CLRIRWKVLHRSPGQIHVVQRHAPSEETLAFQLNALIGYDVTDVSNVHDDELEFTRRRL 180

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;  TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
;  TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
;  FILE REFERENCE: 038602/1543
;  CURRENT APPLICATION NUMBER: US/10/334,143
;  CURRENT FILING DATE: 2002-12-31
;  PRIOR APPLICATION NUMBER: 60/343,169
;  PRIOR FILING DATE: 2001-12-31
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 4
;  LENGTH: 1103
;  TYPE: PRT
;  ORGANISM: Homo sapiens

US-10-334-143-4

Query Match             95.6%;   Score 5538;   DB 12;   Length 1103;
Best Local Similarity   95.3%;   Pred. No. 0;
Matches 1050;   Conservative   20;   Mismatches   32;   Indels   0;   Gaps   0;

Qy    1  MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEPVLPTSQRNTKTPETALLH   60
         |||||||||||||||||||||||||||||||||||:|||||||||||||||:|||||||
Db    2  MELENYKQPVVLREDNCRRRRRMKPRSAAASLSSMELIPIEFVLPTSQRKCKSPETALLH   61

Qy   61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
         |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db   62  VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD  121

Qy  121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
         |||||:|||||||||:||||||||||:::::||||||||||||||||||||||||||||
Db  122  CLRYWKATHRSPGQIHLVQRHPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL  181

Qy  181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
         |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db  182  VTPRMAEVASRDPKLYAMHPWTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT  241

Qy  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
         |||||||||||||||||||||||||||::|||||||||||||||||||||||||||||||
Db  242  PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG  301

Qy  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  302  EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  361

Qy  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
         |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db  362  FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  421

Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY  480
         ||||||||||||||||||:|||||||||:|||:|||||||||||||||||||||||||||
Db  422  KDLPKGALLNLQIYCGKAPALSSKASARSPSSSKGKVQLLYVNLLLIDHRFLLRRGEY  481

Qy  481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTDPDEG  540
         ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  482  VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTDPDEG  541

Qy  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  542  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ  601

Qy  601  QEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  602  QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  661

Qy  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  662  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  721

Qy  721  LRGCGTAMLHDFTCQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  722  LRGCGTAMLHDFTCQVVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP  781

Qy  781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   782  ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  841
          ||:||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Qy   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   842  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG   901

Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          ||||||||:|||||:|||||||||||||||||||||||||||||||||||||||:||||
Db   902  AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL  961

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHPQKFQDVCVKAYLAL  1020
          |||||||||||||||||||||||||||||||||||||||||||:|:|||||:||||||||
Db   962  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL  1021

Qy  1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW   1080
          ||||||||||||||||||||||||||||||||||||||:|:||||||||||||||||||
Db  1022  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEBDAKKYFLDQIEVCRDKGW   1081

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA  1102
          ||||||||||||||||||||||
Db  1082  TVQFNWFLHLVLGIKQGEKHSA  1103
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RESULT 3
US-10-101-235A-4
; Sequence 4, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.
;   APPLICANT: Caron, Marc G.
;   TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
;   FILE REFERENCE: 033072-064
;   CURRENT APPLICATION NUMBER: US/10/101,235A
;   CURRENT FILING DATE: 2002-03-19
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 1110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-101-235A-4

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  Query Match        95.4%;   Score 5523.5;   DB 12;   Length 1110;
  Best Local Similarity  95.2%;   Pred. No. 0;
  Matches 1049;  Conservative 21;  Mismatches 31;  Indels 1;  Gaps  1;

Qy     1  MELENYEQPVLREDNRRRRRMKPRSTRAASLSSMELIPIEFVLPTSQRNTKIPETALLH    60
          |||||:|:|||||||:|||||||||||:|||||||||||||||||||||:|:|||||||
Db     1  MELENYKQPVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH    59

Qy    61  VAGHNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
          ||||||||||||||||||||||||||||||||||:|||||||||||||:|||||||||
Db    60  VAGHNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD  119

Qy   121  CLRYWKVLHRSPGQIHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
          |||||:||:|||||||||||:||||:||||||:||:|||||||||||||||||||||||
Db   120  CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL  179

Qy   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKTTNNCVFIVIHRSTTSQTIKVSADDT  240
          ||||||||:||||||||||||||||||||||||:|||||:||||||||||||||||:||
Db   180  VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT  239

Qy   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
          ||:||||||||||||||||||||||||:||||||||||||||||||||||||||:|||||
Db   240  PGAIIQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG  299

Qy   301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK  360
          ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300  EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK  359
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```
Qy   361  FRVKIRGIDIPVLPRTADLTVPEAANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEPSIKI  420
          |||||||||||||||:|||||||||||:||:|||||||||||||||||||||||||||||
Db   360  FRVKIRGIDIPVLPRNTDLTVPEAANIQHGGQVLCQRRTSPKPFTEEVLWNVWLEPSIKI  419

Qy   421  KDLPKGALLNLQIYCGKAPALGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY   480
          |||||||||||||||||||||:|:||:||:||:||:||:::|||||||||||||||:|||
Db   420  KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY  479

Qy   481  VLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
          |||||:||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   480  VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG  539

Qy   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
          |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   540  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ  599

Qy   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
          |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db   600  QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  659

Qy   661  LQIVQAVKFEPYHDSALARFLLKRGLNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAY  720
          ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660  LQLVQAVKFEPYHDSALARFLLKRGLNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAY  719

Qy   721  LRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSAEKYDVSSQVISLQKQLENLQNLNLP  780
          |||||||||||||||||:|::|||||:||||||||||||||||||||||||||||||:||
Db   720  LRGCGTAMLHDFTQQVVIEMLQKVTLDIKSLSAEKYDVSSQVISLQKQLENLQNSQLP   779

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
          :||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db   780  ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  839

Qy   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG   899

Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          |||||||:||||||:|||||||||||||||||||||||||||||||||||||||:||||
Db   900  AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL  959

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHPQKFQDVCVKAYLAL  1020
          |||||||||||||||||||||||||||||||||||||||||||:|:|||||:||||||||
Db   960  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL  1019

Qy  1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW   1080
          ||||||||||||||||||||||||||||||||||||||:|:||||||||||||||||||
Db  1020  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEBDAKKYFLDQIEVCRDKGW   1079

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA  1102
          ||||||||||||||||||||||
Db  1080  TVQFNWFLHLVLGIKQGEKHSA  1101
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RESULT 4
US-10-101-235A-6
; Sequence 6, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.
;   APPLICANT: Caron, Marc G.
;   TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
;   FILE REFERENCE: 033072-064
;   CURRENT APPLICATION NUMBER: US/10/101,235A
;   CURRENT FILING DATE: 2002-03-19
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1076
;   TYPE: PRT
;   ORGANISM: Homo sapiens

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Qy  652 EDDDVLHYLLQLVQAVKFEPYHDSALARFLLKGLRNKRIGHFLFWFLRSEIAQSRHYQQ 711
            ::::  |||: || |.|::||| :::||:|||||||||||| |::|||||
Db  604 TDDELFQYILQLQVLKYESYLDCELTKFLLDRALANKRIGHFLFWHLRSEM----HVPS 659

Qy  712 ---RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLK 768
           |||::||||| |||  :::::::  : :: |:||:|  ||:
Db  660 VALRFGLILEAYCRG-STHHMKVLMKQGEALSKL-KALNDFVLXLSSQKTP--------K 708

Qy  769 QKLENLQNLNLPQS---------RRVPYDPGLKAGALVIEKCKVMASKKPLWLBFKCADP 820
         ::: : :.|:|    :: :: ||
Db  709 PQTKELMHICMRQEAYLEALSHLQSPLDPSTLLAEVCVEQCTFMDSKMKPLWIMY--SNE 766

Qy  821 TALSNETIGIIFKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIE 880
          | ||:.|||||:|||||||||:|:|::::: |  |||:|  |||| ::|||: |:||
Db  767 EAGSGGSVGIIFKNGDDLRQDMLTLQMQLMDVLMKQEGLDLRMTPYGCLPTGDRTGLIE 826

Qy  881 IVKDATTIAKIQ-QSTVGNTGAFKDBVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVA 938
          :: ||:|| ||  .: ::.|  :|| :|.||| |: |   ||| :|||| |||||||
Db  827 VVLRSDTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIEEFTLSCAGYCVA 885

Qy  939 TFVLIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTS 998
          |:|||||||.|||||  :|.|||||||||||| |: |||.||||| ||.||| ||.
Db  886 TYVLIGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRERVPFILTYDFVHVIQQG 945

Qy  999 GKKTSLSHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVG 1058
          |  .|| ||.::  ||: | | ||| .||: :|::: : |.| ||::|||||:||:|: |
Db  946 KTNNSEKFERFRGYCERAVTILRRHGLLFLHLFALMRAAGLPELSCCSKDIQYIKDSLALG 1005

Qy 1059 KSEBDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
          |:| : ||:| ::.| :: | ||| ||| |:.
Db 1006 KTEEBALKHFRVKFNEALRESWKTKVNWLAHNV 1038
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RESULT 7
US-10-027-591-2
; Sequence 2, Application US/10027591
; Publication No. US2002016101014A1
; GENERAL INFORMATION:
; APPLICANT: SADHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Human p110delta protein
US-10-027-591-2

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Query Match     23.3%;  Score 1351.5; DB 14; Length 1044;
Best Local Similarity     32.5%;  Pred. No. 1.7e-113;
Matches   362;  Conservative  197;  Mismatches 401;  Indels  153;  Gaps   40;

Qy   38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRL-GPD 94
          ::::||::::|   :: .||||   |||| :::.| :::|||:||::|.||||:  |||
Db   20 VVVDFLLPTG--------VYLNFPVSRNANLSTIKQLLWHRAQYEPL---FHMLSGPE 66

Qy   95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
          ||:: |:::. ::::||| : : .|  ||| :::
Db   67 AYVFTCINQTAEQQELEDEQR-RLCDVQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy  154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPL---- 207
          : |:||  :|.|:|:|||||||||||||||||||||||||||||||||:  |||
Db  117 ISLLIGKGLHEFDSLCDPEVNDFRAKMC--QFCEEAAARRQQLGWEAWLQYSFPLQLEPS 174

Qy  208 -----PEYILLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSL 258
              ||: :::: .:: .: : |||||||||||||||||||||||||||||  ||||
Db  175 -RLPNRALLVNKFEGSEESFTFQVSTKDVPLAIMACALRKKATVFRQPL 232

Qy  259 MDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVL------------- 307
          :|:|:: ::|.|:| |||||||||:||:|.|:  ::|| :.||:||:|
Db  233 VEQPE----DYTLQVNGRHEYLYGNYPLCQFQYICSCLHSGLTPHLTMVHSSSILAMRD 287

Qy  308 -DTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWMDCDRKFRVK-I 365
           :|| | ::::: |:  |   |:||||:|||::|||  :|||.|||||:  |:||::|
Db  288 EQSNPAPQVQKPRAKPPP-----------------TPAKKPSS---VSLWSLEQPFRIELI 328

Qy  366 RGIDIPVLPRTAD--LTVFVEANIQYGQGVLCQRRTSPK-PFTEEVLMNVWLEFSIKIKD 422
          :|: .|:|   :  ||| ||| :|:||  | |:|  |   ||:||:| ||||:||: |
Db  329 QGSKV-----NADERMKLVVQAGLFHGNEMLCKITVSSSEVSVCSEPVWKQRLEFDINICD 383

Qy  423 LPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYL 482
          || .|:| :: |   :  : :::|  :||  || |||:::::|:| ||  | :|| |
Db  384 LPRMARLCFALYA----VIEKAKKARSTKKKSKSKADCPIAWANLMLFDYKDQLKTGERCL 439

Qy  483 HMWQLSGKGBDQGSFNADKLTSATNPDKENSMSISILLDNYC-HPIALP---------KH 532
          :||  | : : | :::| |   ||: |: : |   ||:::: ||: |:        ||
Db  440 YMW--PSVPDEKGELLNPTGVRSNNTDSAAALLICLPEVAPHFVYYPALEKILELGH 497

Qy  533 RPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPK 591
          ||||||:||||||:|||||||||:|::::|:|||||||||:| |:|||||||| ||||||
Db  498 ------SECVHVTEEEQL--QLREILERRGSGELYEHEKDLVWKLRHEVQEHFPEALAR 548

Qy  592 LFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESL 651
          : :::||: |::: :  :| :  | ||: ||: ||::|||  ::||| ||| |:|  :|
Db  549 LLLIVTKWNKHEDVAQMLYLLCS---WPE--LPVLSALELLDFSFPDCHVGSFAIKSLRKL 603
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RESULT 8
US-10-162-160-1
; Sequence 1, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
; APPLICANT: Van Haesebroeck, Bart
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. US20030099627Alel Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; PRIOR FILING DATE: 1996-06-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-160-1

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Query Match     23.3%;  Score 1349.5; DB 15; Length 1044;
Best Local Similarity     32.5%;  Pred. No. 2.6e-113;
Matches   362;  Conservative 197;  Mismatches 401;  Indels  153;  Gaps   40;

Qy   38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRL-GPD 94
          ::::||::::|   :: .||||   |||| :::.| :::|||:||::|.||||:  |||
Db   20 VVVDFLLPTG--------VYLNFPVSRNANLSTIKQLLWHRAQYEPL---FHMLSGPE 66

Qy   95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
          ||:: |:::. ::::||| : : .|  ||| :::
Db   67 AYVFTCINQTAEQQELEDEQR-RLCDVQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy  154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPL---- 207
          : |:||  :|.|:|:|||||||||||||||||||||||||||||||||:  |||
Db  117 ISLLIGKGLHEFDSLCDPEVNDFRAKMC--QFCEEAAARRQQLGWEAWLQYSFPLQLEPS 174

Qy  208 -----PEYILLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSL 258
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; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-2

Query Match        18.5%;    Score 1074;  DB 14;  Length 1686;
Best Local Similarity  28.9%;  Pred. No. 8.3e-88;
Matches  309;  Conservative 178;  Mismatches 343;  Indels 238;  Gaps 32;

Qy   194  KLYAMHPWTTSKPLPEYLLKKIT--NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT  250
          :    : :::       : :     ||||   |   |  : |   ||:  :  :
Db   390  KLKTKFPYINHRTNPGYLLSPVTAQRNIC------GENASVKVSI-DIEGRQLPVTFT  440

Qy   251  ------KWAKKKSLMDIPESQNERD--FVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
                 : :   ::     :     ||| :|    :||
Db   441  CDVSSTVEIIIMQALCWVHDDLNQVDVGSYVLKVCGQEEVLQNNHCLGSHEHIQNCRKWD 500

Qy   301  EEIHLVL-------------DTPPDPALDEVRKEEWPLVDDCTG------VT  333
          ::                     :  :
Db   501  TEIRIQLLTFSAMCQNLARTAEDDETPVD------LNKHLYQIEKPCKEAMTRHPVEELLD 555

Qy   334  GYHEQ------LTIHGKDH------ESVFTVSLWDCDRKFPRVKIRGIDIPVL  373
          ::                    ::
Db   556  SYHNQVELALQIENQHRAVDQVIKAVRKICSALDGVETLAITESVKKLK--RAVNLP-R  611

Qy   374  PRTADLTVFV-------EANIQYGQQVLCQRRT----------SP-----  401
          |   :  :
Db   612  SKTADVTSLFGGEDTSRSSTRGSLNPENPVQVSINQLTAAIYDLLRLHANSGRSPTDCAQ 671

Qy   402  -----------------------------------------------  401
Db   672  SSKSVKEAWTTEQLQFTIFAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGT  731

Qy   402  -KPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKA  458
Db   732  YKNFFYLIKWDELIIFPIQISQLPLESVLHLTLFGILNQSSGGSSPDSNKQRKGPEALGK- 790

Qy   459  QLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISI  518
Db   791  -----VSLPLCDFRRFLTCGTKLLYLWTSS---------------HTNSVPGTV  824

Qy   519  LLDNY-CHPIALPKGHRPTP-----------DPEGDRVRAE------MPNQLRKQLEAIIATDPL 564
Db   825  TKKGYVWERIVLQVDFPSPAFDIIYTTPQVDRSIIQQHNLETLENDIKGKLLDILHKDSS 884

Qy   565  NPLTAEDKELLWHFRYESLKDPKAYPKLFSSV---KWGQQEIVAKTYQLLAKREVWDQSA 621
Db   885  LGLSKEDKAFLWEKRYYCFKHPNCLPKILASAPNWKWGN--LAKTVSLLHQ---W-PA  936

Qy   622  LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFL 681
Db   937  LYPLIALELLDSKFAQQVRSLAVTWEAISDDELTDLLPQFVQALKYEIYLNSSLVQFL  996

Qy   682  LKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQIDM 741
Db   997  LSRALGNIQIAHNLYWLLKDAL-HDVQFSTRYEHVLGALLSVGGKRLREELLKQTKLVQL 1055

Qy   742  LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKC 801
Db  1056  LGGVAEKVRQASGS----ARQVV-LQRSMERVQSFFQKNKCRLPLKPSLVAKELNIKSC 1109

Qy   802  KVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWETESLD 861
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Db   175  AQTWGPGTL--RLPNRALLVNVKFEGSBESFTFQVSTKDVPLALMACALRKKATVFRQPL 232
Qy   259  MDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWTVRQCLKNGEEIHLVL---  307
Qy   233  VEQPE------DYTLQVNGRHEYLYGSYPLCCQFYICSCLHSGLTPHLTMVHSSSILAMRD 287
Db   308  -DTPPDPALDEVRKEEWPLVDDCTGYTGYHEQLTIHGKDHESVFTVSLWDCDRKFPRVK-I 365
Db   288  EQSNPAPQVQKPRAKPPP------------IPAKKPSS---VSLWSLEQPFRIELI 328
Qy   366  RGIDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTEEVLWNVWLEFSIKIKD 422
Db   329  QGSKV-----NADERMKLVVQAGLFHGNEMLCKTVSSSEVSVCSEPVWKQRLBFDINICD 383
Qy   423  LPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVL 482
Db   384  LPRMARLCFAIYA----VIEKAKKARSTKKKSKKADCPIAWANLMLFDYKDQLKTGERCL 439
Qy   483  HMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC-HPIALP--------KH 532
Db   440  YMW--PSVPDEKGELLNPTG-VRSNPNTDSAAALLICLPEVAPHVYYPALEKILELGRH 497
Qy   533  RPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPK 591
Db   498  ------SECVHVTEEQL-QLREILERRGSGELYEHEKDLVWKLRHEVQEHFPEALAR 548
Qy   592  LFSSVKMGQQEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESL 651
Db   549  LLLVTKWNKHEDVAQMLYLLCS---WPE-LPVLSALELLDFSFPDCHVGSFAIKSLRKL 603
Qy   652  EDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQ 711
Db   604  TDDELFQYLLQLVQVLKYESYLDCELTKFLLDRALLANRKIGHFLFWHLRSEM----HVPS 659
Qy   712  ---RFAVILEAYLRGCGTAMLHDFTQQVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLK 768
Db   660  VALRFGJLILEAYCRG-RTHHMKVLMKQGEALSKI-KALNDFVKLSSQKTP--------K 708
Qy   769  QKLENLQNLNLPQS-------FRVPYDPGLKAGALVIEKCKVVASKKKPLWLEFKCADP 820
Db   709  PQTKELMHLCMRQEAYLEALSHLQSPLDPSTLLAEVCVEQCTFMDSKMKPLWIMY--SNE 766
Qy   821  TALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIE 880
Db   767  EAGSGGSVGIIFKNGDDLRQDMLTLQMIQLMDVLWKQEGLDLRMTPYGCLPTGDRTGLIE 826
Qy   881  IVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVA 938
Db   827  VVLRSDTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIEBFTLSCAGYCVA 885
Qy   939  TFVLGIGDRHNDNIMISETGNLFHIDFGHILGNVKSFLGINKERVPFVLTPDELFVMGTS 998
Db   886  TYVLGIGDRHSDNIMIRESGQLFHIDFGHFLGNFKFGLNRERVPFILTYDFVHVIQQG 945
Qy   999  GKKTSLHFQKFQDVCVKAYLALRHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVG 1058
Db   946  KTNNSEKFERFRGYCERAYTILRRGLLFLHLFALMRAAGLPELSCSKDIQYLKDSLALG 1005
Qy  1059  KSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db  1006  KTEEEALKHPRVKFNEALRESWKIKVNWLAHNV 1038
```

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Qy  369 DIPVLPRTADLTVFVEANIQYGQQVLQRRTSPKPFTEEVLMNVWL-EFSIKIKDLPKGA 427
         :  :   : :.:  :  :       : .     :. .   : :.::
Db  425 DFPA---DVDMYVRIEFSVYVGTLTLASKSTI-KVNAQFAKWNKEMYTFDLIVMKDMPPSA 480

Qy  428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEVLHMWQL 487
         :. : :                   :: ..        ::.::: :.. :: :.:::
Db  481 VLSIRVLYGK------VKLKSEEFE----VGWVNMSLTDWRDELRQGQFLFHLW- 524

Qy  488 SGKGEDQGSFNADKLTSATNPDKEN------SMSISILLDNYCHPIALP--------KH 532
                                           : .: :::..: ::.:.
Db  525 ---------APPTANRSRIGENGARIGTNAAVTIBISSYGGRVRMPSQGQYTYLVKH 573

Qy  533 R---PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
         :       : .        : ..   ::. :.: :::  ..       :::.:.:: ::
Db  574 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWR-RYIQKQE 632

Qy  586 PKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
         :    .: : :.::::  .:. .  ::: .        :  :: ::.
Db  633 PDLLIVLSLAFVWTDRENFSELYVMLEK--WKPPSVAAALT--LLGKRCTDRVIRKFA 687

Qy  645 VQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEI 703
         :.::.. : .:.:  :::.: :::::::::.:  .:::.: :: :::::: :::.::: :
Db  688 VEKLNEQLSPVTFHLFILFLPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEI 747

Qy  704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKY 757
         : .:      : ::::  ::: :::: .   :    :::. :: : ::.
Db  748 ARLRDCDLKSEEYRRISILMERYLRG-NEEHIKIITRQVDMVDELTRISTLVKGMPK--- 803

Qy  758 DVSS----QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWL 813
         :...    :.:..: .:..  .    .       ::: ::. :::.:::.:
Db  804 DVATMKLRDELRSISHKMENMDS-------PLDPVYKLGEMIIDKAIVLGSAKRPLML 854

Qy  814 EFKCADPTA-LSNETIGIIFKHGDDLRQDMLIQILRIMESIWETESLDLCLLPYGCIST 872
         .:: :    .:.  .: .:::::::::::::::.::..:..:: .. ::: ::: .
Db  855 HWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914

Qy  873 GDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIEE--------- 919
         : ::::::.: : ::: .:.  : :::::  .::.:. : :..:::: ::
Db  915 GEMGIIEVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDST 974

Qy  920 -------------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                      ::.:.  ::::::.::: ::::.::: ::::.::::..:.::..:::
Db  975 KNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHID 1034

Qy  965 FGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
         :::::: ::: ::: ::: ::.:: .:. .:  ::::.::.:::.::. :: :::.: .:
Db 1035 FGHILGHGKTKLGIQRDRQPFIITEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYBVMWN 1094

Qy 1023 HTNLLIILFSMMLMTGMPQLTSKEDIEVIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
          ..: . :::.:::.:: ::.:::.:.: .:.:   :.:.:.:   ..  ..  ..:::
Db 1095 NRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEARKFPAGIYEEAFNGGWS 1154

Qy 1082 VQFNWFLHIV 1091
         .. ::::..:
Db 1155 TKTNWLFHAV 1164
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RESULT 11
US-09-844-353A-48
; Sequence 48, Application US/09844353A
; Patent No. US20020037585A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Koweek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005

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Db 1110 SFFSSNAVPLKVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKINLKEGLD 1166
Qy  862 LCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKF 921
Db 1167 LRMVIFKCLSTGRDRGMVELVPASDTLRKIQVE-YGVTGSFKDKPLAEWLRKYNPSEEEY 1225
Qy  922 QAAVERFVYSCAGYCVATYVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKE 981
Db 1226 EKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRD 1285
Qy  982 RVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYALALRHHTNLLIILFSMMLMTGMPQ 1041
Db 1286 RAPFVLTSDMAYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPE 1344
Qy 1042 LTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
Db 1345 LTSIQDLKVVRDALQPQTTDAEATIFFTRLIESSLGSIAT-KFNFFIH 1391
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RESULT 10
US-09-205-658-48
; Sequence 48, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1997-05-15
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-48

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Query Match           17.9%;  Score 1034;  DB 9;  Length 1167;
Best Local Similarity 27.2%;  Pred. No. 2e-84;
Matches  313;  Conservative 227;  Mismatches 400;  Indels 210;  Gaps 44;

Qy   78 ALETSVSADFVHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
         .:: .. .:: :.. ..:  :::.:.    :.  :::.:.:
Db   89 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143

Qy  138 VQRHAPSEETLAFQ--------RQLNALIGYDVTDVSNVHDDEL-EP-------TRR 178
          .. . .  .: .         : :  ::::. ... .:..  :
Db  144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203

Qy  179 RLVT--------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215
          :.          : :.   ..:.  .   ..:  : :. .:.
Db  204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKK-------AEI 256

Qy  216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFKMAKKKSLMDIPESQNERD--FVLR 273
          ::: .     ..  . :.   ..:.:: : .:   ..:  . .::      : ::
Db  257 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK----LDVYDTDDPADEGWFLQ 306

Qy  274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH--LVLD--TPPDPALDE--VRKE 321
          .:::. .:  . :. .  :  ..  .    :.     ..::   :  ::  :  :
Db  307 LAGRTTFVTNPDVKLTSYDGVRSELESYRCPGFVVRRQSLVLKDYCRPKLYEPHYVRAH 366

Qy  322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT---------VSLWDCDRKFRVK---IRGI 368
         :. :.      .:. .:  .. .:.: .:         ::::: : .: :    :  .
Db  367 ERKLALDVLSVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424
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; CURRENT APPLICATION NUMBER: US/09/844,353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857,076
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-844-353A-48

  Query Match         17.9%;    Score 1034;  DB 9;  Length 1167;
  Best Local Similarity   27.2%;   Pred. No. 2e-84;
  Matches  313;  Conservative  227;  Mismatches  400;  Indels  210;  Gaps    44;

Qy      78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
           ::::|::::|::|:|::::|::|:::|||:|:::::::::::::|:|:|::|:::|:|
Db      89 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143

Qy     138 VQRHAPSEETLAFQ--------------RQLNALIGYDVTDVSNVHDDEL-EF------TRR 178
           :|::|     ::            |::|:::::|:::::::::::|:: ::         :
Db     144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203

Qy     179 RLVT------------------------------PRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKI 215
              :|                           |: |:|::|:::::|:::::::::||:|:::::|
Db     204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK--------AEI 256

Qy     216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKVAKKKSLMDIPESQNERD--FVLR 273
           :::|    ::|  |::|::: ||:|::|:|:|:|::|::|::|::::|::::::||   ||
Db     257 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK---LDVYDTDDPADEGWFLQ 306

Qy     274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH--LVLD-TPPDPALDE--VRKE 321
           :: |   :|                |::|:::::||::::: |:::::::  ::::
Db     307 LAGRRTFVTNPDVKLTSYDGVRSELESYRCPGFVVRRQSVLKDYCRPKPLYEPHYVRAH 366

Qy     322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT---------VSLMWDCDRKFRVK---IRGI 368
                  :|  |: ::    |:    ::|         |::::::|:::: ::    ::|:
Db     367 ERKLALDVLSVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424

Qy     369 DIPVLPRTADITVFEANIQYGQQVLCQRRTSPKPFTEEVLNNVWL-EFSIKIKDLPKGA 427
           :||:: |:|:::|:|     |::|::::::::::::::::  ::|:::::::|:::
Db     425 DFPA---DVDMYVRIEFSVVGVGTLTLASKSTT-KVNAQFAKWNKEMYTFDLYMKDMPPSA 480

Qy     428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLIYYVNLLLIDHRFLLRHGEYTLHWWQL 487
              : :::|:                  :   :::::::::: |:::|:|::::|::
Db     481 VLSIRVLYGK---------VKLKSEEFE----VGWVNMSLTDWRDELRQGQFLFHLW-- 524

Qy     488 SGKGEDQGGSFNADKLTSATNPDKEN--------SMSISILLDNYCHPIALP--------KH 532
                                   ::      |::|::::::    ::         ||
Db     525 ------APEPTANRSRIGENGARIGTNAAVTIEIISSYGGRVRMPSQGQYTYLVKH 573

Qy     533 R----PTPDEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
           :      :::|:::::|::|::::|::|:::|:::::|::||:      ::|:|::::|:
Db     574 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWR-RYIQKQE 632

Qy     586 PKAYPKLFS-SVKWGGQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
           |::|:|:   ||:::|:::|:|::::::|:|:|    :|::|:|::::|:|:
Db     633 PDLLIVLSELAFVWTDRENFSELYVMLEK---WKPPSVAAALT--LLGKRCTDRVIRKFA 687

Qy     645 VQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEI 703
           ::|::::|:: ::  :::|::|::::|      :|:|::|:::::::|:|:::
Db     688 VEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEI 747

Qy     704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKY 757
           :|:|      :::::|:::|::|:|||||::|:|::::::::::|::::::|::|:::|
Db     748 ARLRDCDLKSEEYRRISLLMEAYLRG-NEBHIKIITRQVDMVDELTRISTLIVKGMPK--- 803

Qy     758 DVSS---QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLML 813
           |:|    :::|:|:|:|:::::::::::     |||:|::|::::::|:|::::::|:|:
Db     804 DVATMKLRDELRSISHKMENMDS--------PLDPVYKLGEMIIDKAIVLGSAKRPLML 854

Qy     814 EFKCADPTA-LSNETIGIIPKHGDDLRQDMLILQILRIMESIWETESLDLCLLPYGCIST 872
           ::|:|::|  :|::|::|::|:||||::|:|::::|:|::|:::::| :|||||||:::|
Db     855 HWKNKNPKSDLHLPFCAMFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914
```

```
Qy     873 GDKLGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIEE---------- 919
           |::||||||:|:::|:|:|||| ||:|  :||:|:|:|:|:||:|||:||
Db     915 GEMGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSSKKDST 974

Qy     920 ---------------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                         ::|:|   |||::|:|:::::|::|::|::::|::::|:::|:::|
Db     975 KNPIEKKIDNTQAMKKYFPESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTBDGKYVHID 1034

Qy     965 FGHILGNYKSPLGINKERVPFVLTPDFLFVM--GTSGGKKTSLHFQKFQDVCVCAYLALRH 1022
           |||::|||:|:|||:||:|:|:|:|:|:|:  |:|::|::|:|:|||:|::|:::|:|:|
Db    1035 FGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWN 1094

Qy    1023 HTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
           :|:||:::::::|::|::::|:::|::|::|:|::  |:::::|||:|:|:|:|:|:||:|
Db    1095 NRDLFVSLFTLMGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWS 1154

Qy    1082 VQFNWFLHLV 1091
           :|::|::|:|
Db    1155 TKTNWLFHAV 1164
```

```
RESULT 12
US-09-963-693-48
; Sequence 48, Application US/09963693
; Publication No. US2003018136441
; GENERAL INFORMATION:
;  APPLICANT: Ruvkun, Gary
;  APPLICANT: Ogg, Scott
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
;  TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;  FILE REFERENCE: 00786/351004
;  CURRENT APPLICATION NUMBER: US/09/963,693
;  CURRENT FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US/09/205,658
;  PRIOR FILING DATE: 1998-12-03
;  PRIOR APPLICATION NUMBER: 08/888,534
;  PRIOR FILING DATE: 1997-07-07
;  PRIOR APPLICATION NUMBER: 08/857,076
;  PRIOR FILING DATE: 1997-05-15
;  PRIOR APPLICATION NUMBER: US98/10080
;  PRIOR FILING DATE: 1998-05-15
;  NUMBER OF SEQ ID NOS: 328
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-48

  Query Match         17.9%;    Score 1034;  DB 12;  Length 1167;
  Best Local Similarity   27.2%;   Pred. No. 2e-84;
  Matches  313;  Conservative  227;  Mismatches  400;  Indels  210;  Gaps    44;

Qy      78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
           ::::|::::|::|:|::::|::|:::|||:|:::::::::::::|:|:|::|:::|:|
Db      89 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143

Qy     138 VQRHAPSEETLAFQ--------------RQLNALIGYDVTDVSNVHDDEL-EF------TRR 178
           :|::|     ::            |::|:::::|:::::::::::|:: ::         :
Db     144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203

Qy     179 RLVT------------------------------PRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKI 215
              :|                           |: |:|::|:::::|:::::::::||:|:::::|
Db     204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK--------AEI 256

Qy     216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKVAKKKSLMDIPESQNERD--FVLR 273
           :::|    ::|  |::|::: ||:|::|:|:|:|::|::|::|::::|::::::||   ||
Db     257 NGVC------EKMKIQIEFNPNETPKSLLHTFLYEMRK---LDVYDTDDPADEGWFLQ 306

Qy     274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH--LVLD--TPPDPALDE--VRKE 321
```

```
Db   307 LAGRTTFVTNPDVKLTSYDGVRSELESYRCPGVVRRQSLIVLKDYCRPKPLYEPHYVRAH 366
                   :. :   ::    |    |||  :.  . ||  . : |:     . :    |||
Qy   322 EWPIVDDCTGVTGYHEQLTIHGKDHESVFT---------------VSLWDCDRKFRVK---IRGI 368

Db   367 ERKLALDVLSVS--IDSTPKQSKNSDMWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424
             ::  :    :  |:.|     .  .:|  .:: |  : :. ::   : . ::|
Qy   369 DIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLMNVWL-EFSIKIKDLPKGA 427

Db   425 DFPA--DVDMYVRIEFSVYVGTILTLASKSTT-KVNAQPAKWNKEMYTFDLIYMKDMPPSA 480
            ||:     :  :|  ::   | ||.:   .    |.||: .|.:| :.|: | ||:.
Qy   428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQL 487

Db   481 VLSIRVLYGK---------VKLKSEEFE-----VGWVNMSLITDWRDELRQGQPLFHLM-- 524
          :|: .:||           || :       | :.    ::|     :: |  |.  |
Qy   488 SGKGEDQGSFNADKLTSATNPDKN------SMSISILLDNYCHPIALP---------KH 532

Db   525 ---------APEPTANRSRIGNGARIGTNAAVTIEISSYGGRVRMPSQQQYTYLVKH 573
                     :. .:||.:|:.|::|| :  |::|:||.  :: :  :|| || || ||
Qy   533 R----PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585

Db   574 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMR-RYIQKQE 632
            :.|:  :.:|:|| : :  |   ||  ||   :   :: ||:|.|||:.: | :::|:
Qy   586 PKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644

Db   633 PDLLIVLSELAFVWTDRENFSELIYVMLEK--WKPPSVAAALT--LLGKRCTDRVIRKFA 687
            || :|::|  : :|:|.||  :: |: |      |  : : :    || |. :::|:
Qy   645 VQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLR 700

Db   688 VEKLNEQLSPVTFHLFILPLIQALKYEPPAQSEVGMLLTRALCDYRIGHRLFWLLRAEI 747
            ::: :  | ||:  | :|:|:|||:||| ||:|| |||. | | |:||| |||:|| |
Qy   701 SEIAQSRHYQQRFAVILEAYLRGCGTA 727

Db   748 ARLRDCDLKSBEYRRISLLMBAYLRG-NEEHIKIITRQVDMVDELTRISTLVKGMPK-- 803
           |  |  || ||.|| || ||.||||| ||.:|| ||:  :| ||  : ||| |  |:
Qy   704 HYQQRFAVILEAYLRGCGTAMLHDFTOQVQVIDMLQKVTIDIKSLSAEKY 757

Db   758 DVSS---QVISQLKQKLENLQNLNLPQSPRVPYDPGLKAGALVIEKCKVMASKKKPLWL 813
           |.||    | ||:|:|:.| .|:|.||  :|   |.:||  |::::|:|.::|||||| |
Qy   804 DVATMKLRDELRSISHKMENMDS--------PLDPVYKLGEMIIDKAIVLGSSAKRPLML 854

Db   814 EFKCADPTA-LSNETIGIIFKGHGDDIRQDMLILQIRIMESIWETESLDLCLLPYGCIST 872
           :|  |  |   .|::|:||:|.||||:|:| :.|||.|::|:|| : ||:| | ||. |
Qy   855 HWKNKNPKSDDLHLPFCAMIFNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914

Db   873 GDKIGMEIVKDATTIAKIQOST-VGNTG--AFKDEVLSHWLKEKCPIEE---------- 919
           ||:||:|  ||  : | ||.|   ||.|.  .|||: .  |::| ||::
Qy   915 GEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDST 974

Db   920 ---------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                    :|.|::|::| ||| :  |:.|:||:||.:||: ::::| |.:|
Qy   975 KNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMITEDGKYVHID 1034

Db   965 FGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
           ||:|:|.||| | |.:| | |:|.|| |::     ||:||: |:|||:..|||:|:|:|:
Qy   1035 FGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWN 1094

Db   1023 HTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
            ::|:::| ||:||.||||||| |.|| .||::. || ||.||| | :.||. |::|.|
Qy   1095 NRDLFVSLFTLMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWS 1154

Db   1082 VQFNWFLHLV 1091
           ..:|||::.|
Qy   1095 TKTNWLFHAV 1164
```

RESULT 13
US-10-101-235A-2
; Sequence 2, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.

```
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
FILE REFERENCE: 033072-064
CURRENT APPLICATION NUMBER: US/10/101,235A
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
US-10-101-235A-2

Query Match              16.9%;     Score 980;   DB 12;   Length 204;
Best Local Similarity    93.2%;     Pred. No. 8.5e-81;
Matches  193;  Conservative   3;  Mismatches   3;  Indels   8;  Gaps   2;
```

```
Qy   521 DNYCHPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRY 580
           ||:|||||||| :||| .|||||||||||||||||||||||||||||||||||   |||||||
Db     6 DDDKHPIALPKHQPTPD--DRVRAEMPNQLRKQLEAIIATD-----TAEDKELLWHFRY 57

Qy   581 ESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENV 640
           ||||| ||:||||||||||||||||||||||||||:||||||| ||||||||||||||||
Db    58 ESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENV 117

Qy   641 RAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLR 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 RAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLR 177

Qy   701 SEIAQSRHYQQRFAVILEAYLRGCGTA 727
           |||||||||||||||||||||||||||
Db   178 SEIAQSRHYQQRFAVILEAYLRGCGTA 204
```

RESULT 14
US-10-101-235A-9
; Sequence 9, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.

```
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
FILE REFERENCE: 033072-064
CURRENT APPLICATION NUMBER: US/10/101,235A
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
US-10-101-235A-9

Query Match              16.9%;     Score 979;   DB 12;   Length 195;
Best Local Similarity    94.6%;     Pred. No. 9.7e-81;
Matches  192;  Conservative   2;  Mismatches   2;  Indels   1;  Gaps   2;
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```
Qy   525 HPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLK 584
           |||||||| :||| .|||||||||||||||||||||||||||       |||||||||||
Db     1 HPIALPKHQPTPD--DRVRAEMPNQLRKQLEAIIATD-----TAEDKELLWHFRYESLK 52

Qy   585 DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
            ||:||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db    53 HPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIA 112

Qy   645 VQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIA 704
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113 VQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIA 172

Qy   705 QSRHYQQRFAVILEAYLRGCGTA 727
Db   727
```

```
Db  173 QSRHYQQRFAVILEAYLRGCGTA 195
            ||||||||||||||||||||||||

Db  626 ED-----GGKYPVIFKHGDDLRQDQLILQIISLMDKLLRKENLDLXLTPYKVLATSTKHG 680
            :|||||||||| ||||||  :|: ::|||  :|:|||   :::||:
Qy  878 MIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEK----FQAAVERFVYSCA 933

Db  681 FMQFIQ-SVPVAEV-LDTEGS--------IQNFFRKYAPSENGPNGISAEVMDTYVKSCA 730
            :: :: :||||   :|: ||:|      ::|:::|

Qy  934 GYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL---GINKERVPFVLTP 989
            ||||:|:|||:||||:|:| ||||:|||:|||:||||||  ||

Db  731 GYCVITYILGVGDRHLDNLVLTKGKLFHIDFGYILGRDPKPLPPPMKLNKE------- 782

Qy  990 DFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIIFSMMLMTGMPQLTSKED-- 1047
            :::  : :: |: |: :: |    :|    :::|:|: | || |::

Db  783 ---MVEGMGGTQ-SEQYQEFRKQCYTAFLHLRRYSNLILNLFSLMVDPNIPDIALEPDKT 838

Qy 1048 IEYIRDALTVGKSEEDAKKYFLDQIE 1073
            :: :::|:|   :::|:|:

Db  839 VKKVQDKFRLDLSDEEAVHYMQSLID 864
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Search completed: February 15, 2004, 02:10:05
Job time : 89 secs

RESULT 15
US-09-771-161A-192
; Sequence 192, Application US/09771161A
; Patent No. US2002011011A1
; GENERAL INFORMATION:
;   APPLICANT: LEVINE, et al.
;   TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
;   FILE REFERENCE: 802620-2005.1
;   CURRENT APPLICATION NUMBER: US/09/771,161A
;   CURRENT FILING DATE: 2001-01-26
;   PRIOR APPLICATION NUMBER: 09/724,676
;   PRIOR FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: 136776
;   PRIOR FILING DATE: 2000-06-15
;   PRIOR APPLICATION NUMBER: 135619
;   PRIOR FILING DATE: 2000-04-12
;   NUMBER OF SEQ ID NOS: 273
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 192
;   LENGTH: 887
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-771-161A-192

Query Match   12.1%;   Score 698.5; DB 10;   Length 887;
Best Local Similarity   25.9%;   Pred. No. 5.2e-54;
Matches 224;   Conservative 146; Mismatches 259;   Indels 237;   Gaps 30;

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Qy  381 VFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIY----CG 436
            ||:|

Db   63 VFAE-----GKPSALPVRTSYKAFSTRWNWNEWLKLPVXYPDLPRNAQVALIIWDVVGPG 117

Qy  437 KAPALS---------------------------------GKTSAEMPSPESKGKAQ 459
            |||:|                                    :|:|

Db  118 KAVPVGGTTVSLFGKYGMSRQGMHDLKVWPNVEADGSEPTNTPGRTSSTLSEDQMSRLAK 177

Qy  460 LL----YVVNLLLIDHRFLLRHGEYVLH---------MWQLSG------KGEDQ------ 494
            ||

Db  178 LTKAHRQGHMVKVDWLD-RLTFREIEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYY 236

Qy  495 --GSFNADKLTS---ATNPDKENSMSISILLDNYCHPIALPKH--------RPTPDP 538
            :|

Db  237 EKDGDESSPILTSPFLVKVPDPQ--MSLENLVESKHH--NLPRSLRSGPSDHDLKPYPSP 292

Qy  539 EGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKW 598

Db  293 ------RDQLKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW 339

Qy  599 GQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLH 658

Db  340 DLPQGAKQALALLGK---W---NPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLM 394

Qy  659 YLLQIVQAVKFEPYHD 674
            ||:|:|:|:|:

Db  395 YLSQIVQALKYENFDDIKNGLEPTKKDSQSSVSGNVSNSGINSAEIDSSQIITSPLPSVS 454

Qy  675 -----------------------SALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVI 716

Db  455 SPPPASKTKEVPDGENLEQDLCTFLISRASKNSTLANYLWYVIVE-CEDQDTQQRDPKT 513

Qy  717 LEAYLRGCGTAMLHDFTQQVQVIMLQKVTIDIKSLSAEKYDVSSQVISQL-------- 767

Db  514 HEMYLN-----VMRRFSQALLKGDKSVRV---MRSLLAAQQTFVDRLVHLMKAVQRESGN 565

Qy  768 -KQKLENLQ-------NLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPIWLEFKC 817

Db  566 RKKKNERLQALLGDNEKOMLSDVELIPLPLEPQVKIRGIIPETATLFKSALMPAQLFKT 625

Qy  818 ADPTALSNETIGIIPKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCISTGDKIG 877
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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
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Run on: February 15, 2004, 02:08:37 ; Search time 9655 Seconds
(without alignments)
4669.333 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO spool/US09974573/runat_11022004_180013_18093/app_query.fasta_1.1287
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974573_@CGN_1_6581 @runat_11022004_180013_18093 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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11: gb_sts:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5785	99.9	3808	4	SSP120	Y10743 S.scrofa mR
2	5726	98.9	3808	6	AR026673	AR026673 Sequence
3	5726	98.9	3808	6	AR026679	AR026679 Sequence
4	5726	98.9	3808	6	AR029062	AR029062 Sequence
5	5726	98.9	3808	6	AR033966	AR033966 Sequence
6	5538	95.6	3860	9	BC035683	BC035683 Homo sapi
7	5534	95.6	3410	9	AF327656	AF327656 Homo sapi
8	5534	95.6	5162	6	AR026677	AR026677 Sequence
9	5523.5	95.4	5397	9	AX327655	AX327655 Sequence
10	5523.5	95.4	5397	9	HSIDEM	X83368 H.sapiens m
11	5506	95.1	4725	10	MMU249280	AJ249280 Mus muscu
12	5505	95.1	4330	10	BC051246	BC051246 Mus muscu
13	5499.5	95.0	4137	6	A50265	A50265 Sequence 3
14	5476.5	94.6	3342	10	AF208345	AF208345 Mus muscu
15	5440	94.0	4134	6	A50263	A50263 Sequence 1
16	3318	57.3	107527	9	AC005018	AC005018 Homo sapi
17	3291	56.8	186349	9	AC073420	AC073420 Homo sapi
18	3287	56.8	2080	10	MMU249413	AC249413 Mus muscu
c 19	3286.5	56.8	146761	2	AC132894	AC132894 Mus muscu
c 20	3286.5	56.8	164211	2	AC115801	AC115801 Mus muscu
c 21	3286.5	56.8	198298	2	AC140314	AC140314 Mus muscu
22	3280.5	56.7	221422	2	AC129663	AC129663 Rattus no
23	1470.5	25.4	3452	5	AF001076	AF001076 Gallus ga
24	1466.5	25.3	3424	9	AX327651	AX327651 Sequence
25	1466.5	25.3	3424	9	HSPHI3K	Z29090 H.sapiens m
26	1465.5	25.3	3207	4	BOVPHOS3KN	M93252 Bovine phop
27	1465.5	25.3	3207	6	A75936	A75936 Sequence 36
28	1465.5	25.3	3207	6	AR048987	AR048987 Sequence
29	1465.5	25.3	3207	6	AR064288	AR064288 Sequence
30	1465.5	25.3	3207	6	AR164681	AR164681 Sequence
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34	1460.5	25.2	3240	6	AR064287	AR064287 Sequence
35	1460.5	25.2	3240	6	AR164680	AR164680 Sequence
36	1460.5	25.2	3412	9	A75939	A75939 Sequence 39
37	1460.5	25.2	3412	6	AR048985	AR048985 Sequence
38	1460.5	25.2	3412	6	AR064286	AR064286 Sequence
39	1450.5	25.1	3412	6	AR164679	AR164679 Sequence
40	1450.5	25.1	3207	10	MMU03279	U03279 Mus musculu
41	1450.5	25.1	3389	14	AF001075	AF001075 Avian sar
42	1366	23.6	225277	2	AC129863	AC129863 Rattus no
43	1362	23.5	3213	10	RNO012482	AJ012482 Rattus no
44	1358	23.5	1921	3	AK113227	AK113227 Ciona int
45	1354.5	23.4	3213	6	AR116356	AR116356 Sequence

ALIGNMENTS

RESULT 1

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LOCUS       SSP120                   3808 bp    mRNA    linear   MAM 12-MAY-1998
DEFINITION  S.scrofa mRNA for p120-PI3K protein.
ACCESSION   Y10743
VERSION     Y10743.1  GI:3133115
KEYWORDS    p120-PI3K protein.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
AUTHORS     Stephens,L.R., Eguinoa,A., Erdjumen-Bromage,H., Lui,M., Cooke,F.,
            Coadwell,J., Smrcka,A., Thelen,M., Cadwallader,K., Tempst,P. and
            Hawkins,P.T.
TITLE       The G beta gamma sensitivity of a PI3K is dependent upon a tightly
            associated adaptor, p101
JOURNAL     Cell 89 (1), 105-114 (1997)
MEDLINE     97248491
PUBMED      9094719
REFERENCE   2
AUTHORS     Stephens,L.R.
TITLE       Direct Submission
JOURNAL     Submitted (23-JAN-1997) L.R. Stephens, Babraham Institute,
            Babraham, Cambridge, CB2 4AT, UK
REMARK      revised by [3]
REFERENCE   3  (bases 1 to 3808)
AUTHORS     Stephens,L.R.
TITLE       Direct Submission
JOURNAL     Submitted (24-APR-1998) L.R. Stephens, Babraham Institute,
            Babraham, Cambridge, CB2 4AT, UK
COMMENT     On May 15, 1998 this sequence version replaced gi:1935003.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /dev_stage="adult"
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                     /protein_id="CAA71731.1"
                     /db_xref="GI:3133116"
                     /db_xref="SWISS-PROT:O02697"
                     /function="catalytic subunit of G-beta-gamma-activated
                     PI3K"
                     /translation="MELENYEQPVVLREDNRRRRRRRRMKPRSTAASLSSMELIPIEFVL
                     PTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQK
                     KGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGY
                     DVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNN
                     CVFIVIHRSTVSTSQTIKVSADDTPGTILQSFFTKWAKKKSLMDIPESQNERDFVLRVCG
                     RDEYLVGETPIKNFOWVRQCLKNGEIHIVLDTPPDPALDEVRKEWEPLVVDDCTGVTG
                     YHEQLTIHGKDHESVPTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGGQ
                     VLCQRRTSPKPFTEEVLMRNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMP
                     SPESKGKAQLLYVNLLLIDHRFLRHGEYLVHMWQLSGKGEDGGSFNADKLTSRTNP
                     DKENSMSISILLDNYCHPIALPKHRPTDPEGDRVRAEMPNQLRKQLEAIIATDPLNP
                     LTAEDKELLMHFRYESLKDPKAYPKLFSSVKWGGQEIVAKTYQLLAKREVWDQSALDV
                     GLTMQLLDCNPSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLL
                     KRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID
                     MLQKVTIDIKSLSAEKYDVSSQVISQLKQENLQNLNLPQSFRVPYDPGLKAGALVI
                     EKCKVMASKKKPLWLEFKCADTPAUSNETIGIIFKHGDDLRQDMLILQIRIMESIWE
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                     KSFLGINKERVFFVMGTSGKKTSLHFQDKFQDVCVKAYLALRHHTNLLIIL
                     FSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKKYFLDQIEVCRDKGWTVQFNWFL
                     HLVLGIKQGEKHSA"
BASE COUNT     1012 a    971 c    949 g    876 t
ORIGIN
Alignment Scores:
Pred. No.:                0
Score:                 5785.00
Percent Similarity:     99.91%
Best Local Similarity:  99.91%
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Query Match:    99.91%     Indels:      0
DB:              4         Gaps:        0

US-09-974-573-1 (1-1102) x SSP120 (1-3808)

Qy     1 MetGluGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg 20
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Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
Db   149 CGGAGGATGAAGCCGCGAGCACGGCAGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 208

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
Db   209 GAGTTTGTTTTGCCCACGAGCCAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC 268

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
Db   269 GTGGCCGGGCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGGGCTGGAG 328

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
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Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
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Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
Db   449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
Db   509 CACGCGCCCTCCGAGGAGACCATTGGCCTTCCAGCGCCAGCTGAACGCCCTCATCGGCTAC 568

Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu 180
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Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
Db   629 GTCACCCCGCGCATGGCCGAGGTGGCCGGGCGCGACCCCAAGCTTTACGCCATGCACCCC 688

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
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Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
Db   749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC 808

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Db   809 CCAGGCACCATCCTCCAGAGCTTCTTCTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
Db   869 ATCCCTGAAAGCCAGAAACGAACGGGAGACTTTGTGCTGCGGGTCTGCGGGGATGAGTAC 928

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
Db   929 CTGGTGGGTGAGACGCCGCCATCAAGAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy   301 GluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
Db   989 GAGGAGATTCACCTTGTCCTGGACACTCCTCCAGACCCTGGCACCTGGAGGTGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
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Db   3269 GAGGAGGATGCTAAAAAGTATTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328
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Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuIleLysGlnGlyIleLysHis 1100
Db   3329 ACCGTCGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAAACAAGGGAGAAGCAT 3388
          
Qy   1101 SerAla 1102
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Db   3389 TCCGCA 3394


RESULT 2
AR026673
LOCUS        AR026673      3808 bp    DNA       linear   PAT 29-SEP-1999
DEFINITION   Sequence 3 from patent US 5856132.
ACCESSION    AR026673
VERSION      AR026673.1  GI:5937513
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 3808)
  AUTHORS    Stephens,L., Hawkins,P.Thomas, and Braselmann,S.
  TITLE      G-beta-gamma regulated phosphatidylinositol-3' kinase
  JOURNAL    Patent: US 5856112-A 3 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1..3808
                     /organism="unknown"
BASE COUNT     1010 a    965 c    953 g    880 t
ORIGIN

Alignment Scores:
Pred. No.:            0
Score:               5726.00
Percent Similarity:  99.46%            Length:          3808
Best Local Similarity: 98.91%          Matches:         1090
Query Match:         98.89%            Conservative:       6
DB:                  6                 Mismatches:         6
                                       Indels:             0
                                       Gaps:               0

US-09-974-573-1 (1-1102) x AR026673 (1-3808)

Qy      1 MetGluLeuGluAsnTyrGluGlyProValValLeuArgGluArgAspAsnArgArgArgArg 20
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Db     89 ATGGAGCTTGAGAACTATGAAGGACCCGTGGTGCTGAGAGAGAGAGAGGACAACCGCCAGGCGT 148

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 CGGAGGAGGATGAAGCCGCGCAGCACCGGCAGCCTGTCTATGGAGCTCATCCCCATC 208

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGlyHisThrAlaLeuLeuHis 60
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Db    209 GAGTTTGTTCTGCCCACCAGCCAGAGGAACACGAAAACGCCCGGACACACTGCTCCAC 268

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
          |||||||||||||||||| |||:::|||||| |||::||||||||||||||||||||
Db    269 GTGGCCGGCCACGGGAATGTGGAGCAAATGAAGGCCCAGGTGTGTTGCGGCGGCTGGAG 328

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
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Db    329 ACGAGCGTTTCTGCTGGAGGTTTCACCACGGTTCGGGACTTCCACCGGTTCCTCCTGTTC 388

Qy    101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
          |||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db    389 CAGAAGAAGGGGCAGTGGTACGAGATCTATGACAAGTACCAGGTGGTCAGACCCTGGAC 448

Qy    121 CysLeuArgTyrGlyLysTrpLysArgSerProGlyGlnIleHisValValGlnArg 140
          |||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db    449 TGCCTGCGCTACTGGGAGGTGTTGCACCGGAGTCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy    141 HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Qy    161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu 180
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Qy    569 GACGTCACGGACGTCAGCAACGTGCATGACGACGAGCTGGAGTTCACGCGCCGCCTG 628
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Qy    181 ValThrProArgMetAlaGlyValAlaGlyArgAspProLeuTyrAlaMetHisPro 200
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Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal 220
Db    689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAGATCACTAACAACTGCGTC 748

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysSerAlaAspAspThr 240
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Db    809 CCAGGGACCAACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCCTGATGGAT 868

Qy    261 IleProGluSerGlnAsnGluLeuAspPheValLeuArgValCysGlyArgAspGluTyr 280
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Qy    301 GluGlnIleHisLeuValLeuAspThrProAspProAlaLeuAspThrLysArgLys 320
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Qy    321 GluGluIleProLeuValAspAspCysThrGlyValThrGlyValThrHisGluGlnLeuThr 340
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Qy    361 PheArgValLysIleArgGlyTyrIleAspIleProValLeuProArgThrAlaAspLeuThr 380
Db   1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTGCCCCGGACCGCTGACCTCACG 1228

Qy    381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnLeuValLeuCysGlnArgArgThrSer 400
Db   1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCACAGCTGAGCCAAGAGGAACCAGC 1288

Qy    401 ProLysProPhePheThrGluGluGlnTrpLeuTrpLeuGluPheSerIleLysIle 420
Db   1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGACGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy    421 LysAspLeuProLysGlyAlaAlaLeuAsnLeuTyrCysGlyLysAlaProAla 440
Db   1349 AAAGACTTACCCAAAGGGGCTTCGTGAACCTCCAGATCACTGCGGCAAAGCTCCAGCA 1408

Qy    441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeu 460
Db   1409 CTGTCTCTGGCAAGACCTCGCAGAGATGCCCAGTCCCAGTCCAAAGGCAAAGCAAGCTCAGCTT 1468

Qy    461 LeuTyrTyrValAsnLeuLeuLeuLeuGlyLeuArgHisGlyHisGlyGluTyr 480
Db   1469 CTGTACTATGTCAACCTATTGCTGATAGCACCACCGCTTCCTCCTGCGCCATGGGCAGTAT 1528

Qy    481 ValLeuHisMetTrpLeuSerGlyLeuGlyGlnIleHisValSerPheAsnAlaAsp 500
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Qy    501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeuLeu 520
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Qy    521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
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Db  1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuTrpHisPheArgTyr 580
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Qy   581 GluSerLeuLysAspProLysAlaTyrProLysPheSerValLysTrpGlyGln 600
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Db  1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTTAGCTGCGTGAAATGGGGACAG 1888

Qy   601 GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysGluValTrpAspGlnSer 620
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Db  1889 CAAGAAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValLeuValGlyAsnGlnLeuLeuAspCysAsnPheSerGluAspAsnVal 640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1949 GCTTTGGATGTGGGGTTAACCATCGAGCTCCTGACTGCACTTCTCCGATGAAAAGTG 2008

Qy   641 ArgAlaIleAlaValGlnLysLeuGluSerGluAspAspValLeuHisTyrLeu 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2009 AGAGCCATTGCAGTCCAGAAACTGGAGAGCGAGGATGATGACGTGCTCCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
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Db  2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCACGACAGTGCCCTAGCCAGATTT 2128

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
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Db  2129 CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTGTTTTGGTTCTTCGAGA 2188

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyr 720
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Db  2189 AGTGAGATTGCCCAGTCCAGGCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleAsp 740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy   741 MetLeuGlnLysValThrIleAspPheIleLysSerLeuSerArgAlaGlyLysTyrArgAspValSer 760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2309 ATGTTACAAAAGGTCACCATTGACTTTATAAAGTCCTTCTCGCGTGAAAAGTATCGACGTCAGT 2368

Qy   761 SerGlnValIleSerArgGlnLeuLysLeuGlnAsnLeuGluAsnLeuGlnAsnLeuAsnLeuPro 780
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Db  2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAATTTGAATCTTCCCC 2428

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysLysLeuAlaGlyIleValAlaLeuValIleGluLysLys 800
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Qy   801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuProLeuLysCysAlaAspPro 820
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Db  2489 TGTAAAGTGATGGCCTCCAAGAAGAAGAGCCCCTGGCTTGAGTTTAAATGTGCCGATCCT 2548

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
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Db  2549 ACGGCTCTATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA 2608

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
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Db  2609 GACATGCTTATTTTACAGATTCTACGGATTATGGAGAGTATTTGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
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Db  2669 GATCTGTGTCCTCCTGCCATATGGCTGCATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysSerIleGlnIleAsnSerThrValGlyAsnThrGly 900
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Db  2729 ATCGTGAAGGACGCCACGACAATCGCCAAAAGTCAGCAAAGCCACAGTGGGCAACACGGGT 2788
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Qy   901 AlaPheLysAspArgSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
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Db  2789 GCCTTTAAAGATGAAGGTCCTGAGTCACTGGCTCAAGAAAAATGCCTATTGAGAAAAG 2848

Qy   921 PheGlnAlaAlaValGluHisArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
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Db  2849 TTTCAGGCAGCTGTGGAGAATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT 2908

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
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Db  2909 GTTCTTGGAATAGGCGACAGACACAATGACATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
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Db  2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
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Db  3029 GAGAGGGTGCCATTTGTCCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy  1001 LysThrSerLeuHisProPheGlnLysAspPheGlnLysLysTyrLeuAlaLeu 1020
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Db  3089 AAGACAAGTCTCACACTTCCAGAAATTTCAGGATGTGTGCGTCAAGCTTACCTAGCCCTT 3148

Qy  1021 ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetThrGlyMetPro 1040
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Db  3149 CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATGACAGGAATGCCC 3208

Qy  1041 GlnLeuThrSerLysGluGluValIleTyrIleArgArgAspAlaLeuArgValGlyLysSer 1060
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Db  3209 CAGTTAACCAGCAAAGAAGAAGCAATTTACATTCGGAGAGATGCCCTCCACAGTGGGCAAAAGT 3268

Qy  1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluGluValCysArgGlyLysGlyTrp 1080
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Db  3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328

Qy  1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLysGlyGluLysHis 1100
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Db  3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy  1101 SerAla 1102
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AR026679
LOCUS        AR026679                3808 bp    DNA        linear    PAT 29-SEP-1999
DEFINITION   Sequence 3 from patent US 5856133.
ACCESSION    AR026679
VERSION      AR026679.1    GI:5937519
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 3808)
  AUTHORS    Stephens,L. and Hawkins,P.Thomas.
  TITLE      G-beta-gamma regulated phosphatidylinositol-3'kinase
  JOURNAL    Patent: US 5856133-A 3 05-JAN-1999;
FEATURES     Location/Qualifiers
     source  1..3808
             /organism="unknown"
BASE COUNT   1010 a   965 c   953 g   880 t
ORIGIN

Alignment Scores:
Pred. No.:                0           Length:         3808
Score:                 5726.00        Matches:        1090
Percent Similarity:    99.46%         Conservative:      6
Best Local Similarity: 98.91%         Mismatches:        6
Query Match:           98.89%         Indels:            0
DB:                        6          Gaps:              0
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US-09-974-573-1 (1-1102) x AR026679 (1-3808)

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Qy      1  MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg   20
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Db     89  ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGCGTGAGGAGGACAACCGCCGCAGGCGT  148

Qy     21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluSerLeuIlePro Ile   40
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Db    149  CGGAGGATGAAGCCGCGCAGCACGGCAGCCTGTCTCCATGGAGTCTCATCCCCATC  208

Qy     41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209  GAGTTTGTTTTGCCCACCAGCCAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC  268

Qy     61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaValGlnValTrpLeuArgAlaLeuGlu   80
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Db    269  GTGGCCGGCCACGGCAATGTGGAGCAAATGAAGGCCGTGCAGGTGTGGCTGCGCGCCTGGAG  328

Qy     81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyTyrProAspHisPheLeuLeuTyr  100
           |||||||||||||||||||||||||||||||||||||:::::::
Db    329  ACGAGCGTTTCTTGGGACTTCTACCACCGGTTCGGGCCCCGACCCTGTTCCTGTGTTTC  388

Qy    101  GlnLysLysGlyIleTrpTyrTyrGluIleTyrAspLysTyrGlnValGlnThrLeuAsp  120
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Db    389  CAGAAGAAGGGGACTACTGGAGGTGCACCGGCAGCCCCTGCGTGTCCACCGTGTCCAGGAC  448

Qy    121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
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Db    449  TGCCTGCGCTACTGGAAGGTGCTCCACCGGAGTCCAGGCCAGATCCACGTGGTCCAGCGG  508

Qy    141  HisAlaProSerGluGluThrProGluLeuTyrTyrAspLysAspAspAlaLeuGluArgLeuTyr  160
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Db    509  CACGCGCCCTCGGAGGAGACAATTGGCCTTCCAGCGCGCCAGCTGCCTCATCGGCTAC  568

Qy    161  AspValThrAspValSerAlaAsnValHisAspAspArgHisLeuGluPheThrArgArgLeu  180
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Db    569  GACGGTCACCGACGTCAGCAAGTGCATGACGATGAGGTTCACGCGGCGGCCGCTG  628

Qy    181  ValThrProArgMetAlaGluValAlaGlyAlaArgAspLysArgTyrAlaMetHisPro  200
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Db    629  GTCACCCCGCGCATGGCCGAGGTCGCCGGGGCCCGCGACAAGCGCTATGCCATGCACCCC  688

Qy    201  TrpValThrSerProLeuProGlyTyrProGluLeuLysLeuLysThrAsnAsnCysVal  220
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Db    689  TGGGTGACATCCCAAGCCCCTCCCCTGAGTACCCTTCTGAAGAAGAGTCACTAACAACTGCGTC  748

Qy    221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
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Db    749  TTCATCGTCATTCACCGCAGCACCACCTCCCAGACCATCAAAGTGTCCGCCGATGACACC  808

Qy    241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerGluLeuMetAsp  260
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Db    809  CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAGAAATCTGATGGAT  868

Qy    261  IleProGluSerGlnAsnGlnIleArgAspPheValLeuArgValCysLeuLysAsnGly  280
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Db    869  ATCCCTGAAAGCCAGAACCAGATCCGCGACTTTGTGCTGCGCGTCTGCCTGAAGAATGGG  928

Qy    281  LeuValG:lyThrProIleLeuLysAsnPheGlnIleTrpValArgValCysLeuLysAsnGly  300
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Db    929  CTGGTGGGTGAGACGTCCCATCAAAAATTTCAGTGGGTGAGGCAGTGCCTCAAGAATGGG  988

Qy    301  GluGlnLeuHisLeuValLeuAspThrProProAlaLeuAspGluGluValArgLys  320
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Db    989  GAGGAGATTCACCTTGTGCTGGACACTCCTCCAGCCCCTGGACGAGGTGAGGAAG  1048

Qy    321  GlyGluTrpProLeuValAspProCysThrGlyTyrValThrGlyTyrHisGluGlnLeuThr  340
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Db   1049  GGAGAGTGGCCCGTGGTTTAAGAACAACAAGAGAAATTGGTCACTCTTGTTTCGGTTCTTCGAGA  1108

Qy    341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuProAspCysAspArgLys  360
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Db   1109  ATCCACGGCAAGGACCATGAAGTGTGTTTCACCGTGTCCCTGCCTGGGACTGTGACCCCAAG  1168
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Qy    361  PheArgValLysIleArgGlyIleIleAspIleProValLeuProArgThrAlaAspLeuThr  380
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Db   1169  TTCAGGGTCAAAATCAGAGGCATTATCGACATTCCTGTCCTGCCCCGCACCGCTGACCTCACG  1228

Qy    381  ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer  400
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Db   1229  GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGGTGCTCTGCCAAGGAGAACCAGC  1288

Qy    401  ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle  420
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Db   1289  CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC  1348

Qy    421  LysAspLeuProLysGlyIleAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla  440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349  AAAGACTTACCCAAAGGGCTGCTGACCTCACTGCGGCAAAGTCTCCAGCA  1408

Qy    441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu  460
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Db   1409  CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGTCCAAAGGCAAAGCTCAGCTT  1468

Qy    461  LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyr  480
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Db   1469  CTGTACTACGTCAACCTATTCGTGATAGACCATCGCTTCCTCCTGCGCCATGGCGAGTAT  1528

Qy    481  ValLeuHisMetTrpGlnValAspLysGlyGlyAspPheAsnAlaAsp  500
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Db   1529  GTGCTCCACATGTGGCAGGTTGACAAGGGAGGGAAGGACTTCAATGGCGAC  1588

Qy    501  LysLeuThrSerAlaThrArgAsnProAspLysAsnSerMetSerIleSerIleLeuLeu  520
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Db   1589  AAGCTCACGTCGGGAACCACCCGGAACCAAGGAGCTTCAATGTCCATTCCATTCTCCTG  1648

Qy    521  AspAsnTyrCysHisProIleAlaLeuProLysProHisProAspProGluGly  540
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Db   1649  GACAATTACTGCCACCCCATAGCCTTGCCTAAGATATGGCCTACCCCTGACCCCAGAAGGG  1708

Qy    541  AspArgValAlaArgAlaGluMetProAsnGlnLeuArgGlyGlnLeuGluAlaIleIleAla  560
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Db   1709  GACCGGGTTGCGGCGCAGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGCTCGAGGCAATCATAGCC  1768

Qy    561  ThrAspProLeuAsnProLeuThrAlaGluAspLysLysGluLeuLeuTrpHisPheArgTyr  580
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Db   1769  ACGGATCCGCTTAACCCACTCACAGCTGAAGACAAAGAAGAACTGCTCTGGCATTTCAGATAT  1828

Qy    581  GluSerLeuLysAspProLysAlaTyrProLysPheSerGluValLysTrpGlyLysGln  600
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Qy    601  GlnGluIleValAlaLysThrGlnValThrArgGluValValTrpAspTrpGlnSer  620
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Db   1889  CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGAGGTCTGGATCAGAGT  1948

Qy    621  AlaLeuAlaIleAlaValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
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Db   1949  GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGATGAAAACGTG  2008

Qy    641  ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspAspValLeuHisTyrLeu  660
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Db   2009  AGAGCCATTGCAGTGCAGAAACTGGAGAGCTTGGAGGATGATGAGGCTGCCATTACCTG  2068

Qy    661  LeuGlnLeuValGlnAlaValLysPheGlnLeuProTyrHisAspSerAlaLeuAlaArgPhe  680
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Qy    681  LeuLeuValArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheLeuPheArg  700
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Db   2129  CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTTGTTTCTGTTTCGGAGA  2188

Qy    701  SerGluIleGluAlaGlnHisSerArgHisTyrGlnLeuArgPheAlaValIleLeuGluLeuAlaTyr  720
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Db   2189  AGTGAGATTGCCCAGTCAGGCACTATCAGCAGAGGTTTGCAGTTCTGGAAGCCTAC  2248
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Qy  721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp 740
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Db 2249 CTGCGAGGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy  741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
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Qy  781 GlnSerPheArgValProTyrAspProGlyLeuLysLysGlyAlaLeuValIleGluLys 800
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Qy  801 CysLysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
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Qy  861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyArgGlyIleGlyMetIleGlu 880
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Db 2669 GATCTGTGCCTCCTGCCATATGGCTCATTTGCAATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy  881 IleValLysAspAlaThrThrIleAlaLysIleGlnAsnSerThrValGlyAsnThrGly 900
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Db 2729 ATCGTGAAGGACGCCACGACAATGCCAAAATTCAGCAAAGCACAGTGGCAACACCGGGT 2788

Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
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Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAGAAAG 2848

Qy  921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
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Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGCGCAGGCTACTGTGTGGCAACCTTT 2908

Qy  941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
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Db 2909 GTTCTCGGAATAGGCGACAGACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
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Db 2969 TTTCATATTGATTTCGGACACATTCTTGGAAATTACAAAAGTTTCCTTGGCATTAATAAA 3028

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Db 3029 GAGAGGGTGCCATTTGTCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisThrArgAsnLeuIleLeuIleLeuAspValCysValLysAlaAlaLeu 1020
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Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTTGCGTCAAGGCTAACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrArgAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
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Db 3149 CGTTCATCACCACAACCTACACTTGATCATCCTTCTCCATGATGCTGATGACAGGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspIleLysArgIleGluThrValIleGlyLysLysSer 1060
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Qy 1061 GluGluAspValThrAspValSerAsnValHisAspGluGluThrArgArgLeu 1080
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Db 3269 GAGGAGGATGCTAAAAAGTATTTTCGGATCAGAATTGAGAGTTCAGAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleIleLysGlnLeuGlyLysHis 1100
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Db        GACGTCACCGACGTCAGCAACGTGCATGACGAGGAGACTCGGAGGTTCACGCGGCGCCCCTG 628
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Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
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Db 3389 CCCGCA 3394
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RESULT 4
AR029062

LOCUS	AR029062	3808 bp	DNA	linear	PAT	29-SEP-1999
DEFINITION	Sequence 3 from patent US 5859201.
ACCESSION	AR029062
VERSION	AR029062.1 GI:5941035
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 3808)
AUTHORS	Stephens,L. and Hawkins,P.Thomas.
TITLE	G-beta-gamma regulated phosphatidylinositol-3' kinase
JOURNAL	Patent: US 5859201-A 3 12-JAN-1999;
FEATURES	Location/Qualifiers
source	1..3808
	/organism="unknown"
BASE COUNT	1010 a 965 c 953 g 880 t
ORIGIN	

Alignment Scores:

Pred. No.:		Length:	3808
Score:	0	Matches:	1090
Percent Similarity:	5726.00	Conservative:	6
Best Local Similarity:	99.46%	Mismatches:	6
Query Match:	98.91%	Indels:	0
DB:	98.89%	Gaps:	0
	6		

US-09-974-573-1 (1-1102) x AR029062 (1-3808)

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Qy    1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluArgArgArgArg 20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACCCGCAGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuSerProIle 40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149 CGGAGGATGAAGCCGCGGAGCACGCGGCAGCCTGTCCTCCATGAGCTCATCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209 GAGTTTGTTTTGCCCACCAGCCAGCGCAACACCAAGACCCCGAAACGGCACTGCTGCAC 268

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
            ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db  269 GTGGCCGGCCACGGCAATGTGGAGAGATGAAGGCCCAGGTGTTGTTGCGGCGCTGGAG 328

Qy   81 ThrSerValSerAlaAspTheTyrHisArgLeuGlyProAspHisArgLeuLeuLeuTyr 100
            ||||||||||||||||||||||||:::|||||||||||||||||||||||::::|||||
Db  329 ACGAGCGTTTCTTGGGACTTCTACCACCGGTTCGGCCCGACCATGACAACTTCCTCCTGTCTTC 388

Qy  101 GlnLysLysGlyValGlnLysTrpTyrGluIleTyrArgArgAsnValValGlnThrLeuAsp 120
            ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db  389 CAGAAGAAGGGGGTGCAGAAGTGGTACGAGATCTATAGACAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleHisValArgGlnIleArg 140
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Db  449 TGCCTGCGCTACTGGGAGGTGTTGCACCGCAGCCCCGGGGGCAGATCCACGTGGTCCAGGGA 508

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Db  509 CACGGCGCCCTGCGGAGAGACAATTGGCCTTCCAGCGCCCAGCTCAACGCCCTCATCGGCTAC 568

Qy  161 AspValThrAspValSerAsnValHisAspGluGluThrArgArgLeu 180
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Db  569 GACGTCACCGACGTCAGCAACGTGCATGACGAGGAGACTCGGAGGTTCACGCGGCGCCCCTG 628
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Qy  181  ValThrProArgMetAlaGluValAlaGlyAlaGlyArgAspProLysLeuTyrAlaMetHisPro  200
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Db  629  GTCACCCCGCGCATGGCCGAGGTGGCCGGCGCGGGACCCCGAGCTTACGCCATGCACCCC  688

Qy  201  TrpAspAsnProLeuThrLysAlaGluAspLysTrpLeuLysGluLeuTrpHisPheArgTyr  220
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Db  689  TGGGTGACATCCAAGCTCCCCGAGTACCTTCGAGATCACTAACAACTGCGTC  748

Qy  561  ThrAspAsnProLeuAsnThrLeuAlaGluAspLysTrpLeuLysGluLeuTrpHisPheArgTyr  580
Db 1769  ACGGATCCGTTAACCCACTCACAGCTGAAGACAAAGAACTGCTCTGGAAATTTCAGATAT 1828
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[Page consists of dense DNA/protein sequence alignment data in paired Qy (query) / Db (database) rows with translated amino-acid sequences and corresponding nucleotide sequences separated by match bars, numbered at right and left margins from residues 181–920 and nucleotides 629–2788.]

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Db  2789  GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG  2848
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Qy    89  ATGGAGCTGGAGAACATGAACAGCCCGTGGTGCTGAGAGGAGCAACCGCGCAGGCGCGT   148

Db   921  PheGlnAlaAlaValAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
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Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluSerLeuProIle    40

Db  2849  TTTCAGGCAGCTGTGGAGAGATTTGTTATTCGTGCCGGCTACTGTGTGGCCAACCTTT  2908
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Qy   149  CGGAGGATGAAGCCGCGCAGCACGGCAGCCGCTCCTCCTGAGAGTCCATCCCCATC   208

Db   941  ValLeuGlyValIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
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Qy    41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGlnThrProAlaLeuLeuHis   60

Db  2909  GTTCTTCGGAATAGGCGACGAGACACAATATTATGATCTTCAGAAACAGGAAATCTTA  2968
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Qy   209  GAGTTTGTTTGCCACGCCAGGCGAACACCAAGACCCCGAAACGGCACTGCTGCAC   268

Db   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys   980
          |||||||||||||||||||||||||||||||||
Qy    61  ValAlaGlyHisGlyAsnValGluGlnValMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80

Db  2969  TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAGTTTCCTGGGCATTAATAAA  3028
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Qy   269  GTGGCCGGCCACGGCAATGTGGAGCAGGTGATGAAGGCCCAGGTGTTGTTGCGGGCGCTGGAG  328

Db   981  GluArgValProPheValThrProAspPheLeuPheValMetGlyThrSerGlyLysLys  1000
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Qy    81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100

Db  3029  GAGAGGGTGCCATTTGTGACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG  3088
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Qy   329  ACGAGCGTTTCTTGGGGACTTCCACCACCGGAGTTCCTCCTCCTGGTTCTTC   388

Db  1001  LysThrSerLeuHisPheGlnLysAspValCysValLysAlaTyrLeuAlaLeu  1020
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Qy   101  GlnLysLysGlyGlnInTrpTyrTyrGlnIleTyrArgAspLysTyrGlnInThrLeuAsp  120

Db  3089  AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT  3148
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Qy   389  CAGAAGAAGGGGAGTGGTACCAGATCTATCGAGACAAGTACCAGCAGACCCTGGAC  448

Db  1021  ArgHisHisThrAsnLeuIleLeuIleIleLeuProSerMetMetLeuMetThrGlyMetPro  1040
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Qy   121  CysLeuArgTyrTrpLysValHisArgSerProGlyGlnIleHisValGlnInIleValGlnArg  140

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Qy   141  HisAlaProSerGluThrLeuAlaPheGlnInLeuAsnAlaLeuIleLeuGlyTyr  160

Db  3209  CAGTTAACCAGCAAAGGACCAAAGAAGATGTATTTCGGATACATTCGGGATGCCCTTCACAGTGGGCAAAAGT  3268
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Qy   509  CACGCGCCCTCGGAGGAGACAATTGGCTTCCAGCTCAACGCGCTCATCGGCTAC  568

Db  1061  GluGluLysAspAlaLysLysTyrPheLeuAspTyrPheLeuGlnIleGluValCysArgAspLysGlyGlyTrp  1080
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Qy   161  AspValThrArgMetAlaGluValAlaGlyValAlaGlyProLysLysTyrAlaMetHisPro  180

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Qy   569  GACGTACCGACGTCAGCAACGTGCATGACAGCGGCCGGCCAAGCTTTACGCCATGCACCCC  628

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Qy   181  ValThrProArgMetAlaGluValAlaGlyArgAspProLysProLeuArgAlaMetHisPro  200

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Qy   629  GTCACCCCGCGCATGGCCGAGGTGGCCGGCCGACACCCAAGCTTTACGCCATGCACCCC  688

Qy   201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleLeuThrAsnAsnCysVal  220
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Qy   689  TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC  748

Qy   221  PheIleValIleHisArgSerThrThrSerGlnInThrIleLysValSerAlaAspAspThr  240
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Qy   749  TTCATCGTCATTCACCCGAGCACCACCAGCCAGATCAAGGTGTCTGGCCGATGACACC  808

Qy   241  ProGlyThrIleLeuGlnInSerProPhePheThrLysMetAlaLysLysSerLeuMetAsp  260
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Qy   809  CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  868

Qy   261  IleProGluSerGlnInAsnGluArgAspPheValLeuArgValCysGlyGlyArgGluTyr  280
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Qy   869  ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTCTGCGGCGGGATGAGTAC  928

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Qy   929  CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG  988

Qy   301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspThrGlyValAlaArgLys  320
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Qy   989  GAGGAGATTCACCTTGTCTGACACTCCTCCAGACCCAGCCCTGGACACCGGAGTGAGGAAG  1048

Qy   321  GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyTyrHisGluGlnInLeuThr  340
          |||||||||||||||||||||||||||||||||
Qy  1049  GAAGAGTGGCCCGTGGTGGCTGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGTGACC  1108

Qy   341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuProArgAsnLys  360
          |||||||||||||||||||||||||||||
Qy  1109  ATCCACACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGCCGGGACTGTGACCGGAAG  1168

Qy   361  PheArgLysIleArgGlyIleAspIleProValValLeuArgGluArgAspAsnArgArgArgArg  380
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RESULT 5
AR033966
LOCUS   AR033966   3808 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5869271.
ACCESSION   AR033966
VERSION   AR033966.1 GI:5949571
KEYWORDS   Unknown.
SOURCE   Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 3808)
AUTHORS   Stephens,L. and Hawkins,P.Thomas.
TITLE   G-beta-gamma regulated phosphatidylinositol-3' kinase
JOURNAL   Patent: US 5869271-A 3 09-FEB-1999;
FEATURES   Location/Qualifiers
source   1..3808
                     /organism="unknown"

BASE COUNT   1010 a   965 c   953 g   880 t
ORIGIN

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 6   Gaps: 0

US-09-974-573-1 (1-1102) x AR033966 (1-3808)
Qy   1 MetGluLeuGluAsnTyrGluGlnInProValValLeuArgGluArgAspAsnArgArgArgArg 20

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Qy    741 MetLeuGlnLysValThrIleAspIleSerLeuSerAlaGluLysTyrAspValSer 760
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Db   2309 ATGTTACAAAAGTCACCATTGATATCCCTCTCTGCTGAAAAGTATGAGTCAGT 2368

Qy    761 SerGlnValIleSerGlnLeuLysGlnLysGluAsnLeuGlnAsnLeuAsnLeuPro 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAATTTGAATCTCCCC 2428

Qy    781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGTCTGAAAGCCGGGGCACTGGTGATCGAAAAA 2488

Qy    801 CysLysValMetAlaSerLysLysProLeuTrpLeuCysPheLysGluAspPro 820
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Db   2489 TGTAAAGTGATGGCCTCCAAGAAGAAGAGCCCCTGTGGCTTGAGTTTAAATGCCGATCCT 2548

Qy    821 ThrAlaLeuSerAsnGluThrIleGlyIleLeuGluPheLysHisGlyTyrAspLeuArgGln 840
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Db   2549 ACGGGCTCATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA 2608

Qy    841 AspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG 2668

Qy    861 AspLeuCysLeuLeuProTyrGlyTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
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Db   2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy    881 IleValLysAspAlaThrThrIleAlaLysIleGluGlnAsnSerThrValGlyAsnThrGly 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2729 ATCGTGAAGGACGCCACGACATCGCCAAAATTCAGCAACAGCACAGTGGGCAACACCGGGT 2788

Qy    901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
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Db   2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy    921 PheGlnAlaAlaValGlnArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
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Db   2849 TTTCAGGCAGCTGTGGAGAGATTTGTTATTCCTGTCCGCTACTGTGTGGCAACCTTT 2908

Qy    941 ValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
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Db   2909 GTTCTCGGAATAGGCGACAGACAATGACAATATATGATCTCAGAAACAGGAAATCTA 2968

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
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Db   2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy    981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyTyrSerGlyLys 1000
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Db   3029 GAGAGGGTGCCATTTGTCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

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Db   3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT 3148

Qy   1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
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Db   3149 CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC 3208

Qy   1041 GlnLeuThrSerLysGluAspArgIleGluTyrIleLeuArgAspAlaLeuThrValGlyLysSer 1060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3209 CAGTTAACCAGCAAAGAAGACAGGATTGAGTACATTCTGAGAGATGCCCTCACAGTGGCAAAAGT 3268

Qy   1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspArgGlyTrp 1080
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Db   3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGATAGAGGATGG 3328

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleIleGluGlyLysHis 1100
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Db   3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAAGGGGAGAAGCAT 3388
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Db   1169 TTCAGGGTCAAATCAGAGGCATTGATATCCCTGTCTGCCCGCGACCTCACG 1228
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Db   1229 GTGTTTGTTGGAGCCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAACCAGC 1288

Qy    401 ProLysProThrGluGluValLeuTrpAsnValTrpLeuPheSerIleLysIle 420
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Db   1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTGTTCAGTATTAAAATC 1348

Qy    421 LysAspLeuProLysProGlyAlaLeuLeuAsnLeuAsnLeuTyrCysGlyLysAlaProAla 440
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Db   1349 AAAGACTTACCCAAAGGGCTCTGCTGAACCTTCAGATCTACTGCGGCAAAGCTCCAGCA 1408

Qy    441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyGlyLysAlaGlyLeu 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGTCCAAAGGGCAAAGCTCAGGTT 1468

Qy    461 LeuTyrTyrValAsnLeuLeuLeuLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
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Db   1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCTGCGACATGGCGAGTAT 1528

Qy    481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyValGlnAspGlySerPheAsnAlaAsp 500
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Db   1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC 1588

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Db   1589 AAGCTCACAGTCGGCAACACCCTTAACCCGGACAAGGAGGACTTCAATG 1648

Qy    521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
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Qy    541 AspArgValAlaArgAlaLysMetProAsnLeuArgGlnLeuGlnLeuAlaIleIleAla 560
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Qy    581 GluSerLeuLysAspProLysProLysSerValLysSerTrpGlyValTrpGlyGln 600
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Qy    601 GlnGluIleIleValAlaAlaLysThrTyrGlnLeuLeuAlaLysArgGlnValTrpAspGlnSer 620
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Db   1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTCGAGCTCTGCAACTTCTCGGATGAAAACGTG 2008

Qy    641 ArgAlaIleAlaAlaValGlnLysLeuGluSerLeuGluAspAspAspAlaLeuHisTyrLeu 660
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Db   2009 AGAGCCATTGCAGCTGTTCAGAAACTGGAGAGCTTGGAGGATGATGACGCTGCCATTACCTG 2068

Qy    661 LeuGlnLeuValGlnAlaValAlaLysProArgSerAlaAlaLeuAlaArgPhe 680
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Db   2069 CTCCAGCTGGTCCAGGCTGTGTGCAAAAGGGGAAATTTGAAAATTGAACCAGCACCAGATTT 2128

Qy    681 LeuLeuLeuArgGlyLeuArgAspAsnLysArgIleGlyHisProLeuTrpPheLeuArg 700
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Db   2129 CTCCTACTGCGTGGTTTAAGGAACAACAAAAGAAGAAATTGGTCACTTCTGTTTTGGTTCTTGAGA 2188

Qy    701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluLeuAlaTyr 720
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Db   2189 AGTGAGATTGCCCAGTCTAGGCACTATCAGATCAGGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy    721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleValLeuLysHis 740
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Db   2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCCAGCAAGTCCAAGTCCAAGTAATTGAC 2308
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Qy    1101 SerAla 1102
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Db    3389 CCCGCA 3394
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RESULT 6
BC035683
LOCUS       BC035683              3860 bp    mRNA       linear      PRI 23-SEP-2002
DEFINITION  Homo sapiens, phosphoinositide-3-kinase, catalytic, gamma
            polypeptide, clone MGC:46206 IMAGE:5749986, mRNA, complete cds.
ACCESSION   BC035683
VERSION     BC035683.1  GI:23274229
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3860)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), National Institutes of Health, Mammalian
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: m Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21237724.
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BASE COUNT   1111 a     924 c     932 g     893 t
ORIGIN
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Alignment Scores:
Pred. No.:                  0              Length:         3860
Score:                5538.00             Matches:        1050
Percent Similarity:     97.10%            Conservative:     20
Best Local Similarity:  95.28%            Mismatches:       32
Query Match:            95.65%            Indels:            0
DB:                                       Gaps:              0
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US-09-974-573-1 (1-1102) x BC035683 (1-3860)

Qy    1 MetGluLeuAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
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Db   54 ATGGAGCTGAACTATGAGCAGCCCGTGGTGCTGAGAGAGGACAATAGACGGCGC 113

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
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Db  114 CGGAGGATGAAGCCGCGCAGTGCTGCGGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 173

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
        ||||||||||||||||||||||| | ||||||||    |||||||||||||||||
Db  174 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGAGCCCGAAGCCGCTGCCAC 233

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
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Db  234 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 293

Qy   81 ThrSerValSerAlaAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
        |||||||||| ||::|||||||||||||||||||||||||   |||||||||
Db  294 ACCAGCGTGAGCGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT 353

Qy  101 GlnLysGlyGlnTrpTyrGlnTrpIleTyrAspLysTyrGlnValValLeuThrLeuAsp 120
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Db  354 CAGAAGAAGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 413

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
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Qy  141 HisAlaProSerGluGluThrGlnAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Db  474 CACCCCGCCCCCGGAGGAGTCCCAAGCCTTCCAGCGCTGGCAGCTACCTGCGGCTGATTGGCTAT 533

Qy  161 AspValThrAspValSerAsnValHisAspAspLeuGluPheThrArgArgGlyLeu 180
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Db  534 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG 593

Qy  181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
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Db  594 GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGCGACCCCAAGCTCTACGCCATGCACCCG 653

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
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Db  654 TGGGTGACGTCCAAGCCCCTTCCCGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC 713

Qy  221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr 240
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Sun Feb 15 18:14:36 2004   us-09-974-573-1.rge

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Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLeuLysLysSerLeuMetAsp  260
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Db   774 CCCGGGCCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAAATCTCTGATGGAT  833

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr   280
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Db   834 ATTCCCGAAAGCCAAAGCGAACAGGGATTTGTGCTGCGCGTGTGCGGCCGGGATGAGTAC    893

Qy   281 LeuValGlyGluThrProIleLysPheGlnPheValArgGlnCysLeuLysAsnGly      300
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Db   894 CTGGTGGGCGAAACGCCCATCAAAAAACTTCCAGTGGGTCAGCCACTCCTCAAGAACGGA   953

Qy   301 GluGlyIleHisLeuValLeuAspAspThrProAspProAlaLeuAspGluAspValArgLys 320
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Db   954 GAAGGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCCTAGACGAGGTGAGGAAG  1013

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyValThrGlyGlnLeuGlnLeuThr 340
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Db  1014 GAAGAGTGGCCGCTGGTGACGACTGCACGGAGTCACCGGGTACCCATGAGCAGCTTACC   1073

Qy   341 IleHisGlyLyLysAspGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
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Db  1074 ATCCACGGCAAGACCACGAGAGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG    1133

Qy   361 PheArgValLysAspGlyIleTyrIleAspAspProValProLeuProArgThrAlaAspLeuThr 380
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Qy   381 ValPheValGlnAlaAsnIleGlnTyrGlyGlnGlnArgArgThrSer               400
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Db  1194 GTTTTTGTAGAGGCAAACATCCAGTACGGGCCAACAAGTCCTTTGCCAAAGGAGAACCAGC  1253

Qy   401 ProLysProPheThrGluValLeuTrpTrpAspAspValPheLeuGluProSerIleLysIle 420
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Qy   421 LysAspLeuProLysGlyValAlaLeuAsnLeuAsnLeuIleTyrCysGlyLysAlaProAla 440
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Db  1314 AAAGACTTGCCCAAAGGGGCTTCACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA   1373

Qy   441 LeuSerArgLysThrSerAlaGluMetProSerProGluSerLysGlyGlyLysAlaGlnLeu 460
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Db  1374 CTGTCCCAGAAGACCTCTGCAGAGTCCCCCAGTTCTGAGTCCAAGGGCAAAGTTCAGCTT  1433

Qy   461 LeuTyrPheTyrValAlaAsnLeuLeuLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
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Db  1434 CTCTATTTATGTGACCAACCTGCTGCTGATAGACCACCGGTTTCTCCTGCGCGGTGAGAATAC 1493

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLyGluAspGlnGlySerPheAsnAlaAlaAsp     500
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Db  1494 GTCCTCCACATGTGGCAGATCTGGGAGGGCAGAAGACCAAGGAAAGCTTCAATGCTGAC   1553

Qy   501 LysLeuThrSerAlaThrAsnProAspLysProLysGluAsnSerMetSerIleLeuLeuLeu 520
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Db  1554 AAACTCACGTCTGCAACTAACCCAGACAAGCCCAAGGAGAACTCAATGTCCATTCCATTCTTCTG 1613

Qy   521 AspAsnTyrCysHisProLeuAlaAlaLeuProThrProAspProGluGly            540
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Qy   541 AspArgValArgAlaGluMetProAsnGlyLysGluArgLysGlyGlnLeuGlnLeuAlaIleIleAlaAla 560
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Qy   601 GlnIleGluIleAlaAlaLysThrTyrGlnLeuLeuLeuAlaLysArgGluValTrpAspArgGlnSer 620
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Db  1854 CAAGAAATTGTGGCCAAAACATACCAATGTTGGCCAGAGGGAGTCTGGGATCCAAAGT   1913

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerGluAsnVal       640
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Db  1914 GCTTTGGATGTTGGGTTAACAATGCAGTTGCTTGACTGCAACTTCTCAGATGAAAATGTA   1973

Qy   641 ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu    660
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Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe     680
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Qy   681 LeuLeuLysArgGlyLeuAsnLysAsnArgIleGlyHisPheLeuPheTrpPheLeuArg     700
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Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaTyr     720
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Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnAsnValIleLeuAspAsp    740
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Qy   741 MetLeuGlnLysValThrIleAspIleSerLeuSerAlaGluLysTyrAspValSer      760
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Qy   761 SerGlnValIleSerGlnLeuLysGlnLeuLysGluGlnLeuAsnLeuGlnAsnLeuAsnLeuPro 780
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Db  2334 TCCCAAGTTATTTCACAACTTAAACAAAGCTTGAAAATCCAGAAATTCTCAACTCCCC     2393

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuGluGluLys     800
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Db  2394 GAAAAGTTTAGAGTTCCATATGATCCTGGACTGAAGAAGCAGGAGGCCCTGGCAATTGAAAAA  2453

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluLysHisGlyCysAlaAspPro    820
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Db  2454 TGTAAAGTAATGGCCTCCAAGAAAAACCCATGGCTTGAGTTTAAATGTGCCGATCCT     2513

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyTyrIleIlePheLysHisGlyAspLeuArgGln    840
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Db  2514 ACAGCCCTATCAAATGAAACAATTGGATATATCATTTAAACATGGTGATCTGCGCCAA     2573

Qy   841 AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
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Db  2574 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG   2633

Qy   861 AspLeuCysLeuProTyrGlyCysIleSerSerThrGlyLysMetIleGlu            880
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Db  2634 GATCTATGCCTCCCTATGGTTGCATTTCAACTGGTGACAAAATAGGAATAATGATCGAG    2693

Qy   881 IleValLysAspAlaThrArgLysThrIleLeuGlnIleSerThrValGlyAsnThrGly    900
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Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGlyCysGlyProLeuGluLys      920
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Db  2754 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG    2813

Qy   921 PheGlnAlaAlaValGlyAlaArgPheValTyrSerCysSerValAlaThrPhe         940
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Db  2814 TTTCAGGCAGCAGTGGGAGAGATTTGTTTATTCCTGTGCAGCTACTGTGTGGCAACCTTT   2873

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu    960
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Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys    980
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EKCKVMASKKKPLMLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQIRIMESIWE
TESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEK
SPTEEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMITETGNLFHIHFDGHILGNY
KSFLGINKRVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIIL
FSMMLMTGMPQLTSEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGWTVQFNWFL
HLVLGIKQGEKHSA"
```

```
BASE COUNT     950 a    861 c    849 g    750 t
ORIGIN
```

Alignment Scores:

```
Pred. No.:                0
Score:                 5534.00
Percent Similarity:      97.10%
Best Local Similarity:   95.19%
Query Match:             95.58%
DB:                       9
```

```
Length:        3410
Matches:       1049
Conservative:    21
Mismatches:      32
Indels:           0
Gaps:             0
```

US-09-974-573-1 (1-1102) x AF327656 (1-3410)

```
Qy    1 MetGluGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArg 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGGAGGAGAACTATAAACAGCCCGTGGTGCTCAGAGAGGACAACCGCCGCCGC 60

Qy   21 ArgArgMetLysProArgSerThrAlaAlaAlaSerLeuSerMetGluLeuIleProIle 40
        |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db   61 CGGAGGATGAAGCCGCGCAGTGCTGCGGCAGCCTGTCCATGGAGCTCATCCCCATC 120

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
        |||||||||||||||||||||||||::::||||||||||||||||||||||
Db  121 GAGTTCGTGCTCCCCACCAGCCAGCGCAAATGCAAGAGCCCGGAAACTGCCCTGCTGCAC 180

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 240

Qy   81 ThrSerValAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
        |||||||||||||||||||||||||:||||||||||||||||||||||||||
Db  241 ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTGCTCTAT 300

Qy  101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CAGAAGAAGGGCCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 360

Qy  121 CysLeuArgTyrTrpLysValTrpLysValHisArgSerProGlyGlnIleHisValGlnArg 140
        |||||||||||||||||||||||||||||||||||||||
Db  361 TGCCTGCGCTACTGGAAGGCCACGCACCGGAGCCCGGGCCAGATCCACCTGGTGCAGCGG 420

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnAlaPheGlnLeuAsnAlaLeuIleGlyTyr 160
        |||||||:::|||||||||||||||||||||||||||||||||
Db  421 CACCCGCCCTCCGAGGAGACTTTCAGCCAAGCCTTCCAGCGCCAGCTCACGGCGCTGATTGGCTAT 480

Qy  161 AspValThrAspValSerAsnValHisAspAspGluLeuGluGlyPheThrArgArgGlyLeu 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 2934 TTCATATTGACTTCGGCGACATCTTGGGAATTACAAAAGTTCCTCTGGGCATTAATAAA 2993
Qy 981 GluArgValProPheValThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db 2994 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3053
Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspIleCysValLysAlaTyrLeuAlaLeu 1020
Db 3054 AAGACAAGCCCACACTTCCAGAAATTTCAGGACATCTGTGTTAAGGCTTATCTAGCCCTT 3113
Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
Db 3114 CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCC 3173
Qy 1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
Db 3174 CAGTTAACAAGCAAGGAAGACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAT 3233
Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
Db 3234 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG 3293
Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis 1100
Db 3294 ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAGGGAGAGAAACAT 3353
Qy 1101 SerAla 1102
Db 3354 TCAGCC 3359

Left column

```
Db  481  GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCTGGCCTTG  540
Qy  181  ValThrProArgMetAlaGluValAlaGlyTyrArgAspProLeuLysArgAlaMetHisPro
Db       ValThrProArgMetAlaGlyValAlaGlyTyrArgAspProLeuLysArgAlaMetHisPro  200
Db  541  GTGACCCCGCGCATGGCGGGAGTGGCCAGCCGCCCGACCCCAAGCTCTCACGCCATGCACCCG  600

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLysLysIleThrArgAsnCysVal
Db       PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr  240
Db  601  TGGGTGACGTCAAAGCCCCTCCCGGAGTACCTGTGGAAGAGATTGCCAACAACTGCATC  660

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr  240
Db       ProGlyThrIleLeuGlnSerPheThrArgLysMetAlaLysSerLysLeuSerLeuMetAsp  260
Db  661  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACCACACC  720

Qy  241  ProGlyThrIleLeuGlnSerPheThrArgLysMetAlaLysSerLysLeuSerLeuMetAsp  260
Db       IleProGluSerGlnAsnGluArgAspPhePheValLeuArgValCysGlyArgAspGluTyr  280
Db  721  CCCGGCGCCACCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAGAAATCTCTGATGGAT  780

Qy  261  IleProGluSerGlnAsnGluArgAspPhePheValLeuArgValCysGlyArgAspGluTyr  280
Db       LeuValGlyGluThrProIleLysLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
Db  781  ATTCCCGAAAGCCAAAGCGACAAGGATTTTGCTGCACGGAGATTGCCGGTCTGTGCCCGGA  840

Qy  281  LeuValGlyGluThrProIleLysLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
Db       GluIleLeuHisIleLeuValLeuAspThrProProAlaLeuAspGluValLeuValArgLys  320
Db  841  CTGGTGGGCGAAACGCCCATCAAAAAACTTCCAGTGGGTGAGGCACTGGCCTCAAGAACGGA  900

Qy  301  GluIleLeuHisIleLeuValLeuAspThrProProAlaLeuAspGluValLeuValArgLys  320
Db       GluGluTrpProLeuValAspAspCysGlyValThrGlyValThrGlyTyrHisGluGlnLeuThr  340
Db  901  GAAGAGATTCAGTGGTACTGGACACGGCCCTCCAGACCCGGGCCTAGACGAGGTGAGGAAG  960

Qy  321  GluGluTrpProLeuValAspAspCysGlyValThrGlyTyrHisGluGlnLeuThr  340
Db       IleHisGlyLysAspHisGluSerValPheGlyLysValSerLeuSerGlnThrSer  360
Db  961  GAAGAGTGGCCGCTGGTGGACGACTGCGGAGTCACCGGCTACCATGAGCAGCTTACC  1020

Qy  341  IleHisGlyLysAspHisGluSerValPheGlyLysValSerLeuSerGlnThrSer
Db       SerGluIleAlaGlnAsnSerArgHisTyrGlnGlnIleLeuHisAspPheThrGlnIleValGlnIleLeuAsp  720
Db  1021 ATCCACCGGCAAGGACCACCAGAGAGTGTGTTCACGGGTTCCCTGTGGGGACTGCGACCGCAAG  1080

Qy  361  PheArgValLysAspHisGluLeuArgGlyIleTyrIleAspIleProArgTyrValLeuProValLeuProAlaLeuProAlaGlyArgThrAlaAspLeuThr  380
Db       LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnIleValGlnIleLeuAsp  740
Db  1081 TTCAGGGTCAAGATCAGAGACATCAGGAGGCTCACCGGGTTCCCTGTGGGGACTGCGACCGCAAG  1140

Qy  381  ValPheValGlnAlaAsnIleGluGlnTyrGlyLeuGlnGlnValLeuCysGlnInArgArgThrSer  400
Db       MetLeuGlnIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuAsnLeuPro  780
Db  1141 GTTTTGTAGAGGCAAAACATCCAGCATGGGCAACAAGTCCTTTGCCAAAGGAGAACCAGC  1200

Qy  401  ProLysProPheThrGluLeuValLeuAspHisValProValTrpProValTrpPheLeuGluProSerIleLysIle  420
Db       SerGlnInValIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro  800
Db  1201 CCCAAACCCTTCACAGAGCTGGTGTTGGATCGTGTGGTCGAGTTGGACCATGTCAATCAAAATC  1260

Qy  421  LysAspLeuProLysGlyAlaAlaLeuAsnLeuGlnIleTyrCysGlyTyrGlyLysAlaProAla  440
Db       GlnSerPheArgValProTyrArgAspProGlyLeuLysAlaGlyAlaLeuValIleGluLuLys  820
Db  1261 AAAGACTTGCCCAAAGGGGCTCACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA  1320

Qy  441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerGlyLysGlyLysAlaGlnLeu  460
Db       CysLysValMetAlaSerLysLysProProLeuPheLysTrpLeuGluPheLysCysAlaAspPro  840
Db  1321 CTGTCCCAGCAAGGCCTTGCAAGTCCCAGTTCTGACGTCCAGGGCAAAGTTCGGCTT  1380

Qy  461  ValHisLysMetTrpGlnLeuSerGlyLysGlyGlnGlyTyrGlySerPheAsnAlaAlaAsp  480
Db       ThrAlaLeuSerAsnGluThrIleGluGlyTyrIleIleGlyTyrGlyIleIleGlyIleGluGlu  860
Db  1381 CTGTCCATTATGTGAACCTGCTGCTAGAGACCATCGGGATGGCAGATATCTTCAATGGAAT  1440

Qy  481  ValLeuHisSerAlaThrAsnProAspLysProAspAspLeuArgTyrHisArgProGluLeuGluGluAsp  500
Db       AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyIleLeuGlyIleMetIleGlu  880
Db  1441 GTCCTCCACATGTGGCAGATATCTGGGAAGGAGAAGACCAAGGAAGCTTCAATGCTGAC  1500

Qy  501  LysLeuThrSerAlaThrArgAsnProAspAspLeuArgHisArgProGluGlnSerSerIleLeuSerIleLeuSerIleLeuSerIleLeuLeuSerIleLeuLeu  520
Db       IleValLysAspAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly  900
Db  1501 AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTTCAATGTCCATCTCCATTCTCTG  1560

Qy  521  AspAsnTyrCysHisArgProAlaLeuProLysHisArgProThrProAspProGluGly
Db       IleValLysAspAlaThrArgIleAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly  900
Db  1561 GACAATTACTGCCACCGACCCTGCCTAAGCATCAGCCCCACCCCTGACCCGGAGGGG  1620
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Right column

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Qy  541  AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuAlaAlaIleIleAla  560
Db       AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuAlaAlaIleIleAla
Db  1621 GACCGGGTTCGAGCAGAGAATGCCAACCAGCTTCGCAAGCAATTGGAGGCGGATCATAGCC  1680

Qy  561  ThrAspProLeuAsnProLeuThrPheAlaGluAspLysGluLeuLeuTrpHisPheArgTyr  580
Db       ThrAspProLeuAsnProLeuThrPheAlaGluAspLysGluLeuLeuTrpHisPheArgTyr
Db  1681 ACTGATCACTTAACCCTCTCACAGCAGAGGACAAAGAATTGCTCTGGCATTTTAGATAC  1740

Qy  581  GluSerLeuLysAspProLysAlaTyrProLeuPheSerSerValLysTrpGlyGln  600
Db       GluSerLeuLysAspProLysAlaTyrProLeuPheSerSerValLysTrpGlyGln
Db  1741 GAAAGCCTTAAGCACCCAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG  1800

Qy  601  GlnIleLeuValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer  620
Db       GlnIleLeuValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer
Db  1801 CAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAAGAGGGAAGTCTGGGATCAAAGT  1860

Qy  621  AlaLeuAspAlaValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
Db       AlaLeuAspAlaValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal
Db  1861 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAAATGTA  1920

Qy  641  ArgAlaIleAlaValGlnLeuLysLeuGluSerLeuGluAspAlaAspValLeuHisTyrLeu  660
Db       ArgAlaIleAlaValGlnLeuLysLeuGluSerLeuGluAspAlaAspValLeuHisTyrLeu
Db  1921 AGAGCCATTGCAGTTCAGAAACTGAGAACTGAGAGCCTTGGAGGACGATGAGTGTTCTCATTACCTT  1980

Qy  661  LeuGlnLeuValGlnIleAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe  680
Db       LeuGlnLeuValGlnIleAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe
Db  1981 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCGCCCTTGCCAGATTT  2040

Qy  681  LeuLeuLysArgGlyLeuArgAsnLysSerArgIleGlyHisArgPheLeuPheTrpLeuArg  700
Db       LeuLeuLysArgGlyLeuArgAsnLysSerArgIleGlyHisArgPheLeuPheTrpLeuArg
Db  2041 CTGCTGAAGCGTGGTTGGTTAAGAAACAAAGAAATTGGTCACTTTTTGTTTTGGTTCTTGAGA  2100

Qy  701  SerGluIleAlaGlnAsnSerArgHisTyrGlnGlnIleLeuHisAspPheThrGlnIleValGlnIleLeuAlaTyr  720
Db       SerGluIleAlaGlnAsnSerArgHisTyrGlnGlnIleLeuHisAspPheThrGlnIleValGlnIleLeuAlaTyr
Db  2101 AGTGAGATAGCCCAGAACAGCCGACACTATCAGCAGATCCTCCACGACTTTACCCAAGTCATTCTTGCCTAT  2160

Qy  721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnInValGlnInValIleGluAsp  740
Db       LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnInValGlnInValIleGluAsp
Db  2161 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATTGAGGAG  2220

Qy  741  MetLeuGlnIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuSer  760
Db       MetLeuGlnIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuSer
Db  2221 ATGTTACAAAGTCACCCTGATATTAAATCGCCCTGTGAAAGTATGACGTCAGT  2280

Qy  761  SerGlnInValIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro  780
Db       SerGlnInValIleSerGlnInLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro
Db  2281 TCCCAAGTTATTTCAACAACTTAAACAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC  2340

Qy  781  GlnSerPheArgValProTyrArgAspProGlyLeuLysAlaGlyAlaLeuValIleGluLuLys  800
Db       GlnSerPheArgValProTyrArgAspProGlyLeuLysAlaGlyAlaLeuValIleGluLuLys
Db  2341 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCAGGCCTGGCAATTGAAAAA  2400

Qy  801  CysLysValMetAlaSerLysLysProProLeuPheLysTrpLeuGluPheLysCysAlaAspPro  820
Db       CysLysValMetAlaSerLysLysProProLeuPheLysTrpLeuGluPheLysCysAlaAspPro
Db  2401 TGTAAAGTAATGGCCTCCAAGAAAAAACCTACTATGTCTGAGTTTAAATGGCCCATCCT  2460

Qy  821  ThrAlaLeuSerAsnGluThrIleGluGlyTyrIleIleGlyTyrGlyIleIleGlyIleGluGluGln  840
Db       ThrAlaLeuSerAsnGluThrIleGluGlyTyrIleIleGlyTyrGlyIleIleGlyIleGluGluGln
Db  2461 ACAGCCCTATCAAATGAAACAATTGAATATCTTAAACATGGTATGATCTGCGCCAA  2520

Qy  841  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyIleLeuGlyIleMetIleGlu  860
Db       AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyIleLeuGlyIleMetIleGlu
Db  2521 GACATGCTTATTTTACAGATTTCACGAGTCTATTTTGGGGAGACTCATTTTG  2580

Qy  861  IleValLysAspAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly  880
Db       IleValLysAspAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly
Db  2581 GATCCATGCCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAAATGATGCGGAG  2640

Qy  881  IleValLysAspAlaThrArgIleAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly  900
Db       IleValLysAspAlaThrArgIleAlaThrArgIleAlaLysIleGluGlnSerThrValGlyLysThrGly
Db  2641 ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAGCACAGTGGGCACCACGCGGA  2700
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Qy    1  MetGluLeuGluAsnTyrGluGlnProValLeuArgLeuAspAsnArgArgArgArg        20
Db   84  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC    143

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle        40
Db  144  CGGAGGATGAAGCCGCGAGCACTGCTGCGGCACCCAGCCTGTCTCCATGGAGCTCATCCCATC  203

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrGluThrAlaLeuLeuHis        60
Db  204  GAGTTCGTGCTGCCCACCAGCCAGCGAAATGCAAGAGCCCGAAACGGCGTCTGCTGCAC    263

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysGlyAlaGlnValTrpLeuArgLeuGlu      80
Db  264  GTGGGCCGGCCACGGCAACGTGGAGCAGATGAAGGGCCAGGTGTGGCTGCAGCGCTGGAG    323

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisProPheLeuLeuTyr    100
Db  324  ACCAGCGTGCGCGGGACTTCTACCACCGGCTGGGACCCGGACCACCCCTTCCTCCTCTAT    383

Qy  101  GlnLysLysGlyGlnTrpProTyrGluIleTyrAspGlyTyrGlnValValGlnThrLeuAsp  120
Db  384  CAGAAGAAGGGCCAGTGGCCATACGAGATCTACGACAGTACCAGGTGGTGCAGACTCTGGAC    443

Qy  121  CysLeuArgTyrTrpLysTyrTrpValLeuHisSerArgSerProGlyGlnIleHisValGlnArg  140
Db  444  TGCCTGCGCTACTGGAAGGCCACGGACCCCGGCCAGATCCACGTGGTACCAGCGGGCGG    503

Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnIleLeuAsnAlaLeuIleGlyTyr        160
Db  504  CACCCCGCCCTTCCGAGGAGACCCTGGCAGTTCCAGCGGCGGTTCACGGCGCTGATTGGCTAT  563

Qy  161  AspValThrAspValSerArgAsnValHisAspAspLeuGluPheThrArgArgLeu        180
Db  564  GACGTCACTGACGTCAGCAGCAATGTGCACGACGATGAGGTTCACGCGCGTGGCTTG    623

Qy  181  ValThrProArgMetAlaGluValAlaAlaGlyArgArgProLysLeuTyrAlaMetHisPro   200
Db  624  GTGACCCCGCGATGGCGGAGGTGGCCGCAGGGTCGCAGCCCCAAGCTCTACGCCATGCACCCG  683

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal        220
Db  684  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGATTGCCAACAACTGCATC    743

Qy  221  PheValIleHisArgSerThrSerGlnThrIleLysValSerValSerAlaAspThr        240
Db  744  TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCGACCACACC    803

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaAlaLysLysSerLeuMetAsp      260
Db  804  CCCGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT    863

Qy  261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr      280
Db  864  ATTCCCGAAAGCCAAAGCAACAGGGATTTTGTGCTGCGAGTCTGCGGCCGGGATGAGTAC    923

Qy  281  LeuValGlyThrProLeuLysAspPheAsnProIleLysTrpValArgGlnCysLeuLysAsnGly  300
Db  924  CTGGTGGGCACGCCCCTCAAAGACTTCAACCCTATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA  983

Qy  301  GluGluIleHisLeuValLeuAspAspArgProAlaLeuAspProLysValArgLys        320
Db  984  GAAGAGATTCACGTGGTACTGGACGACCGCCCTGCACTGGACCCCAAGGTGAGGAAG    1043

Qy  321  GluGluTrpProLeuValAspAspCysThrGlyValThrGlyLeuThrGlyLeuThr        340
Db 1044  GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCATGAGCAGTTACC    1103

Qy  341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuLeuTrpAspCysAspArgLys   360
Db 1104  ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGCTGTGGGACTGCGACCGCAAG  1163
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Qy  901  AlaPheLysLysAspGluValLeuSerHisHisTrpLeuTrpLeuLysGluLysCysProIleGluGluLys  920
Db 2701  GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATCCCTACTGAAGAAAAAG                    2760

Qy  921  PheGlnAlaAlaValAlaArgPheValTyrSerAlaGlyTyrCysValAlaThrPhe       940
Db 2761  TTTCAGGCAGCAGTGGCAGATTTGTTTATCCTGCAGGCTACTGTGTGGCAACCTTT            2820

Qy  941  ValLeuGlyValIleGlyGlyAspAlaArgHisAsnAspAsnIleMetIleSerGluThrGlyThrLysAsnLeu  960
Db 2821  GTTCTTGGAATAGGCACAGCAGACACCATATTGATCACCGAGACAGGAAACCTA            2880

Qy  961  PheHisIleAspPheGlyHisPheLeuAspGlyAsnTyrLysSerPheLeuGlyAsnLys       980
Db 2881  TTTCATATTGACTTCGGGCACATTCTTGGGATTACAAAAGTTTCCTGGGCCATTAATAAA         2940

Qy  981  GluArgValProPheValLeuProPheAspPheValMetGlyThrSerGlyLysLys      1000
Db 2941  GAGAGAGTGCCATTTGTCCTAACCCCTGACTTCCTTTGTGATGGGACTTCTGGAAAG           3000

Qy 1001  LysThrSerLeuHisPheGlnLysPheGlnAspLysValCysValLysAlaTyrLeuAlaLeu  1020
Db 3001  AAGACAAGCCCACACTTCCAGAACATTCAGGATAAGGTTGTGTTAAGGCTTATCTAGCCCTT       3060

Qy 1021  ArgHisHisThrAsnLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro      1040
Db 3061  CGTCATCACAACTTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC           3120

Qy 1041  GlnLeuThrSerGluSerProIleGlyTyrIleAspAspAlaLeuThrValGlyLysSer   1060
Db 3121  CAGTTAACAAGCGAAAGACAATTGAATATATCCGGATGCCCTCCACAGTGGGAAAAT            3180

Qy 1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluGlyCysArgAspGlyTyr      1080
Db 3181  GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTGCAGACAAAGGATGG          3240

Qy 1081  ThrValGlnProAsnTrpPheHisHisLeuValLeuGlyIleLeuLysGlnGlyLysHis   1100
Db 3241  ACTGTGCAGTTTAATTGGTTTCATCATTTGTTCTTTGGCATCAAACAGGAGAAACAT           3300

Qy 1101  SerAla  1102
Db 3301  TCAGCC  3306
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RESULT 8

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AR026677
LOCUS        AR026677          5162 bp    DNA        linear        PAT   29-SEP-1999
DEFINITION   Sequence 13 from patent US 5856132.
ACCESSION    AR026677
VERSION      AR026677.1  GI:5937517
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 5162)
  AUTHORS    Stephens,L., Hawkins,P.Thomas. and Braselmann,S.
  TITLE      G-beta-gamma regulated phosphatidylinositol-3' kinase
  JOURNAL    Patent: US 5856132-A 13 05-JAN-1999;
FEATURES             Location/Qualifiers
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ORIGIN
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Alignment Scores:

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Best Local Similarity: 95.58%     Conservative:     21
Query Match:                      Mismatches:       32
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US-09-974-573-1 (1-1102) x AR026677 (1-5162)

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2 others

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Db  1164  TTCAGGGTCAAGATCAGAGGCCATTGATATCCCGTTGCCTCGGACACACCGACCTCACA 1223

Qy   381  ValPheValGluAlaAsnIleGlnTyrTyrGlnValLeuCysGlnArgArgThrSer 400
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Db  1224  GTTTTTGTTGAGGCAAACATCCAGTACTACCAAGTCCTTTGCCAAAGGAGAACCAGC 1283

Qy   401  ProLysProThrGluTrpGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
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Db  1344  AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCAACCAGATCTACTGCGGTAAAGCTCCAGCA 1403

Qy   441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyGlyLysAlaGlnLeu 460
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Db  1404  CTGTCCCAGAAGGCCTCTGCAGAGTCCCCAGTTCTGAGTCCAAGGGCAAAGTTCCGGCTT 1463

Qy   461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
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Db  1464  CTCTATTATGTGAACCTGCTGCTAATAGACCACCGTTTCCTCCTGCGCCGTCATGGAGAATAC 1523

Qy   481  ValLeuHisMetTrpGlnLeuSerGlyGlyValGluAspGlySerPheAsnAlaAsp 500
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Qy   501  LysLeuThrSerAlaThrAsnProAspLysGluSerMetSerIleLeuSerLeuLeu 520
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Db  1584  AAACTCACGTCTGCAACTAACCCAGACAAAGAGAACAATGTCCAATTGTCCATTCTTCTG 1643

Qy   521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProGluGlyGly 540
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Db  1644  GACAATTACTGTCACCCGATAGCCCTGCCTAAGCATCAGCCGACCCCTGACCCGGAAGGG 1703

Qy   541  AspArgValArgAlaGluAlaGluMetProAsnGlnLeuArgLysArgGlnLeuGluAlaIleIleAlaAla 560
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Db  1704  GACCGGGTTCGAGCAGAGAAATGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 1763

Qy   561  ThrAspProLeuAsnProLeuThrAlaGluLeuProLysAspLysLeuLeuTrpHisPheArgTyr 580
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Db  1764  ACTGATCCACTTAACCCTCTCACAGCAGAGGAATTGCCTAAGGACAAGCTTCTGTGGCATTTTAGATAC 1823

Qy   581  GluSerLeuLysAspProLysGlnAlaTyrProLeuLeuPheSerSerValLysTrpGlyGln 600
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Db  1824  GAAAGCCTTAAGGACCCCAAAGCATACCCACTATTAGTTCAGTGAAATGGGGGACAG 1883

Qy   601  GlnGluIleGluValAlaLysLysThrTyrArgLeuIleLeuLeuAlaArgLysTrpAspTrpGlnSer 620
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Db  1884  CAAGAAATTGTGGCAAAAACATACCAATTGTTGCTCCAGAAGGGAAGTCTGGGATCAAAGT 1943

Qy   621  AlaLeuAspAspArgValGlyLeuThrMetGlnLeuAsnLeuAspProAspCysAsnPheSerAspGluAsnVal 640
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Db  1944  GCTTTGGATGTTGGGTTAACAATGCAGCTCCTCGCTGCAACTTCTCCAGATGAATGAAAATGTA 2003

Qy   641  ArgAlaIleAlaValGlnLysLysLeuGlnLysSerLeuGluHisSerLeuValLeuHisTyrLeu 660
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Qy   661  LeuGlnLeuValGlnAlaLysValLysAspProTyrHisSerAlaLeuAlaLeuArgPhe 680
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Db  2064  CTACAAATTGGTCCAGGCGTTGAAATTTGAAACCATACCATAGCGCCCTTTGCCAGATTTT 2123

Qy   681  LeuLeuLysArgGlyLeuArgAsnLeuArgIleGlyTyrIleGlyPheLeuTrpPheLeuArg 700
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Qy   701  SerGluIleGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluLeuAlaTyr 720
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Db  2184  AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAAGCCTAT 2243

Qy   721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnIleLeuGlnIleValIleLeuAsp 740
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Db  2244  CTGAGGGGCTGTGGCACAGCCATGCTGCGACGACTTACCCAACAGTCCAAGTAATCGAG 2303
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Qy   741  MetLeuGlnLysValThrArgLeuAspIleLysSerLeuSerArgAlaGluLysTyrAspValSer 760
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Qy   761  SerGlnValIleSerGlnLeuLeuLysGlnLeuAsnLeuGluAsnLeuAsnLeuPro 780
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Db  2364  TCCCAGGTTATTTCACAACTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC 2423

Qy   781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
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Db  2424  GAAAGCTTTAGAGTTCCATACGATCCTGGACTGAAAGCAGGAGCGCTGGCAATTGAAAA 2483

Qy   801  CysLysValMetAlaSerLysLysLysProLeuPheLysCysGlyAlaAspPro 820
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Db  2484  TGTAAAGTAATGGCCTCCAAGAAAAAACCCTTGTTTAAAATGTGCCGATCCT 2543

Qy   821  ThrAlaLeuSerAsnGluThrIleGlyIleIleIleHisGlyAspAspLeuArgGln 840
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Db  2604  GACATGCTTATTTTACGAATTCATGAGAGTCATTTGGGAGACTGAATCTTTG 2663

Qy   861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspLysIleGlyMetIleGluGlu 880
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Db  2724  ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAGCACACGGGA 2783

Qy   901  AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys 920
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Qy   921  PheGlnAlaAlaValGlnArgPheValTyrSerCysAlaGlyTyrTyrCysValAlaThrPhe 940
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Db  2844  TTTCAGGCAGCAGTGCAGAGATTTGTTATCCTGTGCAGGCTACTGTGTGGCAACCTTT 2903

Qy   941  ValLeuGlyIleGlyIleGlyValAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
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Db  3024  GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3083

Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
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Db  3264  GAGGAGGATGCTAAAAAGTATTTCCTGATCAGATCGAAGTTGCAGAGACAAAAGGATGG 3323

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ACCESSION   AX327655
VERSION   AX327655.1 GI:18097985
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REFERENCE   1
  AUTHORS   Sadhu,C.
  TITLE   Phosphatidyl inositol 3-kinase delta binding partner
  JOURNAL   Patent: WO 0185986-A 9 15-NOV-2001;
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ORIGIN

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US-09-974-573-1 (1-1102) x AX327655 (1-5397)

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Qy   901  AlaPheLysAspGluValLeuSerHisTrpLeuValLysSerProIleGluGlyLysLys  920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3021  GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCCTACTGAAGAAAAG  3080

Qy   921  PheGlnAlaAlaValGlyArgPheValSerCysSerAlaGlyTyrCysValAlaThrPhe  940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3081  TTTCAGGCAGCAGTGGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT  3140

Qy   941  ValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
          ||||||||||||||||||||||||||||||||||:::||
Db  3141  GTTCTTGGAATAGGGGACAGGCACAATGACAATATTATGATCTCCGAGACAGGAAACCTA  3200

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
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Db  3201  TTTCATATTGACTTCGGGCACATTCTGGGAATTACAAAGTTTCCTGGGCATTAATAAA  3260

Qy   981  GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys  1000
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Db  3261  GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG  3320

Qy  1001  LysThrSerLeuHisPheGlnLeuGlnAspAlaValLysAlaTyrLeuAlaLeu  1020
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Qy  1041  GlnLeuThrSerLysGluAspIleGluLyTyrIleGluThrValIleArgAspAlaLeuThrLysArgAspArgGlyLyLysSer  1060
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Qy  1061  GluGluAspProAlaLysLysGlnIleLeuValLeuGlyGlnLysArgAspProLyLysSer  1080
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Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLysGluGlyLysHis  1100
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Db  3621  TCAGCC  3626

RESULT 10
HSIDEM
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DEFINITION   H.sapiens mRNA for phosphatidylinositol 3 kinase gamma.
ACCESSION    X83368
VERSION      X83368.1  GI:1507821
KEYWORDS     phosphatidylinositol 3-kinase.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Stoyanov,B., Volinia,S., Hanck,T., Rubio,I., Loubtchenkov,M.,
             Malek,D., Stoyanova,S., Vanhaesebroeck,B., Dhand,R., Nuernberg,B.,
             Gierschik,P., Seedorf,K., Hsuan,J.J., Waterfield,M.D. and
             Wetzker,R.
  TITLE      Cloning and characterization of a G protein-activated human
             phosphoinositide-3 kinase
  JOURNAL    Science 269 (5224), 690-693 (1995)
   MEDLINE   95350661
   PUBMED    7624799
REFERENCE    2
  AUTHORS    Waterfield,M.D.
  TITLE      Direct Submission
  JOURNAL    Submitted (08-DEC-1994) M.D. Waterfield, Ludwig-Inst. for Cancer
             Research, Courtauld Building, 91 Riding House Street, London, W1P
             8BT, UK
  REMARK     Revised by [3]
REFERENCE    3   (bases 1 to 5397)
  AUTHORS    Waterfield,M.D.
  TITLE      Direct Submission
  JOURNAL    Submitted (23-AUG-1996) M.D. Waterfield, Ludwig-Inst. for Cancer
             Research, Courtauld Building, 91 Riding House Street, London, W1P
             8BT, UK
COMMENT      On Aug 26, 1996 this sequence version replaced gi:940513.
             X83368 is homologous to M93252.
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                     LQKVTLDIKSLSAEKYDVSSQVISQLKQLNSQLPESFRVPYDLKAGALAIE
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BASE COUNT     1534 a   1224 c   1207 g   1432 t
ORIGIN
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Score:                  5523.50            Matches:        1049
Percent Similarity:       97.10%           Conservative:     21
Best Local Similarity:    95.19%           Mismatches:       31
Query Match:              95.40%           Indels:            1
DB:                                        Gaps:              1

US-09-974-573-1 (1-1102) x HSIDEM (1-5397)
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Qy     1 MetGluLeuGlnAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
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Db   324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
         ::      ||||||||   |||                  |||  |||||||||||||||
Db   384 CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 440

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
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Db   441 GAGTTCGTGCTGCCCACCAGCCAGAGAAATGCAAGAGCCCCGAAACGGCGTGCTGCAC 500

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
         |||||||||||||||||   |||||||||     |||    |||   ||||||  ||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         |||    ||   |||   |||||          |||||||||||||||||||||  |||
Db   561 ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT 620

Qy   101 GlnLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
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Db   621 CAGAAGAGGGGCCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTCGAC 680

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
         |||   |||||||||||||||||||::|||||||||||||||||||:::||||||||||
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         ||| |||||||||  |||   |||||  ||| |||:::|||||| |||||||||||  |||
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Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgGlyLeu 180
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Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
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Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleLeuThrAsnAsnCysVal 220
         |||||||||||||||||||||||||:::|||  |||||||   |||||||:::
Db   921 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC 980

Qy   221 PheValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
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Db   981 TTCATCGTCATTCACCGGAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1040

Qy   241 ProGlyThrLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
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Qy   261 IleProGluSerGlnAsnGluAspPheValLeuArgValCysGlyArgAspGluTyr 280
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Qy   281 LeuValGlyGluThrProIleLysAsnProGlnTrpValArgGlnCysLeuLysAsnGly 300
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Qy   301 GluGlnIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
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Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
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Qy   341 IleHisGlyLysGlyAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
Db 1341 ATCCACGGCAAGGACACCACGAGAGTGTGTCCCTGTCCCTGGGACTGCGACCGCCAAG 1400

Qy   361 PheArgValLysIleArgGlyIleLeuProValLeuProArgThrAlaAspLeuThr 380
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Qy   381 ValPheValGluLeuAlaAsnIleGlnTyrGlyGlnGlnIleValLeuCysGlnArgArgThrSer 400
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Db 2181 GCTTTGGATACGCGGTACCTGATGCAGCTCCTGGACAAGTTCTCGGACTGCGATAATGTTAACAATGTA 2240

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Qy   661 LeuGlnLeuValGlnAlaValGlyPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
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Qy  1101  SerAla  1102
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Db  3621  TCAGCC  3626
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RESULT 11
MMU249280
LOCUS   MMU249280   4725 bp   mRNA   linear   ROD 02-NOV-2000
DEFINITION Mus musculus mRNA for phosphoinositide 3-kinase gamma (PI3Kg1 gene).
ACCESSION   AJ249280
VERSION   AJ249280.1 GI:7668042
KEYWORDS   phosphoinositide 3-kinase gamma; PI3Kg1 gene.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Hirsch,E., Wymann,M.P., Patrucco,E., Tolosano,E.,
            Bulgarelli-Leva,G., Marengo,S., Rocchi,M. and Altruda,F.
TITLE   Analysis of the murine phosphoinositide 3-kinase gamma gene
JOURNAL   Gene 256 (1-2), 69-81 (2000)
MEDLINE   20509993
PUBMED   11054537
REFERENCE   2 (bases 1 to 4725)
AUTHORS   Wymann,M.P.
TITLE   Direct Submission
JOURNAL   Submitted (31-AUG-1999) Wymann M.P., Inst. Biochemistry, University
            of Fribourg, Rue du Musee 5, Fribourg CH-1700, SWITZERLAND
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                     EKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQDMLILQLRIMESIWE
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                     CPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNY
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     mat_peptide   322..3627
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BASE COUNT     1251 a   1194 c   1134 g   1146 t
ORIGIN

Alignment Scores:
Pred. No.:                0          Length:        4725
Score:                5506.00        Matches:       1039
Percent Similarity:     97.10%       Conservative:    31
Best Local Similarity:  94.28%       Mismatches:      32
Query Match:            95.09%       Indels:           0
DB:                                  Gaps:             0

US-09-974-573-1 (1-1102) x MMU249280 (1-4725)

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Qy    1  MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
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Db  322  ATGGAGCTGGAGAACTATGAACAACCGGTGGTTCTAAGAGAGGACAACCTTCCGCCGGGC  381

Qy   21  ArgArgMetLysProArgSerThrAlaAlaGlySerLeuSerMetGluLeuIleProIle   40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  382  CGGAGGATGAAGCCACGCAGCGCAGGAGCCAGCCTGTCTTCCATGGAGCTCATCCCCATT  441

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
         ||||||||||||||||||||          :::||||||||||||||||||||||
Db  442  GAGTTCGTACTGCCCACCAGCCAGCGCAACACCAAGACTCCAGAAACAACCAGCGGCTGCTGCAT  501

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  502  GTGGCTGGCCATGGCAATGGAACAGATGAAAGCTCAGGTGTGCGTGCGCCACTGGAG  561

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
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Db  562  ACCAGTGTGTCGGCGGAGTTCTACCACCGCCGAGGCCCCGGACCAATTCCTCCTGCTCTAC  621

Qy  101  GlnLysLysGlyGlnTrpThrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
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Db  622  CAGAAGAAAGGACAATGGTATGAGATCTATGACAAGTACCAAGTGGTGCAGACCCTAGAC  681

Qy  121  CysLeuArgTyrTrpLysLeuValHisArgSerProGlyGlnIleHisValValGlnArg  140
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Db  682  TGCCTGCATTACTGGAAGTTGATGCACAAGAGCCCTGGCCAGATCCACGTGGTACAGCGA  741

Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
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Qy  161  AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu  180
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Db  802  GACGTCACTGACATCAGCAATGTGCACGATGAGCTAGAGTTCACTCGCCGCCGTCTG  861

Qy  181  ValThrProArgMetAlaGluValAlaGlyArgAspProLysTyrAlaMetHisPro  200
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Db  862  GTTACGCCCCGCATGGCTGAAGTGGCTGGCCGGGATGCCAAACTCTATGCTATGCACCCT  921

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal  220
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Db  922  TGGGTAACGTCCAAACCTCTCCCAGACTACCTGTCAAAAAGATTGCCAACAACTGCATC  981

Qy  221  PheIleValIleHisArgSerThrThrSerGlnIleThrIleLysValSerAlaAspThr  240
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Db  982  TTCATCGTCATCCACCGCAGCACCACCAGCCAAACCATCAAGGTCTCCGCAGATGATACT  1041

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysKysSerLeuMetAsp  260
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Db 1042  CCTGGTACCATCCTTCTTCACCAAGATGGCCAAGAAGAAGTCCCTAATGAAT  1101

Qy  261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
         ||||||||||||:::||||||||||||||||||||||||||||::||||||||||||
Db 1102  ATCCCAGAAAGTCAAAGTGCAGGATTTTGTATTGCGGGTTTGTGGCCGGATGAGTAC  1161

Qy  281  LeuValGlyGluThrProLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
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Sun Feb 15 18:14:36 2004   us-09-974-573-1.rge

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Qy  1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro  1040
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Qy  1041  GlnLeuThrSerLysGluArgAspAlaLeuTyrIleArgAspAlaLeuThrValGlyLysSer  1060
Db  3442  CAGCTGACAAGCAAGAGAGACATTGAATATATCCGGGATGCCCTCACCGTGGGAAAAAGC   3501
Qy  1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp   1080
Db  3502  GAGGAGGACGCGTAAGAGAAATATTTCCTTGACAGATCGAGATGCTCTGCAGGACAAAGGATGG  3561
Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGlnGluLysHis   1100
Db  3562  ACTGTGCAGTTTAACTGGTTCCTACATCTTGTTCTTGGCATCAAACAACAGGAGAAAAGCAC   3621
Qy  1101  SerArgIle  1102
Db  3622  TCCCGCT    3627
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RESULT 12
BC051246

LOCUS   BC051246   4330 bp   mRNA   linear   ROD 22-APR-2003
DEFINITION Mus musculus phosphoinositide-3-kinase, catalytic, gamma
            polypeptide, mRNA (cDNA clone MGC:58890 IMAGE:6514979), complete
            cds.
ACCESSION   BC051246
VERSION   BC051246.1 GI:30048085
KEYWORDS   MGC.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 4330)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2 (bases 1 to 4330)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (18-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 108 Row: o Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 9937983.
FEATURES   Location/Qualifiers
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                     /strain="FVB/N-3"
                     /db_xref="taxon:10090"
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                     old mouse. Taken by biopsy."
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                     /note="Vector: pCMV-SPORT6"
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                     /db_xref="LocusID:30955"
                     /translation="MELENYEQPVLREDNLRRRRMKPRSAAGSLSSMELIPIEFVL
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                     CIFIVIHRGTSQTIKVSADDTPGTILQSFFTKVAKKKSLMNISSQSEQDFVLRVCG
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                     MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLPESFRVPYPDGLKAGTLVI
                     EKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQDMILQIRIMESIWE
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                     KSFLGINKERVPFVLTPDFLFVMGSSGKKTSPHFQXFQDVCVRAYLALRHTNLLIIL
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                     HLVLGIKQGEKHSA"
BASE COUNT   1168 a   1088 c   1041 g   1033 t
ORIGIN

Alignment Scores:
Pred. No.:   Length: 4330
Score: 5505.00   Matches: 1039
Percent Similarity: 97.10%   Conservative: 31
Best Local Similarity: 94.28%   Mismatches: 32
Query Match: 95.08%   Indels: 0
DB: Gaps: 0
Pred. No.:   0

US-09-974-573-1 (1-1102) x BC051246 (1-4330)
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Sun Feb 15 18:14:36 2004

us-09-974-573-1.rge

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Qy      1 MetGluLeuLeuGlnAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
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Db     62 ATGGAGCTGGAGAACTATGAACAACCGGTGGTTCTAAGAGAGGACAACCTCCGCCGGCGGC 121

Qy     21 ArgArgMetLysProAlaGlySerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
          ||||||||||||||||||||||||||||||||| :||||||||||||||||||||||||
Db    122 CGGAGGATGAAGCCAGCGGGCGCCACCGCAGCCAGCTCGATGGAGCTCATCCCCATT 181

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GAGTTCGTACTGCCCACCAGCCAGCGCAATACCAAGACTCCAGAAACAGCGGCTGCTCAT 241

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnIleValTrpLeuArgAlaLeuGlu 80
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Db    242 GTGGCTGGACATGGCAATGGAAACAGATGAAAGCTCAGGTGTGGCTGCGCCGCCACTGGAG 301

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuTyr 100
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Db    302 ACCAGTGTGTCTGCTGGGGACTTCTACCACCGATTGGGCCCGGACCATTTCCTGCTCTAC 361

Qy    101 GlnLysLysGlyGlyGlnInTrpTyrAspTyrGlnIleTyrGlnValValGlnValGlnAsnThrLeuAsp 120
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Db    362 CAGAAGAAAGGACAATGGTATGAGATCATGACAGGTACCAAGTGGTGCAGACCCTAGAC 421

Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
          |||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db    422 TGCCTGCATTACTGGAAGTTGATGCACAAGAGCCCTGGCCAGATCCACGTGGTACAGCGA 481

Qy    141 HisAlaProSerGluGluThrArgGlnLeuArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Db    482 CACGTCACTGACATCAGCAATGTGCACGATGATGAGTCTAGAGTTCACTCGCCGCCGTCTG 541

Qy    161 AspValThrAspValSerAsnValHisAspAspGluSerLeuGluTyrAlaMetHisPro 180
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Qy    181 ValThrProArgMetAlaGluAlaGlyAlaAlaArgProLeuTyrAlaMetHisPro 200
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Qy    261 IleProGluSerGlnAsnGluArgAspPhePheLysValArgValGlyArgAspGluTyr 280
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Qy    281 LeuValGlyGluThrProIleLeuLysAspProLeuLysAsnPheGlnInCysLeuLysLeuAsnGly 300
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Db    902 CTGGTGGGTGAAACACCCATCCTCAAAAATTTCCAGTGGTGAGGCAGTGCCTCAAGAACGGA 961

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Db    962 GATGAAATACACCTGGTGCTCGACACCGCCTCCAGACCCTTCCAGACCCTGATGAGGTGAGGAAG 1021

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Db   1082 ATCCATGGCAAGGACCACCACGAGAGTGTGTTCACAGTGTTCTTTGTGGGGACTGCGACCGAAAG 1141

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          |||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 GACAGGGTTCGGGCTGAAGCATGCCAATCAGCTTGAAAAGCAATTGGAGGCGGATCATAGCC 1741

Qy    561 ThrAspProLeuAsnProLeuThrHisAlaGluAspLysLysGluLeuLeuTrpHisPheArgTyr 580
          |||||||||||||||||||||||||||||||||::||||||||||||||
Db   1742 ACAGATCCACTTAACCCCCTCACAGCACGAGGACAAAGAATTGCTCTGCATTTTCGATAT 1801

Qy    581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1802 GAAAGCCTGAAGACATCCGAAGGCTTACCCTAAGCTATTCAGCTCAGTGAAAATGGGGCAG 1861

Qy    601 GlnGluIleLeuValAlaLysTyrTyrGlnInLeuAlaLysArgGluValTrpAspGlnSer 620
          ||||||||||||||||||||||||||::||||||||||||||||||||::||
Db   1862 CAAGAAATTGTTGCAGAAAGTTGCCCAGGATCTGGAGAGGGGATCTGGGATCAAAGT 1921

Qy    621 AlaLeuAspValGlyLeuThrMetGlnLeuThrAsnHisMetGlnAsnPheGluAspAsnVal 640
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1922 GCTTTGGACGTTGGCTTAACCATGCAGCTCACCAACCATATGCAACTTTTCAGACGAGAATGTC 1981

Qy    641 ArgAlaIleAlaValGlyLysGlnInLysLeuGluSerLeuGluHisTyrLeu 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1982 CGGGCCATTGCAGTTGCAGTTCAGAAACTTGAGAGCTTAGAGCAGTTTTTACATTACCTT 2041

Qy    661 LeuGlnLeuValGlnInAlaValPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2042 CTCCAGCTGGTACAGGCGTGTGAAATTTGAACCGTACCACGACAGTGCCTGGCCAGATTCC 2101

Qy    681 LeuLeuGlnLeuValArgGlyLeuArgAsnLysArgIleGluGlyHisPheGlyLeuPheTrpPheLeuArg 700
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2102 CTGCTGCAAGCGGTGCTTGGAGGACAAAGAAATTCAGGAAGACCGGTCACTCTTTGTCTGGTTCTCTCGGA 2161

Qy    701 SerGluIleAlaGlnInSerArgHisTyrGlnInArgPheAlaValIleLeuGluAlaTyr 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2162 AGTGAGATCGCCACAGTCCAGACACTCCAGACAGAGGTTCGCTGATCCTGGAGGCGTAC 2221

Qy    721 LeuArgArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnInValGlnIleValIleAsp 740
          |||||||||||||||||||::::
Db
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Db    1101 SerAla 1102
           |||||
Db    3362 TCCGCT 3367
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RESULT 13
A50265
LOCUS   A50265   4137 bp   DNA   linear   PAT 07-MAR-1997
DEFINITION   Sequence 3 from Patent WO9612024.
ACCESSION   A50265
VERSION   A50265.1   GI:2303321
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 4137)
  AUTHORS   Stoyanov,B., Hanck,T. and Wetzker,R.
  TITLE   CLONING, EXPRESSION AND CHARACTERISATION OF A NOVEL FORM OF
             PHOSPHATIDYLINOSITOL-3-KINASE
  JOURNAL   Patent: WO 9612024-A 3 25-APR-1996;
             MAX PLANCK GESELLSCHAFT (DE)
COMMENT   Other publication DE 445562 960404.
FEATURES   Location/Qualifiers
     source   1..4137
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT   1127 a   999 c   1001 g   1010 t
ORIGIN

Alignment Scores:
Pred. No.:   0   Length: 4137
Score: 5499.50   Matches: 1048
Percent Similarity: 96.92%   Conservative: 21
Best Local Similarity: 95.01%   Mismatches: 32
Query Match: 94.98%   Indels: 2
DB: Gaps: 1

US-09-974-573-1 (1-1102) x A50265 (1-4137)
```

```
Qy      1 MetGluLeuGluAsnTyrGluGlnProValLeuProValLeuArgGluArgAsnArgArgArgArg 20
          |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db    324 ATGGAGCTGGAGAACTATAAACAGCCCGTGCTGCCAGTGCTCCGAGAGAGGAACAACCGCGAGGCGC 383

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleLeuIlePheIle 40
          |||||||||||||||||||||||||||||   --GTGCCAGCCTGTCCCCATGGAGCTCATCCCCATC 440
Db    384 CGGAGGATGAAGCCGCGGCAGT---GTGCCAGCCTGTCCCCATGGAGCTCATCCCCATC

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaAlaLeuLeuHis 60
          ||||||||||||||||||||||||||||:||::||||||||||||||||||||||||||||
Db    441 GAGTTCGTGCTGCCCACCAGCCAAAGTGGAGAGCCCGAAACGGCGGCTGCTGCAC 500

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProHisPheLeuLeuLeuTyr 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 ACCAGCGTGGCCGGCGACTTCTACCACCGCCTGGGACCCCATCACTTCCTCCTGCTCTAT 620

Qy    101 GlnLeuThrSerGlyGlyGlyAspIleGluArgIleLeuTyrGlnValValGlnThrLeuAsp 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 CAGAGAGGGCAGTGGTACGAGAGAATCCTGTACCAGGTGGTGCAGAGATCCTGGAC 680

Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleGlyValValGlnArg 140
          ||||||||||||||||||||||||||||:|:||:||||||||||||||||||||||||||
Db    681 TGCCTGCGCTACTGGAAGGTACTGCACCGCAGCCCCGGGCAGATCGGTGTGGTGCAGCGG 740

Qy    141 HisAlaProSerGluGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
          |||||||||||::|||||||||||||||||||||||||||||||||||||||||||||
Db    741 CACCCGGCCCTCCGAGGAGTCCCAAGCCTTCCAGCGGCAGCTCACGCGGCTGATTGGCTAT 800
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Db    2222 CTGGCGAGGCGTGTGGCACAGCCATGTTGCGGGACTTCACACAGCAGGTCCATGTGATTGAG 2281

Qy     741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerLeuLysTyrAspValSer 760
Db    2282 ATGTTACAGAAAGTCACCATTGATATTAAATCGCTCTCGGCAGAAGTATGACGTCAGT 2341

Qy     761 SerGlnValIleSerGlnLeuLysGlnLeuLysGluAsnLeuAsnLeuPro 780
Db    2342 TCCCAAGTTATTTCACAGCTTAAGCAAAGCCTTGAAAGCCTTAGAACTCCAATCTCCCC 2401

Qy     781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyValIleGluGlyLys 800
Db    2402 GAGAGCCTTTAGAGTTCCCATGATCCTGGACTAAAAGCCGGTACCCTGGTGATCGGAGAA 2461

Qy     801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
Db    2462 TGCAAAGTGATGGCCTCCAAGAAGAAGCCCTGGCTTGAGTTTAAGTGTGCTGATCCC 2521

Qy     821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
Db    2522 ACAGCTCTATCCAACGAAACCATTGGAATCATCTTTAAACATGGTGATGATCTGCGCCAA 2581

Qy     841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
Db    2582 GACATGTTGATCTTGCAGATTCTACGCATCATGGAGTCCATTTGGGAGACTGAATCTCTG 2641

Qy     861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
Db    2642 GACCTGTGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGATCGAG 2701

Qy     881 IleValLysAspAlaThrThrIleAlaLysIleGlnAsnSerThrValGlyAsnThrGly 900
Db    2702 ATTGTAAAGGATGCCACAACGATCGCTAAAATTCAGCAAAGCACAGTGGGTAACACGGGG 2761

Qy     901 AlaPheLysAspAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys 920
Db    2762 GCATTCAAAGATGAAGGTCCTGAATCACTGGCTCAAGAAAAGTCCATTGAAGAAAAAG 2821

Qy     921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
Db    2822 TTTCAGGCCGCAGTGGAAAGGTTTGTTTACTCCTGTGCCGGCTACTGTGTGGCCACATTT 2881

Qy     941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db    2882 GTTCTTGGGATCGGTGACAGGCACAACGACAACATTATGATCTCAGAGACAGGAAACCTA 2941

Qy     961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db    2942 TTTCATATAGACTTTGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCAATAAA 3001

Qy     981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db    3002 GAGAGAGTGCCCTTCGTCCTAACCCCAGACTTCTTGTTTGTGATGGGAATCTTCTGGAAA 3061

Qy    1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
Db    3062 AAGACAAGTCCACACTTCCAGAAATTCCAGGATGTCTGTGTTAAGGCTTACCTAGCTCTT 3121

Qy    1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
Db    3122 CGCCATCACACAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGGAATGCCC 3181

Qy    1041 GlnLeuThrSerGlyGluAspIleGluThrValGlyLysSer 1060
Db    3182 CAGCTGACAAGCGGAGAGGACATTGAAACAGTCGGGAAAAGC 3241

Qy    1061 GluGluAspAlaLysLysTyrPheLeuAspLysIleGluValCysArgAspLysGlyTrp 1080
Db    3242 GAGGAGGACGCTAAGAAGTACTTCCTTGATAAGATCGAAGTGTGCAGGGACAAAGGATGG 3301

Qy    1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis 1100
Db    3302 ACTGTGCAGTTTAACTGGTTCCTACACTTGGTTCTTGGCATCAAACAAGGAGAAAAGCAC 3361
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This page is a two-column nucleotide/protein sequence alignment report (Qy = query, Db = database), printed rotated on the page. The alignment consists of paired Qy/Db rows showing the translated protein sequence above the corresponding nucleotide sequence, with residue/base position numbers in the margins.

Left block (selected readable position markers, Qy then Db):

```
Qy  161  AspValThrAspValSerAsnValHisAspAspGluGluThrArgArgArgLeu  180
Db  801  GACGTCACTGACGTCAGCAACGTGCACGATGAGGAGACGCGCCGCTGGCTTG      860
Qy  181  ValThrProArgMetAlaGlyValAlaGlyArgAspProLysLeuTyrAlaMetHisPro  200
Db  861  GTGACCCCGCGCATGGCCGGAGGTGGCCAGCCCCAAGCTCTACGCCATGCACCCG      920
Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
Db  921  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGAAGATTGCCAACAACTGCATC  980
Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
Db  981  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC  1040
Qy  241  ProGlyThrIleLeuGlnSerPheThrLysMetAlaLysLysSerLeuMetAsp  260
Db 1041  CCCGGCACCATCCTGCAGAGCTTCACCAAGATGGCCAAGAAGAGAAATCTCTGATGAT   1100
Qy  261  IleProGluSerGlnAsnGluArgAspPheThrLysValArgGlyArgAspGluTyr  280
Db 1101  ATTCCCGAAAGCCAAAGCGAAAGGAATTTTGTCTGCGCGGTGTCGGGGAGGATGAGTAC  1160
Qy  281  LeuValGlyTyrGluThrProIleLeuLysAsnPheGlnAlaValArgGlnCysLeuLysAsnGly  300
Db 1161  CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGGAGGCACTGCCTCAAGAACGGA  1220
Qy  301  GluGluIleHisLeuValLeuAspAspProAlaLeuAspAspProIleAspAspGluGluGlu  320
Db 1221  GAAGAGATTCACGTGGTACTGGACGACCCCGCCCTAGACGAGGTGAGGAAG      1280
Qy  321  GluGluTrpProLeuValAspAspCysThrGlyThrValThrHisGluGluThr  340
Db 1281  GAAGAGTGGCCGGTGGTGGACGATTGCACGGGACTACCCATGAGCAGCTTACC      1340
Qy  341  IleHisGlyLysLysAspHisGlySerValPheThrValSerLeuTrpAspAspCysArgLys  360
Db 1341  ATCCACGGCAAGGACCAAGGAGAGTGTGTTCACCGTGTCCCTGTGGGACGACCCGCAAG  1400
Qy  361  PheArgValLysIleAspIleAspIleArgGlyIleLysAspIleProValLeuProArgThrAlaAspLeuThr  380
Db 1401  TTCAGGGTCAAGATCAGAGGCATTGAATATCCCCGTCCTGCCTCGGAACACCGACCTCACA  1460
Qy  381  ValPheValGluAlaAsnIleGlnTyrGlyIleGlnValCysGlnArgArgThrSer  400
Db 1461  GTTTTTGTAGAGGCAAACATCCAGTATGGCATGCAAGTCTTGCCAAAGGAGAACCAGC  1520
Qy  401  ProLysProPheThrGlyLeuValLeuTrpAsnValPheLeuGluSerIleLysIle  420
Db 1521  CCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTGTGGTTCAGTATCAAAATC      1580
Qy  421  LysAspLeuProLysGlyLeuValThrSerAlaGlyMetProSerProGlySerLysGlyLysLysAlaProAla  440
Db 1581  AAAGACTTGCCCAAAGGGGGCTTCTACTGACATCTACTGCGGTAAAGTCCAGCA      1640
Qy  441  LeuSerGlyLysLysThrSerAlaGluMetProSerProGlySerLysGlyLysLysAlaGlnLeu  460
Db 1641  CTGTCTCAGCAGAGGCCTCTGCAGAGTCCAGTTCTGAGTCCTGAGTATCAAAATC   1700
Qy  461  LeuTyrTyrValAsnLeuLeuLeuAspHisArgPheLeuLeuAspHisGlyLysGluTyr  480
Db 1701  CTCTATTATGTGAACCTGCTGATAGACCACCGTTTCCTCCTGGAGAATAC      1760
Qy  481  ValLeuHisMetTrpGlnLeuSerTyrLeuGlyAspGlnGlySerPheAlaAsnAlaAsp  500
Db 1761  GTCCTCCACATGTGGCAGATATCTGGCAGAAGAGAAGAAGCTTCAATGCTGAC      1820
Qy  501  LysLeuThrSerAlaThrAsnProAspLysSerGluAsnSerMetSerIleIleSerLeuLeu  520
Db 1821  AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTCAATGTCCATCTCCATTCTTCTG  1880
Qy  521  AspAsnTyrCysHisProIleAlaLeuProAlaLeuHisArgProThrAspProGluGlyGly  540
```

Right block (selected readable position markers, Qy then Db):

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Db 1881  GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCGACCCCGACCCCGGAAGGG  1940
Qy  541  AspArgValAlaArgAlaGluMetProAsnGlnLeuArgLysGlnLeuLeuGluAlaIleAlaIleAla  560
Db 1941  GACCGGGTTCGAGCGAGATCAGCTGGAGTTCAAGAAGCAATTGGAGGGCGATCATAGCC  2000
Qy  561  ThrAspProLeuAsnProLeuThrAlaGluAspGlyLysGluLeuTrpHisProArgTyr  580
Db 2001  ACTGATCCACTTAACCCTCTCACCAGCAGAGAGACAAAGAATTGCTCTGGCATTTAGATAC  2060
Qy  581  GluSerLeuLysAspProLysSerProLysLysPheProLeuPheSerSerValLysTrpGlyGln  600
Db 2061  GAAAGCCTTAAGCACCCAAAAGCAATCCTAAGCTCATTAGTTCAGTGAAATGGGGACAG  2120
Qy  601  GlnGlyIleValAlaLysThrTyrGlnLeuLeuLeuAlaLeuAlaLysArgGluValTrpAspGlnSer  620
Db 2121  CAAGGAAATTGTGCCAAACATACCAATTGTTGGCGCAGAAGGGAAGTCTGGGATCAAAGT  2180
Qy  621  AlaLeuAspHisGlyTyrLeuThrMetGlnLeuLeuAspCysAsnPheSerGluAspGluGluHisGlyTyrLeu  640
Db 2181  GCTTTGGATGTGGGTTAACAATGGCAGCTCCTGGACTGCCACCTCCTCAGATGAAAATGTA  2240
Qy  641  ArgAlaIleAlaAlaValGlnLysLeuGluGluGlnLysAspAspSerAspLeuLeuLeuAlaArgPhe  660
Db 2241  AGAGCCATTGCAGTTGAGGTCCAGGCTGTGAAATTTGAACCATACCATGACACTTACCTT  2300
Qy  661  LeuGlnLeuValGlnIleAlaValAlaLysValPheGluGluProTyrHisAspSerAlaLeuAlaArgPhe  680
Db 2301  CTACAAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGACACTTACCTT      2360
Qy  681  LeuLeuLysArgGlyLeuArgAsnGlnLysAsnAsnAspArgIleGluGlyHisPheGluTrpPheLeuArg  700
Db 2361  CTGCTGAAGCGTGGTTTAAGAAACAAAAGAATTGGTCACTTTTGTTTGGTTCTTCTGAGA  2420
Qy  701  SerGluIleAlaGlnSerArgHisTyrGlnGlnAsnArgPheAlaValIleLeuGluAlaTyr  720
Db 2421  AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAAGGTTCGCTGTGATTCTGGAAGCCTAT  2480
Qy  721  LeuArgGlyCysGlyThrAlaMetLeuHisAspThrGlnGlnGlnValIleAspLeuAsp  740
Db 2481  CTGAGGGGCTGTGGCACAGCCATGCTGCACGACACTTTACCCACAACGTCCAAGTAATCGAG  2540
Qy  741  MetLeuGlnLysGlnLeuThrIleSerAspIleLysSerLeuSerLeuLysTyrAspValSer  760
Db 2541  ATGTTACAAAAGTCACCCTTGATATTAAATCGCTCTCTGAAAAGATGACGTCAGT      2600
Qy  761  SerGlnValIleSerGlnLeuGlnLeuGlnLysLeuGlnAsnLeuGlnAsnLeuAsnLeuPro  780
Db 2601  TCCCAAGTTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC  2660
Qy  781  GlnSerPheArgValProTyrAspProGlyLeuLysLysLeuAlaLeuValIleLeuGlyLeuLys  800
Db 2661  GAAAAGCTTTTAGAGTTCCATAATGATCCTGGACTGAAAAGCAGCAGGAGCGCTGGCAATTGAAAAA  2720
Qy  801  CysLysGlyValMetAlaSerLysLysGlnProLeuTrpLeuGlnPheLeuLysCysAlaAspPro  820
Db 2721  TGTAAAGGTAATGGCCCTGGACTGAAAAAAACCCATGGCCTGAGTTTAAATGTGCCGATCCT  2780
Qy  821  ThrAlaLeuSerAsnGluThrIleGluGlyIleIleGluPheLeuLysHisGlyAspAspLeuLysArgGlyGln  840
Db 2781  ACAGCCCTATCAAATGAAACAAATTGAAATTATCTTTAAACATGGTGATGATCTGCGCGCA  2840
Qy  841  AspMetLeuLeuLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
Db 2841  GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG  2900
Qy  861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerSerThrGlyTyrIleAspLysLysLysMetIleGluGlu  880
Db 2901  GATCTAATGCCTCCTGCGTATATCTGCAGTTCAACTGGTTCAATTCAACTGGTGCAAAATAGGAATGATCGAG  2960
Qy  881  IleValLysAspAlaThrThrIleAlaLysLysIleGlnSerThrValGlyAsnThrGly  900
```

```
Db   2961  ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAGCACAGTGGCAACACGGGA  3020

Qy    901  AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysGluProIleGluGluLys  920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3021  GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCCTACTGAAGAAAAG  3080

Qy    921  PheGlnAlaAlaValGlyArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3081  TTTCAGGCAGCAGTGGGAAGATTTGTTTATTCCTGTGCAGGGTACTGTGTGGCAACCTTT  3140

Qy    941  ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
           |||||||||||||||||||||||||||||||||::|||||||||||||||||||||||||
Db   3141  GTTCTTGGAATAGGCGACAGGCACAATGACAATATTATGATCAGCGAGACAGGAAACCTA  3200

Qy    961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3201  TTTCATATTGACTTCGGGCACATTCTTGGAAATTACAAAAGTTTCCTGGGCATTAATAAA  3260

Qy    981  GluArgValProPheLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys  1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3261  GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG  3320

Qy   1001  LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu  1020
           ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db   3321  AAGACAAGCCCACTCCACTTCCAGAAATTTCAGGACGTGTGTAAGGCTTATCTAGCCCTT  3380

Qy   1021  ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetPro  1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3381  CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC  3440

Qy   1041  GlnLeuThrSerLysGluAspThrValTyrIleArgAspAlaLeuThrValGlyLysSer  1060
           ||||||||||||||||||||||||||||||:|||||||||||||||||||||::|||:||
Db   3441  CAGTTAACAAGCAAAGAAGACACAGTGAATATCCGGGATGCCCTCACAGTGGGGAAAAT   3500

Qy   1061  GluGluAspAlaAlaLysLysTyrPheLeuAspGlnIleGluValCys ArgAspLysGlyTyr  1080
           |||||||||||||||||||||||||||||||||||||||||||::|||::||||||||||
Db   3501  GAGGAGGATGCTGCAAAAAAGTATTTTTCTTGATCAGATCGAAGTTTGGCAGAGACAAAGGATG  3560

Qy   1080  pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHi  1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3561  GACTGTGCAGTTTAATTGGTTTCTTCACCTCTGTTCTTGGCCATCATCAAACAAGGAGAAACA  3620

Qy   1100  sSerAla  1102
           |||||||
Db   3621  TTCAGCC  3627
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RESULT 14
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AF208345
LOCUS       AF208345                3342 bp    mRNA    linear    ROD 19-DEC-2000
DEFINITION  Mus musculus phosphatidyl-inositol 3-kinase gamma isoform (Pik3cg)
            mRNA, complete cds.
ACCESSION   AF208345
VERSION     AF208345.1   GI:11890407
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3342)
  AUTHORS   Chakravarti,S. and McColl,S.R.
  TITLE     Cloning of a murine ortholog of PI 3-kinase gamma
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3342)
  AUTHORS   Chakravarti,S. and McColl,S.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-NOV-1999) Microbiology & Immunology, University of
            Adelaide, Frome Road, Adelaide, SA 5005, Australia
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /db_xref="taxon:10090"
     gene            1..3342
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                     KGQWEYIYDRYQVVQTLDCLHYWKLMHKSPGQIHVQRHVPSEETLAFQKQLTSLIGY
                     DVTDISNVHDDELEFTRRRLVTPRMAEVAGRDAKLYAMHPWVTSKPLPDYLSKKIANN
                     CIFTVIHRGTSQTIKVSADDTPGTILQSFFTKMAKKKSLMNISESQSEQDFVLRVCG
                     RDEYLVGETPLKNFQWVRQCLKNGDEIHLVLDTPPDPALDEVRKBEWPLVDDCTGVTG
                     YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVPVEANIQHGQQ
                     VLCQRRTSRPPFAEEVLMNVWLEFGIKIKIKDLPKGALLNLQIYCCKTPSLSSKASAETP
                     GSESKGKAQLLYYVNLLIDHRFLLRHGDYVLHMWQISGAEEQSFNADKLTSATNP
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                     MLQKVTIDIKSLSAEKYDVSSQVSLQKLESLQNSNLPESFRVPDGLKQLLVI
                     EKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQDMLILQILRIMESIWE
                     TESLDLCLLPYGCISTGDKIGMEIVKDATTIAQIQQSTVGNTGAFKDEVLNHWLKEK
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BASE COUNT      900 a     853 c     837 g     750 t      2 others
ORIGIN
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Alignment Scores:
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Score:                    5476.50              Matches:             1037
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Query Match:              94.59%               Indels:              11
DB:                       10                   Gaps:                1
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US-09-974-573-1 (1-1102) x AF208345 (1-3342)

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Qy     1  MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArg  20
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Db     1  ATGGAGCTGGAGAACTATGAACAACCGGTGGTTCTAAGAGAGGACAACCTTCCGCCGCGC  60

Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CGGAGGATGAAGCCACGCAGCACAGCCGCCAGAGGCAGCCTGTCTTCCATGGAGCTCATCCCCATT  120

Qy    41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
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Db   121  GAGTTCGTACTGCCCACCAGCCAGCCGCATCAGCAAGACTCCAGAAACAGCCGCTGCTGCAT  180

Qy    61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  GTGGCTGGCCATGGCAATGTGGAACAGATGAAAGCTCAGGTGTGGCCGCGACCACTGGAG  240

Qy    81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
          |||||||||||:::||||||||||||||||||||||||||||::||||||||||||||||
Db   241  ACCAGTGTGTCGCGGGAGTTCTACCACCGATTGGGCCGGACCAATTCCTCCTGCTCTAC  300

Qy   101  GlnLysLysGlyGlnTrpGluTyrGluIleTyrAspArgTyrGlnValValGlnThrLeuAsp  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CAGAAGAAAGGACAATGGTATGAGATCTATGACAGGTACCAAGTGGTGCAGACCCTAGAC  360

Qy   121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
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Db   361  TGCCTGCATTACTGGAAGTTGATGCACAAGAGCCCTGGCCAGATCCATGTCCAGCGACGA  420

Qy   141  HisAlaProSerGluGluThrLeuAlaPheGlnLysGlnLeuAsnAlaLeuIleGlyTyr  160
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Db   421 CACGTACCTTCTGAGGAGACCTGGCTTTCCAGAAGCAGCTCACCTGCCTGATTGGCTAT  480

Qy   161 AspValThrAspValSerAsnValHisAspArgGluLeuGluPheThrArgArgLeu      540
         AspValThrAspValSerAsnValHisAspArgGluLeuGluPheThrArgArgLeu
Db   481 GACGTCACTGACATCAGCAATGTGCACGATGAGCTAGAGTTCACTCGCCGCCTG        540

Qy   181 ValThrProArgMetAlaGluValAlaGlyValArgAspProLysLeuTyrAlaMetHisPro 560
         ValThrProArgMetAlaGluValAlaGlyValArgAspProLysLeuTyrAlaMetHisPro
Db   541 GTTACGCCCCGCATGGCTGAAGTGGCTGGCCGGGATGCCAAATCCTATGCTATGCACCCT   600

Qy   201 TrpValThrSerLysProLeuTyrLeuLysLysIleThrAsnAsnCysVal           580
         TrpValThrSerLysProLeuTyrLeuLysLysIleThrAsnAsnCysVal
Db   601 TGGGTAACGTCCAAACCTCTCCAGACTACCTGTCAAAAAAATTGCCAACAACTGCATC    660

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr     600
         PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr
Db   661 TTCATCGTCATCCACCGCAGCACCACCAGCCAAACCATCAAGGTCTCCGCAGATGATACT  720

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp       620
         ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp
Db   721 CCTGGTACCATCCTCCAGAGCTTCTTCACCAAGATGGCCAAGAAGAGTCCCTAATGAAT   780

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr     640
         IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr
Db   781 ATCCCAGAAAGTCAAAGTGAGCGAGATTTTGTATTGCGGGTTTGTGGCCGCGATGAGTAC  840

Qy   281 LeuValGlyThrProIleLeuLysThrAsnPheGlnThrValArgGlnCysLeuLysAsnGly 660
         LeuValGlyThrProIleLeuLysThrAsnPheGlnThrValArgGlnCysLeuLysAsnGly
Db   841 CTGGTGGGTGAAAACCACCCTCAAAAATTTCAGTGGGTGAGGCAGTGCCTCAAGAACGGA   900

Qy   301 GluGluIleHisGluValLeuAspThrProLeuAspAlaLeuAspProLysValArgLys     680
         GluGluIleHisGluValLeuAspThrProLeuAspAlaLeuAspProLysValArgLys
Db   901 GATGAAATACACGGTGCTCGACACGCCTCAGACCCAGCCCTTGATGAGGTGAGGAAG    2040

Qy   321 GluGluTrpProLeuValAspAspAspCysThrGlyValThrGlyValThrGlnLnLeuThr  700
         GluGluTrpProLeuValAspAspAspCysThrGlyValThrGlyValThrGlnLnLeuThr
Db   961 GAAGAAATGGCCGCTGGTGGATGACTGAGCTACTCCACCGAGCTGACC        2100

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys    720
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Db  1021 ATCCATGGGCAAGGACCACGAGAGTGTGTTCACAGTGTCTTTGTGGGACTGCGACCGAAAG  2160

Qy   361 PheArgValLysIleArgGlyTyrIleAspIleProValLeuProValArgAlaAspLeuThr 740
         PheArgValLysIleArgGlyTyrIleAspIleProValLeuProValArgAlaAspLeuThr
Db  1081 TTCAGGGTGAAGATCAGAGGCCATTGATATCCCTGTCCTGCCCGTCCGGAACACCGACCTCACT  2220

Qy   381 ValPheGluGluAlaAsnIleGlnTyrGlyTyrGlyIleGlnValLeuCysGlnArgThrSer  760
         ValPheGluGluAlaAsnIleGlnTyrGlyTyrGlyIleGlnValLeuCysGlnArgThrSer
Db  1141 GTGTTTGTTGGAGGCAGCAACATCCAGTACGGCTACGGGATCCAAGTCCTTTGCCAAAGGAGAACCAGC  2280

Qy   401 ProLysProPheThrGluValLeuGluLeuTrpProAsnValTrpLeuGluProSerGlyIle  780
         ProLysProPheThrGluValLeuGluLeuTrpProAsnValTrpLeuGluProSerGlyIle
Db  1201 CCTAAGCCCTTCACGGAAGTACTCGAGCTGTGGCCTGAGTTTGGCATCAAAATC        2340

Qy   421 LysAspLeuProLysGlyLysLysSerGlyGlyValGlyGluAsnLeuGlnIleProAla    800
         LysAspLeuProLysGlyLysLysSerGlyGlyValGlyGluAsnLeuGlnIleProAla
Db  1261 AAAGACTTGCCCAAAGGGGCTCATTGAACCTACAGATCTACTGCTGCAAAACCCCATCA    2400

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysLysAlaGlnLeu 820
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Db  1321 CTGTCCAGGAAGACTTCTGCAGAACCCTCCGAGCTCCAGGTCCAAGGGCAAAAGCCCAGCTT  2460

Qy   461 LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuHisGlyHisGluTyr    840
         LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuHisGlyHisGluTyr
Db  1381 CTCTATTACGTGAACTTGCTGTTAATAGACCACCGGTTTCCTCCTCCGCACGGGACTAT    2520

Qy   481 ValLeuHisSerMetTrpGlnLeuSerGlyLysLysAspGlnGlySerPheAsnAlaAsp    860
         ValLeuHisSerMetTrpGlnLeuSerGlyLysLysAspGlnGlySerPheAsnAlaAsp
Db  1441 GTGCTCCACATGTGGCAGATATTGGCAAGGCAAGGACAGCTGAGCAGCTGACCTGAC    2580

Qy   501 LysLeuThrSerAlaThrArgAsnProAspLysGluAsnSerMetSerIleLeuLeuLeu    880
         LysLeuThrSerAlaThrArgAsnProAspLysGluAsnSerMetSerIleLeuLeuLeu
Db  1501 AAGCTCACACATCCCGACAAGGAGAACTCAATGTCCATTTCAATCCTCCTGCTG    2640
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Alignment Scores:
Pred. No.:                        0                    Length:            4134
Score:                       5440.00                   Matches:           1046
Percent Similarity:           96.65%                   Conservative:        20
Best Local Similarity:        94.83%                   Mismatches:          35
Query Match:                  93.96%                   Indels:               4
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US-09-974-573-1 (1-1102) x A50263 (1-4134)

Qy      1 MetGluLeuGlnAsnTyrGluGlnProValValLeuGlnProValLeuGlnProValLeuGlnProValLeuAspAsnArgArgArgArg    20
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Db    324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGGAGGACAACTGCCGAAGGCGC   383

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle    40
            |||||||||||||||||||||||||||::|              |||||||||||||||||||
Db    384 CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCCATGGAGCTCATCCCCATC   440

Qy     41 GluPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe    60
            ||||||||||||||||||||||||||||||||||||::::|||||||
Db    441 GAGTTCCAGCTGCTCCCCACCAGCCAGCCGAAATGCAAGAGCCCCTGCGTGCAC   500

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnHisValTrpLeuArgAlaLeuGlu    80
            |||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGGGCGTGGAG   560

Qy     81 ThrSerValSerArgAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
            |||||::|||||||||||||||||||||||||||||||||||||
Db    561 ACCAGCT--GGGCGGACTTCTACCACCGGCTGGGACCCATCACTTCCTCCTGCTCTAT   618

Qy    101 GlnLysGlyGlnIleTrpTyrGluTyrAspLysGluLeuGlnThrLeuAsp   120
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Db    619 CAGAAGAA-GGGCAGTGTACGAGATCTACGACAAGAGAGACTCTGGAC   677

Qy    121 CysLeuArgTyrTrpLysValLeuValLeuHisArgSerProGlyGlnIleHisValValGlnArg   140
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Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuAsnAlaLeuIleGlyTyr   160
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Db    738 CACCCGCCCTCCGAGGAGTCCCAAGCTTCAGCGCGCGCAGCTCCACGCGCGCTGATTGGCTAT   797

Qy    161 AspValThrAspValSerAsnValHisAspAspGluLeuGluThrArgArgArgLeu   180
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Db    798 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG   857

Qy    181 ValThrProArgMetAlaGluAlaGlyAlaAlaGlyAspProLysLeuTyrAlaMetHisPro   200
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Db    858 GTGACCCCGCGGATGGCCGATGGCGGAGGTGGCCAGCCGAAGCTCTACGCCATGCACCCG   917

Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLysIleThrAsnAsnCysVal   220
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Db    918 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGAAGAAGATTGCCAACAACTGCATC   977

Qy    221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr   240
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Db    978 TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCGGACGACACC   1037

Qy    241 ProGlyThrIleLeuGlnSerPhePheLysMetAlaAlaLysLysLeuSerLeuMetAsp   260
            ||||||||||||||||||||||||||||||||||||
Db   1038 CCCGGCCGCCATCCTGCAGAGTTCTTCACCAGATGGCCAAGAAGAATCTCTGATGGAT   1097

Qy    261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGluTyr   280
            ||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATTCCCGAGAGCCAAAGCCAGAGATTTTGTGCTGCCCGTGGCCCGGGATGAGTAC   1157

Qy    281 LeuValGlyGluThrProIleLysPheIleAsnPheGlnIleValArgGlnCysLeuUysAsnGly   300
            |||||||||||||||||||||||||||||::::|||||||
Db   1158 CTGGTGGGCGAAACCCCCATCAAAAACTTCCAGTGGTGAGGCACTGCCCAAGAACGGA   1217

Qy    301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspLeuGluValArgLys   320
            |||||||||||||||||||||||||||||||||||||||||
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Qy    881 IleValLysAspAlaThrThrIleAlaLysIleGluGlnSerThrValGlyAsnThrGly   900
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Db   2641 ATTGTAAAGGATGCCACAACGATCGCTCAAATTCAGCAAAGCACAGTGGGTAACACGGGG   2700

Qy    901 AlaPheGluValAspGluSerHisLeuSerHisTrpLeuLysGluLysGlyProIleGluGluLys   920
            |||||||||||||::||:||||||||||||||||
Db   2701 GCATCAAAGATGAGGTCTGAATCACTGGCTCAAGAGAAAAATGTCCPATTGAGAGAAAG   2760

Qy    921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe   940
            |||||||||||||||||||||||||||||||||||||
Db   2761 TTTCAGGCCGCAGTGGAAAGGTTTGTTTACTCCTGCGCAGGCTACTGTGTGGCCACATTT   2820

Qy    941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
            ||||||||||::||:::|||||||||||||||||
Db   2821 GTTCTGGGATCGGTGACAGGCCACAACGACAACATTATGATCTCAGAGACAGGAAACCTA   2880

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys   980
            |||||||||||||||||||::|||||||||||||
Db   2881 TTTCATATAGACTTCGGACACATTCTTGGAAATTACAAGAGTTTCCTGGGCATCAATAAA   2940

Qy    981 GluArgValProPheValLeuThrProAspPheValMetGlyThrGlySerGlyLys   1000
            |||||||||||||||||||||||||::::|||||||
Db   2941 GAGAGAGTGCCCTTCGTCCTAACCCCAGACTTTTTGGTTGTGATGGGGATCTTCTGGAAAA   3000

Qy   1001 LysThrLeuHisPheGlnLysLysPheGln---------------------   1010
            |||||||:::||||||
Db   3001 AAGCAAGCCACACTTCCAGGAATTCCAGGATTCGTGTGTGTCTACTTACAGTACTAT   3060

Qy   1011 ---AspValCysArgLysAlaTyrLeuAlaLeuArgHisHisAsnLeuLeuIleIle   1029
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Db   3061 GGGGATGTCTGTGTTAGAGCTTACCTGGCTCTTCGCCATCACAAACCTGTTGATCATC   3120

Qy   1030 LeuPheSerMetMetLeuMetThrGlyMetProGlnLeuProGlnLeuThrSerGluLysProIleGlu   1049
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Db   3121 TTGTTCTCCATGATGCTGATGACAGGAATGCCCCAGCTGACAAGCAAGAAGACCATTGAA   3180

Qy   1050 TyrIleArgAspAlaLeuThrValGlyLysLysSerGluGluAspProAlaLysLysTyrPheLeu   1069
            ||||||||||||||||::|||||||
Db   3181 TATATCCGGGATGCCCTCACCGTGGGAAAAAGCGAGGAGGACCCTAAGAAATATTTCCTT   3240

Qy   1070 AspGlnIleGluValCysArgAspAspLysProGlyGlyTrpThrValGlnPheAsnTrpPheLeuHis   1089
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Db   3241 GATCAGATCGAAGTCTGCAGAGACAAGAATGAAGGACTGTGCAGTTTAACTGGGTTCCTACAT   3300

Qy   1090 LeuValLeuGlyIleLysLysGlnGlyGluLysHisSerAla   1102
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Db   3301 CTTGTTCTTTGGCATCAAACAAGGAGAAAAGCACTCCGCT   3339
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RESULT 15
A50263

LOCUS   A50263   4134 bp   DNA   linear   PAT 07-MAR-1997
DEFINITION Sequence 1 from Patent WO9612024.
ACCESSION   A50263
VERSION   A50263.1 GI:2303320
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 4134)
  AUTHORS   Stoyanov,B., Hanck,T. and Wetzker,R.
  TITLE   CLONING, EXPRESSION AND CHARACTERISATION OF A NOVEL FORM OF
            PHOSPHATIDYLINOSITOL-3-KINASE
  JOURNAL   Patent: WO 9612024-A 1 25-APR-1996;
            MAX PLANCK GESELLSCHAFT (DE)
COMMENT   Other Publication DE 4445562 960404.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT   1127 a   999 c   998 g   1010 t
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Qy   681 LeuLeuLysArgGlyArgAsnLysArgIleGlyHisPheLeuTrpPheLeuArg 700
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Db  2358 CTGCTGAAGCGTGGTTAAGAACAAAGAAATTGGTCACTTTTTGTTTGGTTCTTGAGA 2417

Qy   701 SerGlnIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGlyAlaTyr 720
             |||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Db  2418 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGCGATTCCGTGTGATTCTGGAAGCCTAT 2477

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnInValGlnValIleAsp 740
             ||||||||| |||||||| |||| |||||||||  ||||||||||||    :::
Db  2478 CTGAGGGGCTGTGGCACAGCCATGTGCACGACTTACCCAACAAGTAATGATAATCGAG 2537

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysHisTyrAspValSer 760
             :||||:::||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db  2538 ATGTTACAAAAAGTCACCCCTGATATTAAATCGCTCTGCTGAAAAGTATGACGTCAGT 2597

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysGlnLeuGlnAsnLeuGlnAsnLeuAsnLeuPro 780
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  2598 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCAACTCCCC 2657

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
             ::::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2658 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCCCTGGCAATTGAAAAA 2717

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
             ||||||| || |||||||||||||||||||||||||||  |||||||||||||||||
Db  2718 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 2777

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleTyrIleLysGlyAspLeuArgGln 840
             |||||||| ||||| | |||||||||||| ||| ||||||||||||||||||||||||
Db  2778 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAGGGAGACTTGATGAGTCTCAA 2837

Qy   841 AspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlyMetGlu 860
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2838 GACATGCTTATTTCAGATCTCACAATCATGGGAGTCTATTGGGAGACTGGAATCTTTG 2897

Qy   861 AspLeuCysLeuLeuGlyProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2898 GATCTATGCCTCCTGGCCATATGTTGCATTTCAACTGTGTGACAAAATAGGAATGATCGAG 2957

Qy   881 IleValLysAspAlaThrThrIleAlaLeuIleGlnGlnSerThrValGlyIleAsnThrGly 900
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Db  2958 ATTGTGAAAGACGCCACGACCATCGCACAATTCAGCAAAGCAAGTGGGCAACAGCGGGA 3017

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerCysProIleGluLysLys 920
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Db  3018 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAAATCCCCACTAGAAGAAAAG 3077

Qy   921 PheGlnAlaAlaValGluArgPheLeuThrTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
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Db  3078 TTTCAGGCAGCAGTGGAGAGATTTGTTATTCCTGCCAGCTACTGTGTGGCAACCTTT 3137

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluHisGlyAsnLeu 960
             |||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db  3138 GTTCTTGGAATAGGGGACAGACACAATGACAATATTATGATCAGCGAGCAGGAAACCTA 3197

Qy   961 PheHisIleAspPheGlyHisPheLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
             |||||||||||||||||||||||||| :::|||||||||||||||||||||||||||||
Db  3198 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3257

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
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Db  3258 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3317

Qy  1001 LysThrSerLeuHisProGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3318 AAGACAAGCCCACACCCTCAGAAATTTCAGGACGTGTGTGTTAAGGCTTATTCTGCCCTT 3377

Qy  1021 ArgHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
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Db  3378 CGTCATCACAAACCTACTGACATCCTGTTCTCCATGATGCTCATGACAGGAATGCCC 3437
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Db  1218 GAAGAGAGATTCACGTGGTACTGGACACGCCTTCCAGACGCCCTAGACGAGGTGAGGAAG 1277

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Qy   341 IleHisGlyLysLysAspHisGluSerValPheThrValSerLeuTrpAspCysGlyAspCysAspArgLys 360
Db  1338 ATCCACGGCAAGAAGACCACGAGAGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG 1397

Qy   361 PheArgValLysGlyIleArgGlyIleLeuProValLeuProArgThrArgAlaAspLeuThr 380
Db  1398 TTCAGGGTCAAGATCAGAGGCCATTGATAATCCCGTCCTCCTGGACAACCGACCTCACA 1457

Qy   381 ValPheValGluValGluAlaAsnIleGlnTyrGlyGlnIleValLeuCysGlnInArgArgThrSer 400
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Qy   401 ProLysProPheThrGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
Db  1518 CCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTGTGGCTTGGAATTCAGTATCAAAATC 1577

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnInIleTyrCysGlyLysLysAlaProAla 440
Db  1578 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1637

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProLysSerGlyGlyLysAlaGlnInLeu 460
Db  1638 CTGTCCAGAAGGCCTCTGCAGAGTCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1697

Qy   461 LeuTyrTyrValAsnLeuLeuLeuHisAspHisArgPheLeuArgArgHisGlyGluTyr 480
Db  1698 CTCTATTATGTGAACCTGCTGCTTCACGATCACCGTTCCTCCGCCGCGTGAGAATAC 1757

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyGlyValGlyGluAspGlnGlySerPheAsnAlaAsp 500
Db  1758 GTCCTTCCACATGTGGCAGATATCTGGAGGAGGAGAAGATCAAGGAAGCTTCAATGCTGAC 1817

Qy   501 LysLeuThrSerAlaThrAsnProAspLysProGlyAsnSerMetSerIleSerLeuLeu 520
Db  1818 AAACTCACGTCTGCAACTCTGACAACCCAGACAAGACCAGGAAATTCAATGTCCATCTCCTG 1877

Qy   521 AspAsnTyrCysHisHisProIleAlaLeuHisArgProThrProAspProGluGly 540
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Qy   541 AspArgValArgAlaGluMetProAsnGlnInLeuArgGlyLysSerGlnLeuGluAlaIleIleAla 560
Db  1938 GACCGGGTTCGAGCAGAAATGCCAAACCAGCTTCGCCAAGGGATCATAGCC 1997

Qy   561 ThrAspProLeuAsnProLeuThrMetGlnInLeuLeuAspLysGluLeuTrpLeuLeuTrpHisProHisArgTyr 580
Db  1998 ACTGATCCACTTAACCCCTCACACGGACAAGAAGAATTGCTCTGAAGATTTTTAGATAC 2057

Qy   581 GluSerLeuLysAspProLysGlyAlaTyrProLysSerVerLysLysTrpGlyGln 600
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Qy   601 GlnGlnIleValAlaLysThrTyrGlnInLeuAlaLysArgGluValTrpAspGlnSer 620
Db  2118 CAAGAAAAATGTGGCCAAAAAACATACCAATTGTTGGCCAAGAGGGAAGTTCTGGGATCAAAAGT 2177

Qy   621 AlaLeuAspProValGlyLeuThrMetGlnInLeuLeuAspCysAsnPheSerAspGluAsnVal 640
Db  2178 GCTTTGGATCCTGTTGGGTTAACAATGCAACTTCTCTGACTGTGCAACTGTCTCAGATGAAAATGTA 2237

Qy   641 ArgAlaIleAlaGlnValGlnInLysLeuGlyLeuSerLeuGluSerLeuGluAspAspValLeuHisTyrLeu 660
Db  2238 AGAGCAATTGCCAGTTCAGGTTAACAATTCCAGAAAATTTCAGGACATCTGTGTTAAGGCTTTATTCCTGCCCTT 2297

Qy   661 LeuGlnInLeuValGlnInAlaValLysPheGluProTyrHisAspSerArgLeuAlaAlaArgPhe 680
Db  2298 CTACAATTGGTCCAGGCTGTGAAATTTGAACCCTATCATGACTCCCGTTCTCCAGATTT 2357
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Qy   1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
          |||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   3438 CAGTTAACAAGCAAAGAACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT   3497

Qy   1061 GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCys-ArgAspLysGlyTr   1080
          |||||||||||||||||||||||||||||| || |||||||||||||||||||
Db   3498 GAGGAGGATGCTAAAAGTATTTTCTTGATCAGATCGAAGTTTGGCAGAGACAAAGGATG 3557

Qy   1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleIleLysGlnGlyGluLysHi 1100
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3558 GACTGTGCAGTTTAATTGGTTTCTACACTTGTTCTTGGCATCAAACAAGGAGAGAAACA 3617

Qy   1100 sSerAla 1102
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Db   3618 TTCAGCC 3624
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Search completed: February 15, 2004, 05:14:43
Job time : 9973 secs

Copyright   GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 15, 2004, 02:08:02 ; Search time 663 Seconds
                                               (without alignments)
                                               4486.849 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop   6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09974573/runat_11022004_180012_18083/app_query.fasta_1.1287
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974573 @CGN_1_1.434 @runat_11022004_180012_18083 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	5726	98.9	3808	19	AAV04634	Porcine phosphoino
2	5726	98.9	3808	20	AAV74100	Porcine G-protein
3	5726	98.9	3808	21	AAZ86813	Pig p120 regulator
4	5534	95.6	5162	20	AAV74104	Human G-protein re
5	5534	95.6	5162	21	AAZ86814	Human p120 regulat
6	5523.5	95.4	5397	24	ABL59522	Human phosphatidyl
7	5523.5	95.4	5397	24	AAS14367	cDNA encoding huma
8	5499.5	95.0	4137	17	AAT58546	Human phosphatidyl
9	5440	94.0	4134	17	AAT58545	Human phosphatidyl
10	1467.5	25.3	3498	15	AAQ57012	Ptdins 3-kinase 11
11	1466.5	25.3	3424	24	ABL59523	Human phosphatidyl
12	1466.5	25.3	3424	24	AAS14365	cDNA encoding huma
13	1465.5	25.3	3207	14	AAQ51155	p110 cDNA. Homo s
14	1460.5	25.2	3412	21	AAQ51156	Human p110 cDNA.
15	1354.5	23.4	3213	21	AAC65690	Human PI3 kinase p
16	1354.5	23.4	3213	24	ABV78026	Hypoxia-regulated
17	1354.5	23.4	3213	24	AAS14366	cDNA encoding huma
18	1352.5	23.4	5220	19	AAV31340	Human phosphatidyl
19	1352.5	23.4	5220	20	AAX15932	cDNA sequence enco
20	1352.5	23.4	5220	21	AAZ32882	Human PI 3-kinase-
21	1350.5	23.3	3868	21	AAA13154	Human phosphatidyl
22	1350.5	23.3	3868	24	ABK84750	Human cDNA differe
23	1350.5	23.3	3868	24	AAS14363	cDNA encoding huma
24	1349.5	23.3	3387	19	AAV16533	cDNA encoding mamm
25	1290	22.3	3525	24	ABK84381	Human cDNA differe
26	1283	22.2	3773	23	ABL07215	Drosophila melanog
27	1076.5	18.6	5285	18	AAT80199	Phosphatidyl inosi
28	1074	18.5	5061	19	AAV42920	cDNA encoding a hu
29	1074	18.5	5061	25	ABT17093	Androgen-independe
30	1073.5	18.5	7114	23	ABL07214	Drosophila melanog
31	1034	17.9	3504	19	AAV18654	Caenorhabditis ele
32	1034	17.9	3504	24	AAA62300	Caenorhabditis ele
33	922	15.9	5990	24	ABK62570	Rat sequence diffe
34	873.5	15.1	6871	23	ABL10307	Drosophila melanog
35	873.5	15.1	7191	23	ABL20119	Drosophila melanog
36	866.5	15.0	6831	18	AAT80200	Phosphatidyl inosi
37	856.5	14.8	4491	23	AAS71517	DNA encoding novel
38	856.5	14.8	4878	23	ABN59725	Novel human coding
39	785	13.6	4498	23	AAS68360	DNA encoding novel
40	784	13.5	4747	22	ABA08693	Human PI3-kinase h
41	784	13.5	4747	22	AAH99523	Human protein enco
42	773.5	13.4	17344	23	ABL20118	Drosophila melanog
43	773.5	13.4	17358	23	ABL10306	Drosophila melanog
44	767.5	13.3	1074	23	AAS73988	DNA encoding novel
45	709.5	12.3	3063	22	AAI58587	Human polynucleoti

ALIGNMENTS

RESULT 1
AAV04634
ID   AAV04634 standard; cDNA; 3808 BP.
XX
AC   AAV04634;
XX
DT   17-AUG-1998 (first entry)
XX
DE   Porcine phosphoinositide 3OH-kinase p120 subunit cDNA.
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;

KW   therapy; drug screening; ss.
XX
OS   Sus scrofa.
XX
FH   Key   Location/Qualifiers
FT   CDS   89..3397
FT   /*tag= a
XX
PN   WO9749818-A2.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1997;   97WO-US11219.
XX
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1998-077181/07.
DR   P-PSDB; AAW23948.
XX
PT   DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase,
PT   p101 and p120 subunits - useful for diagnosis, drug screening,
PT   clinical trial monitoring and treatment of inflammatory disorders
XX
PS   Claim 54; Fig 3A-C; 151pp; English.
XX
CC   This cDNA sequence codes for the p120 catalytic subunit (see
CC   AAW23948) of pig G-protein regulated phosphatidylinositol-3' kinase,
CC   a heterodimeric enzyme which produces the intracellular messenger
CC   phosphatidylinositol (3,4,5)-triphosphate in response to activation
CC   of trimeric G protein-linked receptors. This novel protein, which
CC   also contains a regulatory subunit, p101 (see AAV04633), is found in
CC   cells of haematopoietic origin and is involved in immune system
CC   responses which cause inflammation. p120 cDNA was obtained from a
CC   pig neutrophil cDNA library using a degenerate oligonucleotide
CC   probe (see AAT99713) based on an isolated p120 tryptic peptide. The
CC   p120 cDNA clone in pcMV3mycp120 is deposited as ATCC 97637. The
CC   invention encompasses pig and human p101 and p120 proteins (see
CC   host cell expression systems, p101 and p120 proteins (see
CC   AAW23946-49), fusion proteins, polypeptides and peptides, antibodies
CC   to these proteins, and transgenic animals and knockout animals.
CC   Compounds which are useful for treating inflammatory response
CC   disorders can be identified by screening assays using a G protein
CC   activated PI3K, or a cultured host cell that expresses the p101
CC   gene. Antagonists of G protein stimulated PI3K (acting through the
CC   p101 subunit, especially by disrupting the interaction between the
CC   p101 and p120 subunits) can be used to treat arthritis, septic
CC   shock, adult respiratory distress syndrome (ARDS), pneumonia,
CC   asthma, allergies, reperfusion injury, atherosclerosis, cancer and
CC   Alzheimer's disease. The nucleic acids and their products can also
CC   be used for diagnosis, drug screening and clinical trial monitoring
CC   of inflammatory diseases.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 19   Gaps: 0

US-09-974-573-1 (1-1102) x AAV04634 (1-3808)

Qy   1 MetGluLeuGlnAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg 20
Db   89 ATGGAGCTGCAGAACTATGAACAGCCCGTGGTCTGCGAGAGGACAACCGCCGCAGGCGT 148
Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40

Db 149 CGGAGGATGAAGCCGCGGCACGGCAGCCTGCCTCCATGGAGCTCATCCCCATC 208
Qy   41 GluPheValLeuProThrSerGlnArgArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
Db 209 GAGTTGTTTTGGCCACCAGCCAGCGCAACACCAAGACCCCAGAAACGGCACTGCTGCAC 268
Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
Db 269 GTGGCCGGCCACGGCAATGTGGAAGAGATGAAGGCCCAGGTGTTGTTGCGCGGCCTGGAG 328
Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyLeuProAspHisPheLeuLeuLeuTyr 100
Db 329 ACGAGCGTTCTTGGGACTTCTACCACCGGTTCGGCCCCGACCACTTCCTCCTGCTCTTC 388
Qy 101 GlnLeuLysLysGlyGlnTrpTrpTyrArgGluIleTyrAspLysSerTyrGlnIleValValGlnThrLeuAsp 120
Db 389 CAGAAGAAGGGGGAGTGGTACAGAGAATCTATGACAAGTACCAGGTGGTGCAGAACCCTGGAC 448
Qy 121 CysLeuArgTyrTrpLysValValLeuHisArgSerProGlyIleIleHisValValGlnArg 140
Db 449 TGCCTGCGCTACTGGAAGGTGGTTGCACCGGGAGATCCACCAGGTGGTCCAGCCG 508
Qy 141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaLeuIleGlyTyr 160
Db 509 CACGCGCCCTCGGAGGAGACATTGGCCTTCCAGCTGCGCCAGCTTAACGCCCTCATCGGCTAC 568
Qy 161 AspValThrAspValSerArgAsnValHisAspAspGluGluGluGlyProThrArgArgArgLeu 180
Db 569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGGAGGAGGGCCCGACGCGGCGGCTG 628
Qy 181 ValThrProArgMetAlaGluValAlaAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
Db 629 GTCACCCCGCGCATGGCCGAGGTGGCCGCGGGCCGCGACCCCAAGCTTACGGCCATGCACCCC 688
Qy 201 TrpValThrSerLysProLeuProLeuGluProThrTyrLeuLysLysIleThrAsnAsnCysSerVal 220
Db 689 TGGGTGACATCCAAGCCCCTCCCTGAGCCTACCTTCCTGAAGAAGATCACTAACAACTGCGTC 748
Qy 221 PheLeuValIleHisArgSerThrSerGlnThrHisIleLysValSerAlaAlaAspAspThr 240
Db 749 TTCATCGTCATTCACCGCAGCACCAGCCAGACCCATATCAAGGTCTCGGCCGATGACACC 808
Qy 241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaAlaLysLysLysSerLeuMetAsp 260
Db 809 CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868
Qy 261 IleProGluSerGlnAsnGluAspAspPheValLeuArgValCysGlyArgAspGluTyr 280
Db 869 ATCCCTGAAAGCCAGAACGAAGACGACTTTGTGCTGCGCGTCTGCGGCCGGGATGAGTAC 928
Qy 281 LeuValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGlnLysLeuLysAsnGly 300
Db 929 CTGGTGGGTGAGACCCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988
Qy 301 GluGluIleHisLeuValLeuAspAsnThrProProAspProAlaLeuAspLeuValArgLys 320
Db 989 GAGGAGATTCACCTTGTGCTGGACAACACTCCTCCAGACCCTGCACTGGACCTGGTGAGGAAG 1048
Qy 321 GluGluTrpProLeuValAlaAspCysSerThrGlyValThrHisGlyLeuTyrHisGluGlnLeuThr 340
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Qy 341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
Db 1109 ATCCACGGCAAGGACCATGAAAGTGTGTTCACGGTGTCCCTGTGGGACTGCGACCGCAAG 1168
Qy 361 PheArgValLysLysIleArgGlyIleAspAspIleProValLeuProValArgThrAlaAspLeuThr 380
Db 1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTGCCCGTGAGGACCGCCGACCTCACG 1228
Qy 381 ValPheValGluAlaAlaAsnIleGlnTyrGlyGlnInValLeuCysGlnArgArgThrSer 400

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Db  1229 GTGTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAACCAGC 1288

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Db  2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTAGAACAAAAGCTTACTACAGAAATTTGAATCTCCC 2428

Qy   401 ProLysProPheThrGluThrLeuTrpAsnValTrpAsnValPheSerIleLysIle 420
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Db  1289 CCCAAACCCTTCACGGAGAGGAGGTGCTCTCGGAACCTGTGCTTCGAGTTCAGTATTAAAATC 1348

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
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Db  2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAGCCGGGCACTGGTCATCGAAAAA 2488

Qy   421 LysAspLeuProLysGlyValAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
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Qy   801 CysLysValMetAlaSerLysLysGlyLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
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Db  2489 TGTAAAGTGATGGCCTCCAAGAAGAGCCCCTGTGGTTAGTTTAAATGTGCCGGATCCT 2548

Qy   441 LeuSerGlyLysLysThrSerAlaGluMetProSerProGlySerLysGlyLysAlaGlnLeu 460
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Qy   821 ThrAlaLeuSerArgAsnGluThrIleGlyIleGlyLysHisGlyAspAlaProLeuArgGln 840
         |||||||||||||||||||||||
Db  2549 ACGGCTCTATCAAATGAAACAATTGGAATTATCTTTAAAACGGTGACGATCTGCCAA 2608

Qy   461 LeuTyrTyrValAsnLeuLeuLeuLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
         |||||||||||||||||||||||
Db  1469 CTGTACTATGTCAACCTATTGCTGATAGACCATCGCTTCCTCCGCCATGGCGGAGTAT 1528

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
         |||||||||||||||||||||||
Db  2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG 2668

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyValGluAspGlnGlySerPheAsnAlaAsp 500
         |||||||||||||||||||||||
Db  1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGGTAGAAGACCAAGGGAGTTCAATGCCGAC 1588

Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
         ||||||||||||||    :::
Db  2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeuLeu 520
         |||||||||||||||||||||||
Db  1589 AAGCTCACGTCGGGAACCAACCCCGACAAGGAGAGACTCAAGTCCATCTCCATTCTCTTG 1648

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlnSerThrGly 900
         |||||||||||||||||||||||
Db  2729 ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGCAAAGCACAGTGGGCAACACGGGT 2788

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
         |||||||||||||||||||||||
Db  1649 GACAATTACTGCCATCCCCATAGCCTTGCCTAAGCATCGGCCTACACCCTGACCCAGAGGG 1708

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuValSerCysProIleGluGluLys 920
         |||||||||||||||||||||||
Db  2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCGTGAGTTGCCCTATTGAAGAAAAG 2848

Qy   541 AspArgValArgAlaGluMetProLeuAsnProLeuAsnLeuArgLysGlnLeuGluLeuIleIleAla 560
         |||||||||||||||||||||||
Db  1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTTCGGAGCAACTGGAGCTCATTATCGCC 1768

Qy   921 PheGlnAlaAlaValGlyArgPheValSerCysAlaGlyTyrCysValAlaThrPhe 940
         |||||||||||||||||||||||
Db  2849 TTTCAGGCAGCTGTGGGAAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT 2908

Qy   561 ThrAspProLeuAsnProLeuAsnProLeuThrArgAlaGluLeuLeuTrpHisTyrPheArgTyr 580
         |||||||||||||||||||||||
Db  1769 ACGGATCCGCTTAACCCACTCACAGCTGAAGCAAGAACTGCTCTGGCATTTCAGATAT 1828

Qy   941 ValLeuGlyIleIleGlyGlyAspArgHisAsnAspAsnIleMetIleSerGluThrArgGlyAsnLeu 960
         |||||||||||||||||||||||
Db  2909 GTTCTCGGAATAGGCGGACAGACCAATGACAATATTATGATCTCGGAAACAAGGAATCTA 2968

Qy   581 GluSerLeuLysAspProLysProLysSerAlaTyrProLysSerValLysTrpProGlyGln 600
         |||||||||||||||||||||||
Db  1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGTCTGTAAAATGGGGACAG 1888

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
         |||||||||||||||||||||||
Db  2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   601 GlnGluIleValAlaLysThrThrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
         |||||||||||||||||||||||
Db  1889 CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT 1948

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
         |||||||||||||||||||||||
Db  3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy   621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
         |||||||||||||||||||||||
Db  1949 GCTTTGGATGTGGGGTTAACCATGCAGCTGCAACTTGGACAAAACGTG 2008

Qy  1001 LysThrSerLeuHisPheGlnLysPheLeuLysAspValCysValLysAlaTyrLeuAlaLeu 1020
         |||||||||||||||||||||||
Db  3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTAAAGGCTTACCTAGCCCTT 3148

Qy   641 ArgAlaIleAlaValGlnLysLeuGluSerLeuLeuSerAspAspAlaValLeuHisTyrLeu 660
         |||||||||||||||||||||||
Db  2009 AGAGCCATTGCAGTCCAGAAACTGGAGAGCTTACAGAGTTGCAGTGATCTGGAAGCCTAC 2068

Qy  1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
         |||||||||||||||||||||||
Db  3149 CGTCATCACCACAAACCTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC 3208

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
         |||||||||||||||||||||||
Db  2069 CTCCAGCTGGTGCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy  1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
         |||||||||||||||||||||||
Db  3209 CAGTTAACCAGCAAAGAAGAGACATTGAATACATTCGGGATGCCCTCACAGTGGCAAAAGT 3268

Qy   681 LeuLeuLysArgGlyLeuAsnLysArgIleGlyHisGluPheTrpPheLeuArg 700
         |||||||||||||||||||||||
Db  2129 CTGCTGAAGCGTGGATTAAGAAAACAAGAGAATTGGTCACTTCTTTGTTTTGGTTCTTGAGA 2188

Qy  1061 GluGluAspAlaLysGlyTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
         |||||||||||||||||||||||
Db  3269 GAGGAGGACGATGCTAAAAGGTTATTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG 3328

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnIleAsnArgPheAlaValIleLeuGluAlaThrTyr 720
         |||||||||||||||||||||||
Db  2189 AGTGAGATTGCCCAGTCTAGGCACTATCAGATCAGAGGTTTGCAGTGATCTGGAAGCCTAC 2248

Qy  1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis 1100
         |||||||||||||||||||||||
Db  3329 ACCGTGCAGTTTAACTTGGTTCTTCACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisLeuAspPheThrGlnInValGlnInValIleAsp 740
         |||||||||||||||||||||||
Db  2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACCTGGACTTCACCCAGCCAAGTCCAATTGAC 2308

Qy  1101 SerAla 1102
         ||||
Db  3389 CCCGCA 3394

Qy   741 MetLeuGlnLysValThrArgIleLeuAspIleLysSerLeuSerAlaGluLeuTyrArgAspValSer 760
         |||||||||||||||||||||||
Db  2309 ATGTTACAAAAAGTCACCATTGACATTAAATCGTCTCTGCTAGCAGAGTTATGACGTCAGT 2368
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RESULT 2
AAV74100
ID   AAV74100 standard; DNA; 3808 BP.
XX
AC   AAV74100;
XX
DT   09-MAR-1999 (first entry)
XX
DE   Porcine G-protein regulated PI3K p120 adapter subunit DNA.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; porcine;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; haematopoietic system;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer; ss.
XX
OS   Sus scrofa.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;   97US-0916917.
XX
PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S,  Hawkins PT,  Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   P-PSDB; AAW90083.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   their fragments, are used as probes and primers for identifying p101 or
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example IX; Fig 3A-C; 75pp; English.
XX
CC   This sequence encodes a novel catalytic subunit, p120, from porcine
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Alignment Scores:
Pred. No.:              0         Length:         3808
Score:            5726.00         Matches:        1090
Percent Similarity: 99.46%        Conservative:      6
Best Local Similarity: 98.91%     Mismatches:        6
Query Match:       98.89%         Indels:            0
DB:                   20          Gaps:              0

US-09-974-573-1 (1-1102) x AAV74100 (1-3808)

Qy    1 MetGluLeuGluAsnTyrGlnGlnProValLeuGlnProValLeuValArgGluAspAsnArgArgArgArg 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGTCAGCCCGTGCTGAGAGGAGGACAACCCGCCCAGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149 CGGAGGATGAAGCCGCGGCAGCACGGCAGCCAGCCTGTCCTCCATGAGCTCATCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209 GAGTTTGTTTTGGCCACCAGCCAGCGCAACACCAAGACCCCGAAACGGCACTGCTGCAC 268

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
          ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db  269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTGTTGGCCGGCGCTGGAG 328

Qy   81 ThrSerValSerArgLeuArgLeuProAspHisArgLeuProAspHisPheLeuLeuLeuTyr 100
          ||||||||||||||||||||||||||||||:|:::|||||||||||||||||||||||||||
Db  329 ACGAGCGTTCTTGGGACTTCTACCACCGGTTCGGCCCGGACCACTTCCTCCCTGGTCTTC 388

Qy  101 GlnLysLysGlyGlnTrpTyrGlnIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
          ||||||||||:|:|:||||||||||||||||||||||||||||||||||||||||||||||
Db  389 CAGAAGAAGGGGGAGTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy  121 CysLeuArgTyrTrpLysTrpLysHisArgSerProGlyGlnIleHisValValGlnArg 140
          |||||||||||||||||||||||:|:||||||||||||||||||||||||||||||||||
Db  449 TGCCTGCGCTACTGGAGGTGGTTGCACCGGAGTCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuLeuIleGlyTyr 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  509 CACGCCCCCTCGGAGGAGACATTGGCCTTCCAGCGCCAGCTGAACGCCCTCATCGGCTAC 568

Qy  161 AspValThrAspValSerAsnValHisAspAspGluAspGlyAspAspAsnAspAspThr 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGGAGTTCACGCGGCGCGCCCTG 628

Qy  181 ValThrProArgMetAlaGluValAlaAlaGlyArgAspProLysProLysLeuTyrAlaMetHisPro 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  629 GTCACCCCGCGCATGGCCGAGGTGGCCGCGGGCCGCGACCCCAAGCTTTAAGCCATGCACCCC 688

Qy  201 TrpValThrSerLysProLeuProGluValTyrLeuLysLysIleThrAsnCysVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  689 TGGGTGACATCCAAGCCCCTCGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC 748

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC 808

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetGluMetAsp 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  809 CCAGGCACCATCCTCCAGAGTTCTTCTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy  261 PheIleValIleHisArgSerGlnAsnGluArgAspPheValCysGlyValArgAspGluTyr 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGGGTCTGCGGCGTCCGGGATGAGTAC 928

Qy  281 LeuValGlyGluThrProIleLeuLysAspPheAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy  301 GluIleHisLeuHisLeuValLeuAspThrProProAspProAlaLeuAspLeuValArgLys 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  989 GAGGAGATTCACCTTGCTGCTGGACACTCCTCCAGACCCTGCGCTGGATCTGGTGAGGAAG 1048

Qy  321 GluGluTrpProLeuValAspAspCysThrGlyValThrHisGlyValTyrHisGluGlnLeuThr 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1049 GAAGAGTGGCCCCTGGTGGATGACTGCACGGGAGTCACTGCTACCACGAGACCAGCTGACC 1108

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1109 ATCCACGGCAGGACCATGAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy  361 PheArgValLysIleArgGlyIleLeuAspIleProValLeuProArgThrAlaAspThrLeuThr 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTGCCCCGGACCGCTGACTTCACG 1228

Qy  381 ValPheValGluAlaAsnIleGlnTyrGlyInValLeuCysGlnArgThrSer 400
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Db  1229  GTGTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAACCAGC  1288

Qy   761  SerGlnValIleSerGlnLeuLysGlnLysGluAsnLeuGlnAsnLeuAsnLeuPro   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2369  TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACTTACAGAATTTGAATCTCCC   2428

Qy   401  ProLysProPheThrGluGluValLeuTrpAsnValPheLysGluSerIleLysIle    420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1289  CCCAAACCCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGACGTTCAGTATTAAAATC  1348

Qy   781  GlnSerPheArgValProTyrAspTyrProGlyLeuLysGlyAlaGlyAlaValIleGluLys   800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2429  CAAAGCTTTAGAGTTCCCATATGATCCCATGGGACTGAAAGGCGGGGCACTGGTGATCGAAAAA  2488

Qy   421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla    440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1349  AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA   1408

Qy   801  CysLysValMetAlaSerLysLysLysProGluPheLeuPheLysCysLysAspPro    820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGTTTAAATGTAAGGATCCT       2548

Qy   441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu   460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1409  CTGTCGGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGAGCAAAGGCAAAGCTCAGCTT   1468

Qy   821  ThrAlaLeuSerAsnGluThrLeuGlyTyrIleIleGlyHisGlyAspLeuArgGln   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2549  ACGGCTCTATCAAATGAACAAATGGATTATCTTTAAACACGGTGACGATCTCCGGCAA     2608

Qy   461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr    480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1469  CTGTACTATGTCAACCTATTGCTAATAGACCACCGCTTCCTCCGCGCCATGGCGAGTAT   1528

Qy   841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu   860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2609  GACATGCTTAATTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG   2668

Qy   481  ValLeuHisMetTrpGlnIleLeuSerGlyLysGlyGluAspGlnGlySerPheAlaAlaAsp   500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1529  GTGCCCCACATGTGGCAGTATCCGGAAGGGGGAAGACCAAGGAGCTCAATGCCGAC        1588

Qy   861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyLysAspLysProIleGlyMetIleGlu   880
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db  2669  GATCTGTGCCTCCTGCCATATGGCTGCATCAGCACTGGCAAAATAGGAATGATCGAG      2728

Qy   501  LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleLeuLeuLeu   520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1589  AAGCTTCACGTCGGGAACCAACCCGGACAAGGAGGACTCAATGTCCATTCCATTCTTCTG   1648

Qy   881  IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGly   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2729  ATCGTGAAGGACGCGCCACGACAATCGCCAAAATTCAGCAAAAGCACAGTGGGCAACACGGGT  2788

Qy   521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1649  GACAATTACTGCCATCCACCCATAGCCTTGCCTAAGCATCGGCCTACCCCTGACCCCAGAAGGG  1708

Qy   901  AlaPheGluLysAspGluValLeuSerHisTrpLeuValSerProIleGluGluLys   920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2789  GCCTTTGAAAAGGATGAAGTCCTGAGTCACTGGCTTGTCAGCCCTATTGAAGAAAAG     2848

Qy   541  AspArgValArgAlaGluMetProAsnGlnLeuArgGlyLysGlnLeuGlnLeuAlaIleIleAla   560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1709  GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAATCATAGCC   1768

Qy   921  PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe   940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2849  TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT   2908

Qy   561  ThrAspProLeuAsnProLeuThrThrAlaGluLeuLeuLeuHisLeuTrpHisHisPheArgTyr   580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1769  ACGGATCCGCTTAACCCACTCACCACTGCAGAACTGCTCCTGCATTTCTGGCATCATTTCAGATAT  1828

Qy   941  ValLeuGlyIleGlyAspAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2909  GTTCTCGGAATAGGCGACGACAGACACAATTGACAATATTATGATCTCAGAAACAGGAAATCTA  2968

Qy   581  GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1829  GAAAGCCTGAAGGATCCCAAAGCGTATCCCAAAGGAGCTCTTCAGCTCTGTCGGTGAAATGGGGGACAGG  1888

Qy   961  PheHisIleLeuProHisGlyPheHisIleLeuGluGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys   980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2969  TTTCATATTGATTTCGGACACATTCTTGAGGGAAATTACAAAAGTTCCCTGGGCATTATAATAAA  3028

Qy   601  GlnGluIleValGlnAlaAlaLysThrTyrGlnIleValThrArgAspValTrpAspGlnSer   620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1889  CAAGAAATTGTGGGCGCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT  1948

Qy   981  GluArgValProLeuGlyPheProAspLeuValAlaAlaTyrLeuAlaLeu  1000
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3029  GAGAGGGTGCCATTGGTATCCTGCTACCCCGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG  3088

Qy   621  AlaLeuAspAspValGlyValThrMetGlnLeuMetGlnLeuLeuAspProCysAsnPheSerGluAspGluAsnVal   640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1949  GCTTTGGATGGGGTTGGGGTTTAACCATCCAGCTCCTGGCAAAACATTCTCGAATGAAAACGTG  2008

Qy  1001  LysThrSerLeuHisPheGlnLysLeuHisPheGlnAsnValCysValLysValLysValHisTyrLeuAlaLeuTyrLeuAlaLeu  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3089  AAGACAAGTCACACTTCCAGAAATTTCAGGAATGTCGTGCGTCAAGGCTTACCTAGCCCTT    3148

Qy   641  ArgAlaIleAlaValGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluLeuAlaTyr   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2009  AGAGCCATTGCAGTGCAGAGTCGACACTATCAGCAGAGGTTTGCAGTTATCCTGGAAGCCTAC  2068

Qy  1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyValMetPro  1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3149  CGTCATCACACACAAACCACTGACTCATCCTCTTCCATGATGCTGATGACAGGAGTGCCC   3208

Qy   661  LeuGlnLeuValGlnAlaValLysProPheGluGlnProTyrHisAspSerArgAlaLeuArgPhe   680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2069  CTCCAGCTGGTCCAGGCTGTGAAATTTGAAGCCTACCATGACAGTAGGGCCCTAGCCAGATTT  2128

Qy  1041  GlnLeuThrSerLysGluAspIleLeuGluTyrIleLeuArgAspAlaLeuGlyIleLysSer  1060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3209  CAGTTAACCAGCAAAGAAGACATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT    3268

Qy   681  LeuLeuLysArgGlyLysAsnLysArgIleGlyHisPheLeuPheLeuArg   700
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2129  CTGCTGAAGCGTGGTTAAGAAAACAAGAGAATTGTCACTTCCTGTTTCTTGAGA   2188

Qy  1061  GluGluIleAlaGlnAlaAlaLysLysProGlnIleGluGluValCysArgArgGlyGlyTyrTrp  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3269  GAGGAGGATGCTAAAGCAGCTAAAAAGCCTCAAATTGAGGAAGTTTGCAGAGACAAAGGATGG  3328

Qy   701  SerGluIleAlaGlnSerArgHisArgGlnArgPheAlaValIleLeuGluLeuAlaTyr   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2189  AGTGAGATTGCCCAGTCTAGGCACACTCTAGGCACTATCAGCAGAGGTTTGCAGTTATCCTGGAAGCCTAC  2248

Qy  1081  ThrValGlnPheAsnTrpPheAsnValIleIleLysGlnValGlyLysGluLysHis  1100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3329  ACCGTGCAGTTTAACTGGTTCTTAACGTTCTTACATCTTGTTCTTGGCATCAAACAGGGGGAGAAGCAT  3388

Qy   721  LeuArgGlyCysCysGlyThrAlaMetLeuHisAspPheThrGlnLeuValGlnValIleIleAsp   740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2249  CTGAGGGGCTGTGCCAGCCATGCTGCACGACCATCACCCAGCAAGTCCAAGTAATTGAC   2308

Qy  1101  SerAla  1102
          ||||||
Db  3389  CCCGCA  3394

Qy   741  MetLeuGlnLysValThrIleAspSerIleLeuLysSerLeuSerGluAlaGlyLysLysTyrAspValSer   760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2309  ATGTTACAAAAAGTCACCATTGATTCAATATCTTTGAAAAGTCTGAGTGAAGCTGGGAAGAAGTATGACGTCAGT  2368
```

```
RESULT 3
AAZ86813
ID   AAZ86813 standard; DNA; 3808 BP.
XX
AC   AAZ86813;
XX
DT   20-APR-2000  (first entry)
XX
DE   Pig p120 regulatory subunit coding sequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; pig; ss.
XX
OS   Sus sp.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
PF   04-JAN-1999;  99US-0225170.
XX
PR   15-AUG-1997;  97US-0916917.
PR   27-JUN-1996;  96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
XX
DR   WPI; 2000-136682/12.
DR   P-PSDB; AAY76802.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Example; Fig 3; 75pp; English.
XX
CC   This sequence encodes the pig p120 regulatory protein.
CC   The invention relates to the human G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Alignment Scores:
Pred. No.:                 0
Score:                     5726.00
Percent Similarity:        99.46%
Best Local Similarity:     98.91%
Query Match:               98.89%
DB:                        21

US-09-974-573-1 (1-1102) x AAZ86813 (1-3808)
```

Length: 3808
Matches: 1090
Conservative: 6
Mismatches: 6
Indels: 0
Gaps: 0

```
Qy    1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACCGCCGAGGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuProIle 40
Db  149 CGGAGGATGAAGCCGCGGCCAGCAGCCAGCCTGTCCTCCATGGAGCTCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrArgAlaLeuLeuHis 60
Db  209 GAGTTTGTTTTGGCCACCAGCCAGCCGCAACACCAAGACCCCGAAACCGCACTGCTGCAC 268

Qy   61 ValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
Db  269 GTGGCGGCCGCACGGCAATGTGGAGAAGATGAAGGCCCAGGTGTGTTGCCGGCGCTGGAG 328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
Db  329 ACGAGCGGTTTCTTGGGACTTCTCACCACCGGTTCGGCCCGACCACTTCCTCTGGTCTTC 388

Qy  101 GlnLysLysGlyGlnTrpTyrGlnIleTyrArgGluTyrAspLysTyrGlnValValGlnThrLeuAsp 120
Db  389 CAGAAGAAGGGGGAGTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
Db  449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCGGGACAGATCCACGTGGTCCAGCGG 508

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuLeuGlyTyr 160
Db  509 CACGCGCCCTCCGAGGAGACATTGGCCTTCCAGCGCCAGCTCAACGCCCTCAACGGCTAC 568

Qy  161 AspValThrAspValSerAsnValHisAspAspGluPheThrArgArgLeu 180
Db  569 GACGTCACCGACGTCAGCAACGTGCATGATGACGAGTTCACGCGCGCGCCTG 628

Qy  181 ValThrProArgMetAlaGluValAlaGlyTyrArgAspProLysLeuTyrAlaMetHisPro 200
Db  629 GTCACCCCGCGGATGGCCGAGGTGGCCGGCTACCGCGACCCCAAGCTTTTACGCCATGCACCCC 688

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleLysThrAsnAsnCysVal 220
Db  689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTTGCGTC 748

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
Db  749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC 808

Qy  241 ProGlyThrIleLeuGlnSerProPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
Db  809 CCAGGCACCATCCTCCAGGTCTTCTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy  261 IleProGluGlnAsnGluArgAspPheValLeuArgValCysGlyTyrArgAspGluTyr 280
Db  869 ATCCCTGAAAGCCGAGAACGGGGACTTTGTGCTGCGCGTCTGCGGCCCGGGGATGAGTAC 928

Qy  281 LeuValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
Db  929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy  301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspAspThrLeuAspThrLys 320
Db  989 GAGGAGATTCACCTTGTGCTGGACACTCCTCCAGACCCTGCAGGTGAGGAAG 1048

Qy  321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluThrLeuThr 340
Db 1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGTGACC 1108

Qy  341 IleHisGlyLysAspHisGluValThrPheThrValSerLeuTrpAspCysAspArgLys 360
Db 1109 ATCCACGGCAAGGACCATGAAAGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy  361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgLeuProArgThrAlaAspLeuThr 380
```

Db 2249 CTGAGGGGCTGTGGCACGACCATGCTGCACGACTCACCCGCAGTCCAAGTAATTGAC 2308
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
Db 2309 ATGTTACAAAAAGTCACCATTGACATTAAATCCCTCTCGCTGAAAAGTATGACGTCAGT 2368

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysGlnLysLeuGlnLeuGlnAsnLeuGlnLeuProLeuAsnLeuAsnLeuGlnProLeuPro 780
Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGTTGAAAACCTACAGAATTTGAATCTCCC 2428

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
Db 2429 CAAAGCTTTAGAGTTCCTATGATCCTGGACTGAAGCCGGGCACTGGTGATCGATGAAAAA 2488

Qy   801 CysLysValMetAlaSerLysLysSerLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGGCTTGAGTTTAAAATGTCCGATCCT 2548

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
Db 2549 ACGGCCTCATCAAATGAACAATTGGAATTATCTTTAAACACGGTAGCATCTGCCCAA 2608

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
Db 2609 GACATGCTTATTTTACAGATTCTCAGGATCATGGAGTCCATTGGGAGACCGAATCTTG 2668

Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleIleGlyMetIleGlu 880
Db 2669 GATCTGTGCCTCCTGCCATATGGCTGCATTCAACTGGTGACAAAATAGGATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGluGlnSerThrValGlyAsnThrGly 900
Db 2729 ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGCAAAGCACAGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys 920
Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy   921 PheGlnIleAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATCCTGGGCTACGTGTGTGCGGCAACCTTT 2908

Qy   941 ValLeuGlyIleGlyAsnArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db 2909 GTTCTCGGAATAGGCGACAGACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db 2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db 3029 GAGAGGGTGCCATTTGTTCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisGlnLeuPheGlnIleAspAspAspValCysValLysAlaTyrLeuAlaLeu 1020
Db 3089 AAGACAAGCTCACACTTCCAGATTTGAGGATGTCGTGCGTCAAGGCTTACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
Db 3149 CGTCATCACACAAACCTACTGATCATCCTTCTCATGATGCTGATGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
Db 3209 CAGTTAACCAGCAAGGAAGACATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT 3268

Qy 1061 GluGluAspAlaLysTyrPheLeuAspGluValCysArgAspTyrLysGlyTyrTrp 1080
Db 3269 GAGGAGGATGCTAAAAGTATTTTCTGATCAGATTGAAGTTGCAGAGACAAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyLysHis 1100
Db 3329 ACCGTGCAGTTAACTGGTTCTTAACATCCTTGTTCTTCGGCAATCGAAGGGAGAAGCCAT 3388

Db 1169 TTCAGGGTCAAAATCAGAGAGCATTGATATCCCTGTTCCTGCCCCGGACCCCTGACCTCACG 1228
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   381 ValPheValAlaAsnIleGlnTyrGlyGlnIleTyrGlnLeuCysGlnArgArgThrSer 400
Db 1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGATCTCCTTTGCCAAAGGAGAACCAGC 1288

Qy   401 ProLysProPheThrGluGluValTrpAsnValTrpLeuGluPheSerIleLeuLys 420
Db 1289 CCCAAACCCTTCACGGAGGAGGTGTCTGGAACGGTGCTGGCTTGAGTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuProLysGlyValAlaLeuLeuAsnLeuGluIleIleTyrCysGlyLysAlaProAla 440
Db 1349 AAAGACTTACCCAAAGGGGCTCTGCTGACCTCCAGATCTACTGCGGGCAAAGCTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerProLysGlyLysAlaGlnLeu 460
Db 1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCTTCGCCAGAGTCCCAAAGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrTyrValAsnLeuLeuIleGluAspHisArgPheLeuLeuArgHisGlyGlyTyr 480
Db 1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCTGCGCCATGGCGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyAspGlnLeuSerPheAsnAlaAsp 500
Db 1529 GTGTTACACATGTGGCAGTTATCCGGAAGGGAGGACCAAGGGAGTTCATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysProLysIleSerSerIleLeuLeu 520
Db 1589 AAGCTTACAGTCGGGACAACCCGGACAAGGAGGACTCAAATGTCCATCTCCATTCTTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
Db 1649 GACAATTACTGCCACCCATAGCCTTGCCTAAGCATCGGCCTACCCCTGACCCCAGAAGGG 1708

Qy   541 AspArgValArgAlaGluMetProAsnProLeuLysGlnLeuArgLysGlnLeuValAlaIleIleAla 560
Db 1709 GACCGGGTTCGGGCAGAAATGCCCAATCCACTCAGCTTCCGAAGCAACTGAGGCCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluLeuAspLysProLysGluLeuTrpHisPheArgTyr 580
Db 1769 ACGGATCCGCTTAACCCACTCACAGCTGAAGACAAAGAACTGCCTCGGCATTTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysAlaTyrProLeuPheSerSerValLysTrpGlyGln 600
Db 1829 GAAAGCCTGAAGGATCCCAAAGCCTATCCAAGCGTATCCTTTAGCTCGGTGAAAATGGGGACAG 1888

Qy   601 GlnLeuIleValAlaLysThrThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
Db 1889 CAAGAAATTGTGGCCAAAACAACCATATTAGCCAAAGGGAGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuLeuAspCysAsnPheSerAspGluAsnVal 640
Db 1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGCTCGACTGCAACTTCTCCGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaAlaValGlnLysLysLeuGluLeuGluAspAspAspValLeuHisTyrLeu 660
Db 2009 AGAGCCATTGCAGCTGTGCAGAAAAAGCTTGAGGAGGATGACGTGCTCCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaValLysLysTyrHisAspTyrHisAspSerAlaLeuAlaArgPhe 680
Db 2069 CTCCAGCTGGTCCAGGCTGTGAAAAATTTGAACCATAACCATGAACACGTGCCCTAGCAGATTT 2128

Qy   681 LeuLeuGlnLysArgGlyLeuValArgLysAsnLysArgIleGlyTyrHisGlyPheLeuArg 700
Db 2129 CTGCTGCAAAAGCGTGGTTTAAGAAAAAACAAGAGAATTGGTCACTTCTTTTGGTTCTTGAGA 2188

Qy   701 SerGlyIleGlnSerArgHisTyrGlnValGlnArgPheAlaValIleIleGluValAlaTyr 720
Db 2189 AGTGAGATTGCCAGTCGTCAGGCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheGlnInValGlnnValIleAspAsp 740
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Qy        1101 SerAla 1102
               |||
Db        3389 CCCGCA 3394

RESULT 4
AAV74104
ID   AAV74104 standard; DNA; 5162 BP.
XX
AC   AAV74104;
XX
DT   09-MAR-1999 (first entry)
XX
DE   Human G-protein regulated PI3K p120 adapter subunit DNA.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; human;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; haematopoietic system;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;    97US-0916917.
XX
PR   15-AUG-1997;    97US-0916917.
PR   27-JUN-1996;    96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   P-PSDB; AAW90089.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example X; Fig 12A-C; 75pp; English.
XX
CC   This sequence encodes a novel catalytic subunit, p120, from human
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 5162 BP; 1471 A; 1173 C; 1149 G; 1367 T; 2 other;

Alignment Scores:
Pred. No.:                     0        Length:          5162
Score:                   5534.00        Matches:         1049
Percent Similarity:       97.10%        Conservative:      21
Best Local Similarity:    95.19%        Mismatches:        32
Query Match:              95.58%        Indels:             0
DB:                           20        Gaps:               0

US-09-974-573-1 (1-1102) x AAV74104 (1-5162)
```

```
Qy    1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg    20
Db   84 ATGGAGCTGGAGAACTATAAACAGCCCGTGTGCTGAGAGAGAACAACTGCCGAAGGCGC   143

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuProIle    40
Db  144 CGGAGGATGAAGCCCGCCAGTGCCGCAGCCTGTCCCATGGAGCTCATCCCCATC   203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis    60
Db  204 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGACCCCGAAACGGGCGCTGCTGCAC   263

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu    80
Db  264 GTGGCGGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCCCTGGAG   323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
Db  324 ACCAGCGTGGCGGCAGCTTCTACCACCGGCTGGGACCGGCATCCCTTCCCCTGCTCTAT   383

Qy  101 GlnLysLysGlyGlnThrTyrGlnLeuTyrAspLysTyrGlnValValGlnThrLeuAsp   120
Db  384 CAGAAGAAGGGGCAGTGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC   443

Qy  121 CysLeuArgTyrTrpLysValHisArgSerProGlyGlnIleHisValValGlnArg   140
Db  444 TGCCTGCGCTACTGGAAGGCCACGCACCGGAGATCCACGGGGCCAGATCCACGTGGTGCAGCCGG   503

Qy  141 HisAlaProSerGluGlnThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr   160
Db  504 CACGCCCCTCCGAGCAGACCCTTCCAGCCGGCAGCTTCACGGCGCTGATTGGCTAT   563

Qy  161 AspValThrAspValSerAsnValHisAspAspAspLeuLeuGluPheThrArgArgLeu   180
Db  564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGTTCAGCGCCGTGGCTTG   623

Qy  181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro   200
Db  624 GTGACCCCGCGTACTGGCGGAGGTGGCCAGCCGGACCCCAAGCTCTACGCCATGCACCCG   683

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleLysThrAsnAsnCysVal   220
Db  684 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC   743

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr   240
Db  744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCGACGACACC   803

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp   260
Db  804 CCCGGCGCCATCTGCAGCTTCTTCACCAAGATGGCCAAGAAGAATCTCTGATGAT   863

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyTyrArgAspGluTyr   280
Db  864 ATTCCCGAAAGCCAAAGCAGAGATTTTGTGCTGCGCGTCTGTGGCCGGGATGAGTAC   923

Qy  281 LeuValGlyGluThrProIleLysSerAsnPheGlnIleTrpValArgGlnCysLeuLysAsnGly   300
Db  924 CTGGTGGGCGAAAACGCCCATCAAAACTTCCAGTGGGTGGTGAGGCACTGCCTCAAGAACGGA   983

Qy  301 GluGluHisLeuValLeuAspThrProProAlaLeuAspProArgGluValAlaValArgLys   320
Db  984 GAAGAGATTCACGTGGTACTGGACACCCGCCCTCCAGACCCGGCCCTCAGCGAGGTGACGAAG   1043

Qy  321 GluGluTrpProLeuValAlaAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr   340
Db 1044 GAAGAGTGGCCGCTGGTGGCAGACTGCACGGGAGTCACCGGCTACCATGAGCAGTTACC   1103

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
Db 1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG   1163

Qy  361 PheArgValIleArgGlyIleAspIleProValLeuProArgValThrAlaAspLeuThr   380
```

```
Qy      1101 SerAla 1102
Db           ||||||
        3384 TCAGCC 3389

RESULT 5
AA286814
ID   AA286814 standard; DNA; 5162 BP.
XX
AC   AA286814;
XX
DT   20-APR-2000 (first entry)
XX
DE   Human p120 regulatory subunit coding sequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; human; ss.
XX
OS   Homo sapiens.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
PF   04-JAN-1999; 99US-0225170.
XX
PR   15-AUG-1997; 97US-0916917.
PR   27-JUN-1996; 96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
XX
DR   WPI; 2000-136682/12.
DR   P-PSDB; AAY76803.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Disclosure; Fig 12; 75pp; English.
XX
CC   This sequence encodes the human p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence 5162 BP; 1471 A; 1173 C; 1149 G; 1367 T; 2 other;

Alignment Scores:
Pred. No.:                0              Length:        5162
Score:                5534.00           Matches:       1049
Percent Similarity:    97.10%           Conservative:    21
Best Local Similarity: 95.19%           Mismatches:      32
```

```
Query Match:   95.58%          Indels:   0
DB:                21          Gaps:     0

US-09-974-573-1 (1-1102) x AA286814 (1-5162)

Qy    1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg  20
Db   84 ATCGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGGACAACTGCCGAAGGCGC   143

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerMetGluLeuIleProIle            40
Db  144 CGGAGGATGAAGCCGCGGAGCCTGTCCTCCATGGAGCTCATCCCCATC             203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
Db  204 GAGTTCGTGCTGCCCACCAGCCAGCGGAAATGCAAGACGCCCGAAACGGGCGCTGCTGCAC 263

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
Db  264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
Db  324 ACCAGCGTGGGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT 383

Qy  101 GlnLysLysGlyGlnTrpTyrGluIleTyrArgGlnValGlnThrLeuAsp           120
Db  384 CAGAAGAAGGGGCAGTGGTACGAGATCTACAGACAAGTACCCAGGTGGTGCAGACTCTGGAC 443

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleIleHisValValGlnArg  140
Db  444 TGCCTGCGCTACTGGAAGGTCCTGCACCGCAGCCCCGGCATCATCCACGTGGTGCAGCGG  503

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
Db  504 CACCCGCCCTCCGAGGAGTCCCAAGCCTTCAGCGGCAGCTCAGGCGCTGATTGGCTAT   563

Qy  161 AspValThrAspValSerAsnValHisAspAspProGlnLeuGluPheThrArgArgLeu  180
Db  564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  623

Qy  181 ValThrProArgMetAlaGluAlaGlyValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
Db  624 GTGACCCCGCGCATGGCCGAGGCGGGAGTGGCCAGCCGCGACCCCAAGCTCTACGCCATGCACCCG 683

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
Db  684 TGGGTGACGTCCAAGCCCCTGCCGGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC  743

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrThrLysValSerAlaAspAspThr  240
Db  744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCACCAAGGTCTCACCGACGACACC   803

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp     260
Db  804 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  863

Qy  261 IleProGluSerGlnAsnGluLysAspPheValLeuAspArgValCysGlyValArgAspGluTyr 280
Db  864 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGGACCGTGTCTGTGGCCGGATGAGTAC 923

Qy  281 LeuValGlyGluThrProIleLysAsnPheGlnProIleValArgGlnCysLeuLysAsnGly 300
Db  924 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGCGCACTGCCTCAAGAACGGA  983

Qy  301 GluGluIleHisLeuValLeuValAspSerThrProProAlaLeuAspProAlaLeuArgLys 320
Db  984 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGGCCCTAGACGAGGTGAGGAAG 1043

Qy  321 GluGluTrpProLeuValLeuAspAspCysThrGlyThrGlyValThrHisGluGlnLeuThr 340
Db 1044 GAAGAGTGGCCCCTGGTGCTGGACGACTGCACGGGAGTCACGGCTACCATGAGCAGCTTACC 1103
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Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG 1163

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1164 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTCGGACAGCCGACCTCACA 1223

Qy   381 ValPheValGluValGlnAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer 400
           ||||||||||| ||| |:::|||||||||||||||||||||||||||||||||||||||
Db   1224 GTTTTTGTAGAGGCAAACATCCAGTATGGGCAACAAGTCCTTTGCCAAAGGAGAACCAGC 1283

Qy   401 ProLysProPheThrGlyGluValLeuTrpAsnValTrpLeuGluPheAsnLeuLysIle 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 CCCAAACCCTTCACAGGAGAGGTGCTGTGGAATGTGTGGCTTGAGTTCAATCTGAAAATC 1343

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1403

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysLysAlaGlnLeu 460
           |||||||||||||||||||||||||||||||||||| :::|||||||||||
Db   1404 CTGTCCAGCAAGACCTCTGCAGAGTCCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1463

Qy   461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1464 CTCTATTATGTGAACCTGCTGCTAATAGACCACCGTTTCCTGCTGCGCCGTGGAGAATAC 1523

Qy   481 ValLeuHisMetTrpGlnIleLeuSerGlyValGlyAspGlnGlySerPheAsnAlaAsp 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1524 GTCCTCCACATGTGGCAGATATTCTGGAGGGGAGGAGAACCAAGGAAGCTTCAATGCTGAC 1583

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleLeuSerLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1584 AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTCCATGTCCATCCTCATCCTTCTG 1643

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
           ||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db   1644 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGACCCCTGACCCCGGAGGGG 1703

Qy   541 AspArgValAlaArgValAlaGluMetProAsnGlnLysGlyGlnLeuGluLeuIleIleAla 560
           ||||||||||||||| |||||||||||||||||||||||||||||||||
Db   1704 GACCGGGTTGCGAGCGAAATGCCCAACCAGCTTCGCCAAGCAATTGGAGGGCGATCATAGCC 1763

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysAspLysLeuGluLeuTrpHisProPheArgTyr 580
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1764 ACTGACCCCACTTAACCCTCCAACAGCAGAGGACAAAGAATTGCCTGGCCATTTTAGATAC 1823

Qy   581 GluSerLeuLysAspProLysProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
           ||||||||||||||||:::||||||||||||||||||||||||||||
Db   1824 GAAAGCCTTAAGGACCCCAAAAGCATATCCTAAGCTATTCAGTGAAATGGGGGACAG 1883

Qy   601 GlnGluValAlaAlaLysThrTyrGlnLeuLeuArgLeuAlaLysArgAlaAspGlnGlnGln 620
           |||||||||||||||||||||||||||||||||||||||||||:::||
Db   1884 CAAGAAATTGTGGCCAAGACATACATCGGGGAGCTTGGCAGAAGTTTCTGGGCATTAATAA 1943

Qy   621 AlaLeuAspValProPheValLeuThrProAspPheGlnAsnPheSerAspAspGluGluAsnVal 640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1944 GCTTTGGTGGATGTTGGGTTAACAATGAGAGCTGCAACTTCTCAGATGAAAATGTA 2003

Qy   641 ArgAlaValValArgGlnGlyTyrLeuThrArgMetGlnLeuAlaValLeuValHisTyrLeu 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2004 AGAGCAGTTGTCAGGCAGGGTTATCTCACAAGAATGCAGCTTGCTGTGGTTGTTCATTACCTT 2063

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluValProTyrHisAspSerAlaLeuAlaArgPhe 680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2064 CTACAATTGGTCCAGGCTGTCAAATTTGAAGTTCCGTATCACGATAGTGCCCTGGCCAGATTT 2123

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
           |||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   2124 CTGCTGAAGCGTGGGTTAAGAAACAAAGAGATTGGTCACTTTTTGTTTTGGTTCTTGAGA 2183

Qy   701 SerGluIleAlaGlnSerArgHisTyrArgLnIleArgPheAlaAlaIleLeuGluAlaTyr 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||

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Db   3264  GAGGAGGATGCTAAAAGTATTTCTTGATCAGATCGAAGTTGCAGAGACAAAGGATGG  3323

Qy   1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis  1100
           ||||||||||||||||||||||||||||||||||||||
Db   3324  ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACACAAGGAGAAACAT  3383

Qy   1101  SerAla  1102
           ||||||
Db   3384  TCAGCC  3389

RESULT 6
ABL59522
ID   ABL59522 standard; cDNA; 5397 BP.
XX
AC   ABL59522;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human phosphatidylinositol-3-kinase gamma cDNA SEQ ID NO:22.
XX
KW   Human; phosphatidylinositol-3-kinase gamma; enzyme;
KW   tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW   chromosome 7q22.1-31.33; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200227028-A1.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US30366.
PR   28-SEP-2000; 2000US-0676052.
XX
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI   Skinner MK, Patton JL, Chaudhary J;
XX
DR   WPI; 2002-402054/43.
XX
PT   Identifying tumor characteristics in a tissue sample taken from a
PT   patient, involves determining the copy number or expression level of
PT   genes associated with lipid metabolism, synthesis or action -
XX
PS   Example 1; Page 80-81; 113pp; English.
XX
CC   The present invention describes a method for identifying tumour
CC   characteristics, comprising measuring a copy number or expression level
CC   of at least two genes associated with lipid metabolism, synthesis, or
CC   action in cells from a patient tissue sample, and comparing the results
CC   with a copy number or expression level of the genes in a normal cell.
CC   Also described is an array of nucleic acid polymers immobilised on a
CC   solid support, comprising a solid support, at least two different nucleic
CC   acid polymers which are each specific for a different gene associated
CC   with lipid metabolism, synthesis or action, where each nucleic acid
CC   polymer is located at a predetermined position on the solid support, and
CC   the array comprises nucleic acid polymers which are specific for less
CC   than 100 genes other than the selected genes. The method is useful for
CC   determining tumour characteristics in a tissue sample taken from a
CC   patient. The present sequence represents a human lipid-associated gene
CC   related cDNA sequence, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 5397 BP; 1534 A; 1224 C; 1207 G; 1432 T; 0 other;

Alignment Scores:
Pred. No.:                              Length:         5397
Score:                    5523.50       Matches:        1049
Percent Similarity:       97.10%        Conservative:     21
Best Local Similarity:    95.19%        Mismatches:       31
Query Match:              95.40%        Indels:            1
                                        Gaps:              1
DB:
```

US-09-974-573-1 (1-5397)

US-09-974-573-1 (1-1102) x ABL59522 (1-5397)

```
Qy     1  MetGluLeuGlnAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg    20
          |||||||||||||||||||||||||||||||||||||||||
Db   324  ATGGAGCTGGAGAACTATAAACAGCCCGGTGGTCGAGAGGACAACTGCCGAAGCGGC   383

Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle    40
          ||||||||||||||||||||||||||||||                ||||||||||||
Db   384  CGGAGGATGAAGCCGCGGCAGT--GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC   440

Qy    41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis    60
          ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db   441  GAGTTCGTGCTCGCTCCCCACCAGCCAGCGCAAATGCAAGACCCCGAAACGGCCTGCTGCAC   500

Qy    61  ValAlaGlyHisHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG   560

Qy    81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
          |||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   561  ACCAGCGTGGGCGGCGGACTTCTACCACCGCCTGGGACCGGACCATCACTTCCTCCTGCTCTAT   620

Qy   101  GlnLysGlyGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621  CAGAAGAGAGGGGGCAGTGGTACCGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC   680

Qy   121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg   140
          |||||||||||||||||||||:::||||||||||||||||||||||:::||||||||||
Db   681  TGCCTGCGCTACTGGAAGGTCCACCGCACCGGGCCAGATCCACCTGGTGCAGCGG   740

Qy   141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaAlaLeuIleGlyTyr   160
          |||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db   741  CACCCGCCCTCCGAGGATCCCAAGCCTTCAGCCGCGCAGCTCACGGCGCTGATTGGCTAT   800

Qy   161  AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   801  GACGTGACTGACGTCAGCAACGTGCACGACGATGAGTCGGAGTTCACGCGCCGTGGCTTG   860

Qy   181  ValThrProArgMetAlaGlyValAlaGlyTyrArgAspProLysLeuTyrAlaMetHisPro   200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861  GTGACCCCGCGCATGGCCGGAGTGGCCGGCTACCGGGACCCCAAGCTCTACGCCATGCACCCG   920

Qy   201  TrpValThrSerLysProGluProLeuProGluTyrLeuLeuLysIleThrArgAsnCysVal   220
          ||||||||||||||||||||||||||||||||||||||||:::
Db   921  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAGAATTCCAACAACTCCATC   980

Qy   221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerValSerAlaAspAspThr   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC   1040

Qy   241  ProGlyThrLeuGlnLeuSerPhePheThrLysMetAlaLysLysLysLysSerLeuMetAsp   260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041  CCCGGCGGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT   1100

Qy   261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr   280
          |||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db  1101  ATTCCCGAAAGCCAAAGCGAACAGGAATTTGTGCTGCGCGTCTGTGGCCGGGATGAGTAC   1160

Qy   281  LeuValGlyGluThrProIleLysGluAsnPheGlnTrpValArgGlnCysLeuLysAsnGly   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161  CTGGTGGGGGAAACGCCCATCAAAGAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA   1220

Qy   301  GluGluIleHisLeuValLeuAspProThrProProAlaLeuAspProLeuValAlaArgLys   320
          ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db  1221  GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCGGGCCTAGCAGACGGGTGAGGAAG   1280

Qy   321  GluGluTrpProLeuValLaAspAspCysThrGlyValThrGlyIleTyrHisGluGlnLeuThr   340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281  GAAGAGTGGCCGGGTGGACGACTGCACGGGAGTCACCGGCTACCACGAGCAGTTACC   1340

Qy   341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341  ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG   1400

Db  3264  ... (continued)
```

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Qy    361 PheArgValLysIleArgGlyTyrIleProIleAspIleProArgThrAlaAspLeuThr 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401 TTCAGGGTTCAAGATCAGAGGATTCAGAGCATTGAATCCCGTCCGCCTCGGAACACCACCA 1460

Qy    381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgThrSer 400
          |||||||||||||||      :::
Db   1461 GTTTTTGTAGAGGCAAACATCCAGTATGGGCAACAAGTCCTTTGCCAAAGGAGAACCAGC 1520

Qy    401 ProLysProPheGlyGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 CCCAAACCCTTCACAGAGAGGAGGTGCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC 1580

Qy    421 LysAspLeuProLysGlyAlaAlaLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 AAAGACTTGCCCAAAGGGGCTGCTCTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1640

Qy    441 LeuSerGlyLysLysThrSerAlaGluMetProSerProGluLysGlyLysGlyAlaGlnLeu 460
          |||||||||||       ||||||||||||||||||       :::||
Db   1641 CTGTCCAGCAAGGCCTTCTGCAGAGTCCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1700

Qy    461 LeuTyrTyrValAsnLeuLeuLeuHisAspHisArgPheLeuLeuArgHisGlyTyrGluTyr 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 CTCTATTATGTGAACCTGCTGCTGCATAGACCACCGTTTCCTCTGCGCCGTGAGAATAC 1760

Qy    481 ValLeuHisMetTrpGlnLeuSerGlyLysValGluAspGlyGlnGlySerPheAsnAlaAsp 500
          ||||||||||||||||||     ::: |||||||||||||||||||||||||||||
Db   1761 GTCCTCCACATGTGGCAGATATCTGGAAGGGAGAAGACCAAGGAAGCTTCAATGCTGAC 1820

Qy    501 LysLeuThrSerAlaAlaThrAsnProAspLysProHisAlaLeuProLysLeuArgProGluLeuLeu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 AAACTCACGTCTGCTGCAACTAACCCAGACAAGGAGAACTCAATGTCCAATCTCCATTCCTG 1880

Qy    521 AspAsnTyrCysHisProIleAlaLeuProLysProHisArgProThrAspProGluGly 540
          |||||||||||||||||      :::|||||||||||||||||||||||||||||
Db   1881 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCCACACAGGCCCACCGACCCGGAGGG 1940

Qy    541 AspArgValAlaArgAlaGluGluMetProAsnGlnLeuArgLysGlnLeuAlaAlaIleIleAla 560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 GACCGGGTTGCGAGGGCAGAATGCCAAACAATTGCGAAAGCAATTGGAGGCGATCATAGCC 2000

Qy    561 ThrAspProLeuAsnProLeuThrAlaGluAspLysAspGlyLeuLeuGluTyrHisProPheArgTyr 580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 ACTGATCCACTTAACCCTCTCACAGCAGAGGACAAAGACGGCCATTTAGAATAC 2060

Qy    581 GluSerLeuLeuAspProLysGlyAlaThrTyrProLysProSerLeuPheSerSerValLysTrpGlyGln 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 GAAAGCCTTCTAGACCCTAAGGCACCAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG 2120

Qy    601 GlnGluValIleAlaLysThrTyrGlnLeuAlaLysPheGluProTyrHisAspSerAlaAlaArgArgPhe 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 CAAGAAAATTGTGGCAAAAACATACCAAGTCTGGGATCAAAGT 2180

Qy    621 AlaLeuAspProValGlyLeuThrMetGlnIleLeuLeuAspCysAsnPheSerAsnGluAspAsnVal 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GCTTTGGATCCTGTGGGTTAACAATGCAGTCTGACTGCAACTTCTCAGATGAAGATAATGTA 2240

Qy    641 ArgAlaIleAlaGluValGlyIleLysSerLeuGluAspSerAspValLeuHisTyrLeu 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 AGAGCCATTGCAGTTGCAGGAAAACTGGAAGACTCTGATGTTCTGCATTACCTT 2300

Qy    661 LeuGlnLeuValGlnAlaLysThrTyrAspSerHisAspSerAlaAlaArgArgPhe 680
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CTACAATTGGTCCAGGCTGAAATTGAACCATATGACTCGGCTGCCCTTGCCCAGATTTT 2360

Qy    681 LeuLeuLysArgGlyLeuArgAsnLysArgIleArgIleGlyHisPheTrpPheLeuArg 700
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361 CTGCTGAAGCGTGGTTTAAGAAACAAAAGAATTGGTCACTTTTGGTTTCTTCGAGA 2420

Qy    701 SerGluIleAlaGlnSerArgHisTyrGlnArgGlnArgAlaAlaValIleLeuGluAlaTyr 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGAGGTTCGCTGTGATTCTGAAGCCTAT 2480
```

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Qy    721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspAsp 740
          ||||||||||||||||||||||||||||||||||||||||||||||  :::
Db   2481 CTGAGGGGCTGTGGCACAGCCATGTTGCACGACTTTACCCAACAGTCCAAGTAATCGAG 2540

Qy    741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerGluAlaGlnLysTyrAspValSer 760
          ||||||||||||||||||||||     :::|||||||||||||||||||||||||
Db   2541 ATGTTACAAAAAGTCACCCTGATATTAAATGTCTTCTCTGAAGCAGAAAGTATGACGTCAGT 2600

Qy    761 SerGlnValIleSerGlnLeuLeuAspLysGluLeuGluGlnLeuAsnLeuGlnAsnLeuAsnLeuAsnLeuPro 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 TCCCAAGTATTTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC 2660

Qy    781 GlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyTyrAlaLeuValIleGluGluLys 800
          :::      |||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAAAGGCTGGCTATGCATTGAAAA 2720

Qy    801 CysLysValMetAlaSerLysLysSerProLeuTrpLeuGluProLysLysCysSerAlaAlaAspPro 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTCCGGATCCT 2780

Qy    821 ThrAlaLeuSerAsnGluThrGlyIleGlyIleIlePheLysHisGlyAspAspLeuArgLeuGln 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTGATGATCTGCGCCAA 2840

Qy    841 AspMetLeuIleLeuGluGlnIleLeuAsnArgIleMetGluSerIleIleThrGluTrpGluSerLeu 860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GACATGTTATTTCAGATTCTACGAATCATGGAGTCTATTGGAACTGAATCTTTG 2900

Qy    861 AspLeuCysLeuLeuProTyrGlyCysIleSerTyrSerThrGlyIleAspLysLysIleGluMetIleGlu 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2901 GATCTATGCCCTCTGCCCTATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2960

Qy    881 IleValLysAspAlaAlaThrThrIleAlaLysIleGlnGlnAsnThrValGlyAsnThrGly 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2961 ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAACACAGTGGGCAACACGGGA 3020

Qy    901 AlaPheLysAspGluValLeuSerHisCysSerProIleGluGluLys 920
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   3021 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAATCCCCTACTGAAGAAAAG 3080

Qy    921 PheGlnAlaAlaValAlaGluArgTyrSerCysValTyrCysValAlaThrPhe 940
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3081 TTTCAGGCAGCAGTGGCAGAGAGATTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT 3140

Qy    941 ValLeuGlyIleGlyValAspArgHisAlaAsnAlaAsnIleMetIleSerGluThrGlyValAsnLeu 960
          ||||||||||||||||||||||||||||||||||||||||||  :::|||||||||||
Db   3141 GTTCTTGGAATAGGCGACAGACACAATGCAAATATTATGATCACCAGGAACAGGAAAACCTA 3200

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3201 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3260

Qy    981 GluArgValProPheValLeuThrProAspPheValMetGlyValThrSerGlyLys 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3261 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCGTGATGGGAGTTACTTCTGGAAAG 3320

Qy   1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3321 AAGACAAGCCCACACTTCCAGAAATTTCAGGACGTCTGTGTTAAGGCTTATCTAGCCCTT 3380

Qy   1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3381 CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC 3440

Qy   1041 GlnLeuThrSerLysGluAspIleLeuTyrIleArgAspAlaLeuThrValGlyLysSer 1060
          |||||||||||||||||||||||||||||||||||||||||||||  :::
Db   3441 CAGTTAACAAGCAAAGAAGACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT 3500

Qy   1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluGlnGlyArgGlyAspLysGlyLysTrp 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3501 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAGCAGGGAAGAGGAGACAAAGGATGG 3560

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGluGlnHis 1100
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Db          3561 ACTGTGCAGTTAATTGGTTCTACATCTGTTCTTGGCATCAAACAAGGAGAGAAACAT 3620
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy          1101 SerAla 1102
                 ||||||
Db          3621 TCAGCC 3626


Score:                5523.50          Matches:        1049
Percent Similarity:   97.10%           Conservative:     21
Best Local Similarity: 95.19%          Mismatches:       31
Query Match:          95.40%           Indels:            1
DB:                                    Gaps:              1

US-09-974-573-1 (1-1102) x AAS14367 (1-5397)

RESULT 7
AAS14367
ID  AAS14367 standard; cDNA; 5397 BP.
AC  AAS14367;
XX
DT  12-MAR-2002 (first entry)
XX
DE  cDNA encoding human p110gamma isoform of PI3-kinase.
XX
KW  Human; phosphatidylinositol 3-kinase; PI3K; p110gamma isoform;
KW  LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW  autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW  Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             324..3629
FT                  /*tag= a
FT                  /product= "p110gamma isoform of PI3-kinase"
XX
PN  WO20185986-A2.
XX
PD  15-NOV-2001.
XX
PF  10-MAY-2001; 2001WO-US15065.
XX
PR  10-MAY-2000; 2000US-203346P.
XX
PA  (ICOS-) ICOS CORP.
XX
PI  Sadhu C;
XX
DR  WPI; 2002-075252/10.
DR  P-PSDB; AAU09689.
XX
PT  Identifying a modulator of p110delta polypeptide binding to SH3
PT  domain-containing polypeptides e.g. LASP-1, comprising allowing the
PT  binding partners to interact in the presence and absence of a test
PT  compound -
XX
PS  Example 1; Page 71-77; 85pp; English.
XX
CC  The present invention relates to identifying a modulator of the
CC  phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC  the catalytic subunit via a SH3 domain-containing polypeptide such as
CC  LASP-1. Also described are methods of assaying the specific binding
CC  affinity of the PI3-kinase binding partner. Such modulators are useful
CC  for the treatment of diseases characterised by the undesirable or
CC  excessive activity of PI3Kdelta. For example the modulators can be used
CC  for inhibiting the growth or proliferation of cancer cells
CC  (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC  Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC  arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC  autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC  bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC  dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC  system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC  and Type I diabetes mellitus. The present sequence encodes for human
CC  p110gamma isoform of PI3k.
XX
SQ  Sequence 5397 BP; 1534 A; 1224 C; 1207 G; 1432 T; 0 other;

Alignment Scores:
Pred. No.:       0                  Length:     5397
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```
Qy     1 MetGluLeuGluAsnTyrGluGlnProValLeuGlnProValLeuArgGluArgArgArgArg 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTCAGAGAGGACAACTGCCGAAGGCGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
           ||||| ||||||||||||||||||       |||||||||||||||||||||||||||
Db   384 CGGAGGGATGAAGCCGCGGCAGT---GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 440

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
           |||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db   441 GAGTTCGTGCTCCCCACCAGCCAGCGAAATGCAAGACGCCCAAACGGCCTGCTGCAC 500

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
           |||||||||||||||:|||:|||||||||||||||||||||||||||||||||||||||
Db   561 ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCGGCATCACTTCCTCTGCTCTAT 620

Qy   101 GlnLysGlyGlnTrpTyrGlnIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 CAGAAGAAGGGGCAGTGGTACCAAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 680

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
           |||||||||||||||||||||||||||||||||||||||||||||||:|::|||
Db   681 TGCCTGCGCTACTGGAAGGTGCTGCACCGCAGCCCCGGGCAGATCCACGTGGTGCAGCGG 740

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuLeuGlyTyr 160
           ||||:|||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db   741 CACCCGCCCTCCGAGGAGACCCTCGCCTTCCAGCGCCAGCTCAACGCGCTGCTGGGCTAT 800

Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu 180
           |||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   801 GACGTCACTGACGTCAGCAACGTGCACGACGACGAGGACGATGAGTTCACGCGCCGTGGCTTG 860

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLeuTyrArgAlaMetHisPro 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861 GTGACCCCGCGCATGGCGGAGGTGGCAGCCGGCCGAGACCCATTAAGGTCTCACCGATGCACCCG 920

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   921 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC 980

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACCACACC 1040

Qy   241 ProGlyThrLeuGlnSerProPhePheThrLysSerMetAlaLysLysLysSerLeuMetAsp 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041 CCCGGGACCCTCCTGCAGAGCTTCTTCACCAAGAGTATGGCCAAGAAGAAGAAATCCTCGATGGAT 1100

Qy   261 IleProSerGlnAsnGluLeuArgAspPheValLeuArgValCysGlyValGlyAspGluTyr 280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1101 ATTCCCAGCCAAAGCCAAAGCAACAGGATTTTGTGCTGCGCGTCTGTGGCGGATGAGTAC 1160

Qy   281 LeuValGlyLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161 CTGGTGGGGCGAAACGCCATCAAAACTTCCAGTGGTGGCACTGCCTCAAGAACGGGA 1220

Qy   301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluValArgLys 320
           ||||||||||:|||:|||||||||||||||||||||||||||||||||||||||
Db  1221 GAAGAGATTCACGTGGTACTGGACACAGCCTCCAGCACCGGCCCTAGACAGGAGGTGGAAGAAG 1280

Qy   321 GluGluTrpProLeuValAspAspAspCysThrGlyValThrGlyValTyrHisGlyValThrLeuThr 340
```

Right column group (positions 2361–3500 / residues 701–1060):

```
Db      CTGCTGAAGCGTGGTTAAGAACAAAAGAATTGTCACTTTTGTTTGGTTCTTGAGA   2420
         |||||||||||
Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnArgThrProAspCysAspArgLys    720
Db 2421 AGTCGAGATAGCCCAGTCGAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAGCCTAT  2480

Qy  721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValValIleAsp        740
         ||:|||||:|||
Db 2481 CTGAGGGGCTGTGGCACAGCTATGCTGCACGACTTTACCCAACAAGTACCAAGTAATCGAG  2540

Qy  741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer   760
         |||  :|||  |||
Db 2541 ATGTTACAAAAAGTCACCCTGATATAAATCGTCCTGCTGAAAAGTATGACGTCAGT      2600

Qy  761 SerGlnValIleSerGlnLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro   780
         |||||||
Db 2601 TCCCAAGTTATTTCACAACTTAAACAAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTTCCCC  2660

Qy  781 GlnSerPheAlaSerValProTyrAspProGlyLeuLysAlaGlyValAlaLeuValLeuGluLys  800
         :::||
Db 2661 GAAAGCTTTAGAGTTCCATATGATCCTGGACTTAAAGCAGGAGCGCGTGGCAATTGAAAAA  2720

Qy  801 CysLysValMetAlaSerLysValLysLysProLeuTrpLeuGluPheLysGluCysAlaAspPro   820
         ||||
Db 2721 TGTAAAGTAATGGCCTCCAAGAAAAAACACTATGGTTTAAATGTCCGATCCT          2780

Qy  821 ThrAlaLeuSerAsnGluThrIleLeuTyrIleIleIlePheHisGlyAspLeuArgGln      840
         |||||:||:|||
Db 2781 ACAGCCCTATCAAATGAACAATTGGAATTATCTTTAAACATGGTGATCTGCGCCAA     2840

Qy  841 AspMetLeuIleLeuGlnIleLeuAsnArgIleMetGluSerIleTrpGluValSerLeu     860
         ||||
Db 2841 GACATGCTTATTTTACAGATCTTACGAGTCTATTTGGGAGACTGAATCTTTG          2900

Qy  861 AspLeuCysLeuLeuProTyrTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu    880
         ||||
Db 2901 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAATAGGAATGATCGAG   2960

Qy  881 IleValLysAspAlaThrThrIleLeuAlaLeuIleGlnGlnSerThrValGlyAsnThrGly    900
         ||||
Db 2961 ATTGTGAAAGACGCCACGACAATTGCCAAATTCAGCAAGACCAGTGGGCAACACGGGA   3020

Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuLysCysAlaGlyGluLys           920
         |||:
Db 3021 GCATTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAATCCCCTACTGAAGAAAAAG  3080

Qy  921 PheGlnIleAlaValAlaArgPheValTyrSerCysAlaGlyTyrCysValValAlaThrPhe   940
         ||||
Db 3081 TTTCAGGCAGCAGTGGCAAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT  3140

Qy  941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu     960
         |::|||
Db 3141 GTTCTTGGAATAGGGGACAGGCACAATGACAATATAATGATCACCGAGACAGGAAACCTA   3200

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys     980
         |||:
Db 3201 TTTCATATTGACTTCGGGCACATTCTGGGAATTACAAAAGTTCCTGGGCATTAATAAA   3260

Qy  981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLys  1000
         ||||
Db 3261 GAGAGAGTCCCATTTGTCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGCAAGAAG  3320

Qy 1001 LysThrSerLeuHisPheGlnLysProGlnAspValCysValLysValLeuAlaLeu      1020
         ||||
Db 3321 AAGACAAGCCCACACTTCCAGAAATTTCAGGACATCTGTGTTAAGGTCTTAGCCCTT     3380

Qy 1021 ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuThrGlyMetPro      1040
         |::||||||
Db 3381 CGTCATCATACCAACCTACTGATCATCCTGTTCTCCATGATGCTGACAGGAATGCCC    3440

Qy 1041 GlnLeuThrSerLysGluAspIleGluTyrIleLeuArgAspAlaLeuThrValGlyLysSer  1060
         ||:::|||
Db 3441 CAGTTAACAAGCAAAGAAGATATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT  3500
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Left column group (positions 1281–2360 / residues 341–720):

```
Db      GAAGAGTGGCCGCTGTTGGACGACTGCACGGAGTCACCGGCTACCATGAGCAGCTTACC   1340
         |||||||||||
Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
Db 1341 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG  1400

Qy  361 PheArgValLysIleArgGlyTyrIleAspIleProValLeuProArgThrAlaAspLeuThr  380
         ||||
Db 1401 TTTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTTCCTGCCTCGGAACACCGACCTCACA  1460

Qy  381 ValPheValGluAlaAsnIleGlyTyrGlyGlnValLeuCysGlnLysValGlnArgThrSer  400
         ||||
Db 1461 GTTTTTGTAGAGGCAAACATCAGACAAGTCCTTTGCCAAAGGAGAACCAGC          1520

Qy  401 ProLysProPheThrGluGluValValLeuTrpAsnValTrpLeuGluPheSerIleLysIle  420
         ||||
Db 1521 CCCAAACCCTTCACAGAGGAGGTGTGTCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC  1580

Qy  421 LysAspLeuProLysGlyLysAlaLeuLeuAsnLeuIleTyrCysGlyLysAlaProAla    440
         ||||
Db 1581 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCATCTACTGCGGTAAAGCTCCAGCA       1640

Qy  441 LeuSerGlyLysThrSerAlaGluMetProSerProGlnSerProLysGlyLysAlaGlnAsnLeu  460
         ||:::|||
Db 1641 CTGTCCAGCAAGGCCTCTGCAGAGTCCCAGTCTCGAGTCCAAGGGCAAAGTTCGGGTT       1700

Qy  461 LeuTyrTyrTyrValAsnLeuLeuIleAspHisArgPheLeuArgHisGlyHisGlyGluTyr   480
         ||||
Db 1701 CTCTATTATGTGAACCTGCTGTGAATAGAACCACCCGTTCCTCCCGCCGTGGAGAAATAC   1760

Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysValGlyGlyAspGlnGlySerPheAsnAlaAsp   500
         |:::|||
Db 1761 GTCCTCCACATGTGGCAGATATCTGGAGATATTGGGGACCAAGGATCTTCAATGCTGAC     1820

Qy  501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleLeuLeuLeu       520
         ||||
Db 1821 AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTCAATGTCCATCCCATTCTCTG     1880

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgThrProAspProGluGly      540
         ||||
Db 1881 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGACCCCTGACCCCGAGGGG       1940

Qy  541 AspArgValArgAlaGlnMetProAsnGlnLeuArgLysGlnLeuGluAlaIleIleAla     560
         ||||
Db 1941 GACCGGGTTCGAGCACAGAAAACGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC  2000

Qy  561 ThrAspProLeuAsnProLeuThrAlaGluLysLysGluLeuTrpHisIlePheArgTyr     580
         ||||
Db 2001 ACTGATCCACTTAACCCTCTCACAGCAGAGAAGAAGGAGCTGTGGCATATCTTCAGATAC    2060

Qy  581 GluSerLeuValGlyProLysProLysLysPheSerSerValLysTrpGlyGln         600
         ||||
Db 2061 GAAAGCCTTAAGGACACCCAAAAGATCATCTCAAGCGTAAAATGGGGACAG            2120

Qy  601 GlnGluLeuValAlaLysThrTyrGlnLeuLeuLysAlaArgGluValTrpAspGlnSer    620
         ||:::|||
Db 2121 CAAGAAATTGTGGCCAAAAACATACCAATTGTTGCCGCATAGAGGGAGTCTGGGATCAAAGT   2180

Qy  621 AlaLeuAspValGlyValLeuMetGlnLysLeuAspAspCysAsnPheSerGluAsnVal    640
         ||||
Db 2181 GCTTTGGATGTTGGGGTTAACAATGCAGCTCCTGACTTCTCAGATGAAAAATGTA        2240

Qy  641 ArgAlaIleAlaValGlnLysLysValGlnLysAspLeuSerLeuGluSerLeuValLeuHisTyrLeu 660
         ||||
Db 2241 AGAGCCATTGCAGTTCAGTTCCAGAAAACTTGGAGACGAAGTTCTGCATTACCTT        2300

Qy  661 LeuGlnLeuValGlnAlaValLysPheSerGluProTyrHisAspSerAlaLeuAlaArgPhe  680
         ||||
Db 2301 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCGCCCTTGCCAGATTT    2360

Qy  681 LeuLeuLysArgGlyLeuArgAsnLysTyrArgIleGlyHisPheLeuTrpPheLeuArg    700
         ||||
```

```
Qy   1061  GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3501  GAGGAGGATGCTAAAAAGTATTTCTTGATCAGATCGAAGTTTGCAGACAAAGGATGG  3560

Qy   1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuGlnGlnLysHis  1100
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   3561  ACTGTGCAGTTTAATTGGTTCACATCTTGTTCTTGGCATCAAACAAGGAGGAGAAACAT  3620

Qy   1101  SerAla  1102
           ||||||
Db   3621  TCAGCC  3626
```

RESULT 8
AAT58546
ID   AAT58546 standard; cDNA; 4137 BP.
XX
AC   AAT58546;
XX
DT   25-MAR-1997 (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   423..3575
FT   /*tag= a
FT   /product= PI3K-gamma
XX
PN   DE4445562-C1.
XX
PD   04-APR-1996.
XX
PF   20-DEC-1994; 94DE-4445562.
XX
PR   13-OCT-1994; 94DE-4436696.
XX
PA   (PLAC) MAX PLANCK GES FOERDERUNG WISSENCHAFTEN.
XX
PI   Hanck T, Stoyanov B, Wetzker R;
XX
DR   WPI; 1996-172545/18.
DR   P-PSDB; AAW11577.
XX
PT   New phosphatidyl;inositol 3-kinase protein - useful as immunogen and
PT   for determn. of kinase activity
XX
PS   Claim 5; Page -; 10pp; German.
XX
CC   A 402 bp cDNA fragment was amplified from a human bone marrow
CC   library using PCR primers corresponding to amino acid sequences
CC   KNGDDLR and HIDFG. The amplified fragment was used to probe a human
CC   U937 cell cDNA library and several overlapping clones were isolated.
CC   The largest clone coded for a protein of 1049 residues. The protein
CC   is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its
CC   regulatory mechanism from the known PI3K-alpha and -beta enzymes.
CC   The new enzyme has been designated PI3K-gamma. Another clone, coding
CC   for a PI3K-gamma of 1050 residues and having the present
CC   sequence, was then isolated. The enzyme can be used as an immunogen.
CC   The enzyme, antibodies against it or nucleic acid encoding it can be
CC   used for modulating cell proliferation, receptor-mediated signal
CC   transmission, histamine secretion, nerve cell differentiation,
CC   glucose transport and anti-lipolytic activity or for treating
CC   Alzheimer's disease.
CC   N.B. Although the claimed sequences are referred to by SEQ.ID.
CC   Numbers, a sequence listing did not appear in the original printed
CC   patent application.

```
XX
SQ   Sequence 4137 BP; 1127 A; 999 C; 1001 G; 1010 T; 0 other;

Alignment Scores:
Pred. No.:                         Length:        4137
Score:                   0         Matches:       1048
Percent Similarity:   5499.50      Conservative:    21
Best Local Similarity: 96.92%      Mismatches:      32
Query Match:          95.01%       Indels:           2
DB:                   94.98%       Gaps:             1
                         17

US-09-974-573-1 (1-1102) x AAT58546 (1-4137)

Qy    1  MetGluLeuGluAsnTyrGluGlnProValValGlnArgGluAspAsnArgArgArgArg  20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCAGAGAGGAGAAGACAACTGCGAAGGCGC  383

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuLeuProIle  40
         |||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Db   384  CGGAGGATGAAGCCCGGCAGT--GCTGCCAGCTGTCTTCCATGGAGCTACTCCCCATC  440

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
         ||||||||||||||||||||||||||    :::||||||||||||||||||||||||||
Db   441  GAGTTCGTGCTGCCCACCAGCCAGGCAAATGCAAGAGCCCGAAACGGCGCTGCTGCAC  500

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnTrpLeuArgAlaLeuGlu  80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGTGGCTGCGCGCTGGAG  560

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561  ACCAGCGTGGGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  620

Qy  101  GlnLysLysGlyGlnTrpTyrTyrGluIleTyrAspArgLeuGlyValValGlnThrLeuAsp  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621  CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAGGTTGGGTGTGGTGCAGACTCTGGAC  680

Qy  121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   681  TGCCTGCGCTACTGGAAGGTCCACCGCAGCCCGGGCCAGATCCACGTGGTGCAGCGG  740

Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnLysArgGlnLeuAsnAlaLeuIleGlyTyr  160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   741  CACCCGGCCCTCCGAGAGTCCCAAGCTTCACGGCAGCTCAACGCACTCATTGGCTAT  800

Qy  161  AspValThrAspValSerAsnValHisAspAspGluPheThrArgArgLeu  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   801  GACGTCACTGACGTCAGCAACGTGCACGACGAGTTCACGCGCGGCTTG  860

Qy  181  ValThrProArgMetAlaGluValAlaGlyArgAspProLeuTyrAlaMetHisPro  200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   861  GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGGGACCCGCTCTACGCCATGCACCCG  920

Qy  201  TrpValThrSerLysProLeuProGluProGlyTyrLeuLeuLysIleThrAsnAsnCysVal  220
         ||||||||||||||||||||||||||||||||||||||||||||||   :::
Db   921  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGCTGAAGAGAATTGCCAACAACTGCATC  980

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981  TTCATCGTCATTCACCGGAGCACCACCAGCCAGACCATTAAGGTCTCACCGACCACACC  1040

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp  260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041  CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGAT  1100

Qy  261  IleProGluSerGlnAsnGluAlaArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
         :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1101  ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGGTCGTGGCGGGGATGAGTAC  1160

Qy  281  LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161  CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA  1220
```

Qy   301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspProAlaLeuAspGluValArgLys 320
           |||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCCTTGAGACCAGGTGAGGAAG 1280

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
           ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db   1281 GAAGAGTGGCCGCTGGTTAAGACGACGTGGACGGGAGTCACCGGCTACCACGAGCAGCTTACC 1340

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspAspCysAspArgLys 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG 1400

Qy   361 PheArgValLysIleArgGlyIleAspIlePheProValLeuProArgThrArgAlaAspLeuThr 380
           |||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db   1401 TTCAGGGTCAAGATCAGAGGCATTGATATCCCGTCCTCCTGCCTCCGGAAACCACCGACCTCACA 1460

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyValLeuCysGlnArgArgThrSer 400
           |||||:::|||||||||||||||||||||||||||||||||||||||||||
Db   1461 GTTTTTGTAGAGGCAAACATCCAGACAGGGCAAACACTCCTTTGCCAAAGGAGACCAGC 1520

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 CCCAAGCCTTTCACAGAGGAGGTGCTGTGGAATGTGTGGCTTGAATTCAGTATCAAAATC 1580

Qy   421 LysAspLeuProLysGlyValAlaLeuLeuAsnLeuGlnIleLeuTyrCysGlyLysAlaProAla 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 AAAGACTTGCCCAAAGGGGTCGCTCTACTGAACCTCCAGATACTGCGTAAAGCTCCAGCA 1640

Qy   441 LeuSerGlyLysLysThrSerAlaGluMetProSerProGluSerLysLysGlyLysAlaGlnLeu 460
           ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db   1641 CTGTCCAGCAAGGCCTCTGCAGAGTCCCCAGTTCCAGAGTCAAGGGCAAAGTTCGGCTT 1700

Qy   461 LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 CTCTATTATGTGAACCTGCTGATAGACCGTTTCCTCCGCCGTGGAGAATAC 1760

Qy   481 ValLeuHisMetTrpGlnIleuSerGlyLysGlyGlnGlySerPheAlaAsnAlaAsp 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 GTCCTCCACATGTGGCAGATATCTGGAAGGGAGCAGGGAAGCTTCAATGCTAAC 1820

Qy   501 LysLeuThrSerArgAlaThrAsnProAspLysGluAsnSerMetSerIleLeuSerLeuLeuLeu 520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 AAACTCACGTCTCGAACTACCAACCCAGACAAGGAGAACTCCATGTCCATTCTCTG 1880

Qy   521 AspAsnTyrCysHisSerProIleAlaLeuProLysHisArgProThrProAspGluGly 540
           ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881 GACAATTACTGCCACTCCCCGATAGCCCTGCCTAAGCATCAGCCCACCCCCGACGAGGG 1940

Qy   541 AspArgValAlaArgGluMetProAsnProLysLeuArgLysGlnLeuGluAlaIleIleAla 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 GACCGGGTTGCTAGAGAAATGCCCAACCCTAAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 2000

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysLysGlnLeuLeuLeuTrpHisProPheArgTyr 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 ACTGATCCACTTAACCCTCTCACAGCAGAGGACAAAGAAGAATTGCTCTGGCATTTTAGGATAC 2060

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysLysTrpGlyGln 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 GAAAGCCTTAAGGACCCAAAAGCATATCCAAAGCTATTCAGTAGTGTCAAGAAATGGGGACAG 2120

Qy   601 GlnGluIleValAlaLeuValAlaLysThrTyrGlnLeuLysLysAlaLysGluValTrpAspGlnSer 620
           ||||||:::|||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121 CAAGAAATTGTGGCCAAAACATACCAAATTGTTGCCAAGAAGGCAAAGGAAGTCTGGGATCAAAGT 2180

Qy   621 AlaLeuAspAspValGlyLeuThrMetGlnLeuThrMetProSerAspCysAsnPheSerAspGluAsnVal 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GCTTTGGATGTTGGGTTAACAATGCAACTGACACTGCCAACCCTGACTTCCTCTTCTGGAGATGAAAATGTA 2240

Qy   641 ArgAlaIleAlaValGlnLeuLysLysLeuGluSerLeuGluAspLysAspAspValLeuHisTyrLeu 660
           ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db   2241 AGAGCAATTGCAGTTCAGTTGAAAAAACTGGAGAGTCTTGAGGACAAGGATGATGTTCTGCATTACCTT 2300

Qy   661 LeuGlnLeuValGlnAlaValLysGlnGluAlaValGlnHisAspTyrHisAspGluGlyArgSerAlaLeuAlaArgPhe 680

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Db  3381 CGTCATCACACAAACCTACTGATCATCCTGTTCCATGATGCTGATGACAGGAATGCCC 3440

Qy  1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db  3441 CAGTTAACAAGCAAGAGACAATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT 3500

Qy  1061 GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCys-ArgAspLysGlyTyr 1080
         ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  3501 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGGCAGAGACAAAGGATG 3560

Qy  1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHi 1100
         ||||||||||||||||||||||||||||||||||||||||||||
Db  3561 GACTGTGCAGTTAATTGGTTTCTTCACATCTTGTTCTTGGCATCAAACAAGGAGAGAAACA 3620

Qy  1100 sSerAla 1102
         |||||||
Db  3621 TTCAGCC 3627
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RESULT 9
AAT58545
ID   AAT58545 standard; cDNA; 4134 BP.
XX
AC   AAT58545;
XX
DT   25-MAR-1997 (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis; ds.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   CDS            423..3572
FT                  /*tag= a
FT                  /product= PI3K-gamma
XX
PN   DE4445562-C1.
XX
PD   04-APR-1996.
XX
PF   20-DEC-1994; 94DE-4445562.
XX
PR   13-OCT-1994; 94DE-4436696.
XX
PA   (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Hanck T, Stoyanov B, Wetzker R;
XX
DR   WPI; 1996-172545/18.
DR   P-PSDB; AAW11576.
XX
PT   New phosphatidylinositol 3-kinase protein - useful as immunogen and
PT   for determn. of kinase activity
XX
PS   Claim 5; Page -; 10pp; German.
XX
CC   A 402 bp cDNA fragment was amplified from a human bone marrow
CC   library using PCR primers corresponding to amino acid sequences
CC   KNGDDLR and HIDFG. The amplified fragment was used to probe a human
CC   U937 cell cDNA library and several overlapping clones were isolated.
CC   The largest clone had the present sequence and coded for a protein
CC   of 1049 residues. The protein is a novel phosphatidylinositol 3-
CC   kinase (PI3K) that differs in its regulatory mechanism from the
CC   known PI3K-alpha and -beta enzymes. The new enzyme has been
CC   designated PI3K-gamma and can be used as an immunogen. The enzyme,
CC   antibodies against it or nucleic acid encoding it can be used for
CC   modulating cell proliferation, receptor-mediated signal transmission,
CC   histamine secretion, nerve cell differentiation, glucose transport
CC   and anti-lipolytic activity or for treating Alzheimer's disease.
```

```
CC   N.B. Although the claimed sequences are referred to by SEQ.ID.
CC   Numbers, a sequence listing did not appear in the original printed
CC   patent application.
XX
SQ   Sequence 4134 BP; 1127 A; 999 C; 998 G; 1010 T; 0 other;
```

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Alignment Scores:
Pred. No.:                        0          Length:           4134
Score:                       5440.00         Matches:          1046
Percent Similarity:          96.65%          Conservative:       20
Best Local Similarity:       94.83%          Mismatches:         35
Query Match:                 93.96%          Indels:              4
DB:                              17          Gaps:                1
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```
US-09-974-573-1 (1-1102) x AAT58545 (1-4134)

Qy     1 MetGluLeuGluAsnTyrGluGlnProValValArgGluAspAsnArgArgArgArg 20
         ||||||||||||||||||||||||||||||||||: :||||||||||||||||||||
Db   324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
         |||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   384 CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCTCCATGGAGCTCATCCCCATC 440

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
         ||||||||||||||||||||||||||||| ::|||||||||||||||||||||||||
Db   441 GAGTTCGTGCTGCCCACCAGCCAGCGCAATGCAAAGACCCCGAAACGGGCCTGCTGCAC 500

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysLysAlaLysGlnValTrpLeuArgAlaLeuGlu 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ACCAGCT--GGCGCGAGCTTCTACCACCGGCTGGGACCCGATCACTTCCTGCTGCTCTAT 618

Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysThrTyrGlnValValGlnThrLeuAsp 120
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   619 CAGAAGAA-GGGCAGTGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 677

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   678 TGCCTGCGCTACTGGAAGGCGGAGCACCGGAGCCCGGGCCAGATCCACGTGGTGCAGCCG 737

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaLeuIleLeuTyr 160
         ||||||||||||||| ::|||||||||||||||||||||||||||||||||||||||||
Db   738 CACCCGCCCTCCGAGGAGACGCTGGCACAGTGCCAAGCCTTCCAGCTGCGCCAGCTGTAT 797

Qy   161 AspValThrAspValSerAsnValHisAspAspGluGluThrArgArgLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGGAGACTCGACGCCCGTGGCTTG 857

Qy   181 ValThrProArgMetAlaGluValAlaGluValAlaGlyArgAspProLeuTyrAlaMetHisPro 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   858 GTGACCCCGCGCATGGCGGAGGTGGCCGAGGTGGCCGGCCGCGACCCCCTCTACGCCATGCACCCG 917

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLysLysIleThrAsnAsnCysVal 220
         |||||||||||||||||||||||||||||||||||||||||::::||||||||||
Db   918 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGAAGAAGATTGCCAACAACTGCGTC 977

Qy   221 PheIleValIleHisArgThrThrSerGlnThrThrIleLeuValSerValSerAlaAspThr 240
         :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   978 TTCATCGTCATTCACCGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1037

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1038 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAATCTCTGATGGAT 1097

Qy   261 IleProGluGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
         |||||||||||||||||||||||||||:::::||||||||||||||||||||||||
Db  1098 ATTCCCGAAGCCAAAGCCAAAGGCGACCAGGATTTTGTGCTGCGCGTGTGCGGGATGAGTAC 1157

Qy   281 LeuValGlyGluThrProIleLeuAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
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Qy   661 LeuGlnLeuValGlnAlaValPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
             |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db  2238 AGAGCCATTGCAGTTCAGAAACTTGGAGAGCTTGGAGACGATGAGGTTCTGCATTACCTT 2297
         ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1158 CTGGTGGGCCAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCACTGCCTCAAGAACGGA 1217

Db  2298 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCGCCCTTGCCAGATTT 2357
Qy   301 GluGluIleHisGluValAlaLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
Qy  1218 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCCTAGACGAGGTGAGGAAG 1277

Db   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheTrpPheLeuArg 700
Db  2358 CTGCTGAAGCGTGGTTTAAGAAACAAAAGAATTGGTCACTTTTGGTTTCTTGAGA 2417
Qy   321 GluGluTrpProLeuValAspAspAspCysThrGlyValThrGlyValHisGlnLeuThr 340
Qy  1278 GAAGAGTGGCCGCTGGTGGACGACGATTGCACCGGAGTCACCGGAGTCCACCAGCTTACC 1337

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaTyr 720
Db  2418 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAAGCCTAT 2477
Qy   341 IleHisIleGlyLysValLysAspHisGlyGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
Qy  1338 ATCCACGGCAAGGACACCAGGAGAGTGTTTCACCGTGTCCCTGTGGGACTGGCACCGGCAAG 1397

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspThrGlnValIleLeuValIleAsp 740
Db  2478 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACACTTTACCCACCAAGTCCAACTAATCGAG 2537
Qy   361 PheArgValLysIleLeuAspIleLeuProValLeuProArgThrAlaAspLeuThr 380
Qy  1398 TTCAGGGTCAAGATCAGAGATCTGCCTGTCCTGCCTCGGAACACCGACCTCACA 1457

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerGluAlaGluLysTyrAspValSer 760
Db  2538 ATGTTACAAAAAGTCACCCTGTGATATTAAATCGCTTCTCTGCTGAAAGTATGACGTCAGT 2597
Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyValAlaLeuCysGlnArgArgThrSer 400
Qy  1458 GTTTTTGTAGAGGCAAACATCCACAGTACGGGTGCAAAGATGTGTGGTTCAAGGAGAACCAGC 1517

Qy   761 SerGlnValIleSerGlnLeuLysGlnLeuGlnLysLeuGlnAsnLeuAsnLeuAsnLeuPro 780
Db  2598 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGAAAATCTCAACTCCCC 2657
Qy   401 ProLysProPheThrGluValLeuTrpAsnValTrpLeuGlnnIleTyrCysGlyLysLysAlaProAlaLys 420
Qy  1518 CCCAAAACCCTTCACGAGACGGAGGTGCTGTGGAATGTGTGGCTTCAGTATCAAAATC 1577

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysLeuProLeuTrpPheLeuGlyAspAspPro 800
Db  2658 GAAAAGCTTTTCAGGGTTCCATATGATCCTGGACTTAAAGCTGCCTTTGGTAAATGTGCCGGATCCT 2717
Qy   421 LysAspLeuProLysValThrSerGlyLyyAlaLeuLeuAsnLeuAsnIleTyrCysGlyLysAlaProAla 440
Qy  1578 AAAGACTTGCCCAAGGGGCTCTGCAGATCCAGATCTACTCGCGTAAAGTCCCAGCA 1637

Qy   801 CysLysValMetAlaSerLysLysLysProGluLeuTrpPheLysHisGlyAspAspPro 820
Db  2718 TGTAAAGTAATGGCCTCCAAGAAAAACCTATGGTTTAAAATGTCCGGATCCT 2777
Qy   441 LeuSerGlyLysProLysMetProSerProGluSerArgLysGlyGlnGlyLysLysAlaGlnLeu 460
Qy  1638 CTGTCCAGCAAGCCGCTTCTGCAGAATGCCCAGTTCTGAGTCCAAGGGCAAGGTTCGGGCTT 1697

Qy   821 ThrAlaLeuSerArgAsnGluThrArgIleGlyIleIleLeuArgIleMetGluSerIleLeuArgIleLeuSerLeu 840
Db  2778 ACAGCCCTATCAAATGAACAATTGAAATTATCTTTAAACATGGTGATGATGATCTGCGCCAA 2837
Qy   461 LeuTyrTyrValAlaAsnLeuLeuLeuLeuGluIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
Qy  1698 CTCTATTATGTGAACCTGCTGCTGCTGGAAATAGACCGTTCCTCCTCCGCGCGTGGAGAATAC 1757

Qy   841 AspMetMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleLeuArgIleLeuSerLeu 860
Db  2838 GACATGTCTTATTTACAGATTCTACAGATCATGGAGTCTATTTGGGAGACTGAATCTTTG 2897
Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyLysGluAspGlyLysGlySerPheAsnAlaAsp 500
Qy  1758 GTCCTCCACATGTGGCAGATATCTGGAGAGGGGAGAAGACCAAGGAAGCTTCAATGCTGAC 1817

Qy   861 AspLeuCysLeuProTyrGlyCysValIleSerGlyThrGlyAspLysProLysIleGlyLysMetIleGluGlu 880
Db  2898 GATCTATGCCCTCCTGCCATATGGTTGCATTATCAACGGTGCAAAATAGGAATGATCGAG 2957
Qy   501 LysLeuThrSerArgAlaThrAsnProAspLysProLysLeuPheSerSerValLysSerTrpGlyGln 520
Qy  1818 AAACTCACGTCTCGAACTAACCCAGACAAGGAGAACTCAATGTCCCATTCTCATTCTCTG 1877

Qy   881 IleLeuValLysAspAlaAspAlaThrThrIleArgIleLeuAlaLysLysIleGlnIleSerGluThrValGlyLysAsnThrGly 900
Db  2958 ATTGTGAAAGACGCCACGACAATTCAGCAGAAGTCAACACGGGCAACACGGGA 3017
Qy   521 AspAsnTyrCysLysHisProIleAlaLeuProLysProThrProAspProGluGly 540
Qy  1878 GACAATTACTGCAAACATCCAGCCCTGCCTAAGCCAACCCCCGACCCGGAAGGG 1937

Qy   901 AlaPheLysAspArgAspAlaValLeuSerHisTrpProLeuLeuLysGlyLysProProLeuGlyGluLysLysLys 920
Db  3018 GCATTTAAAGATGAAGATGCTGTGCTATCACTGGCTCAAATCCCCACTACTGAAGAAAAAG 3077
Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuLysArgLysGlnLeuGluAlaIleIleAlaAla 560
Qy  1938 GACCGGGTTCGAGCAGAAATGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 1997

Qy   921 PheGlnAlaAlaValGluGlyLyTyrCysValAlaGlyThrPhe 940
Db  3078 TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGTACGGCTCGTTGGCAACCTTT 3137
Qy   561 ThrAspProLeuAsnProLeuThrAlaLeuAspProLysLeuLeuLeuLeuTrpPheHisArgTyr 580
Qy  1998 ACTGATCCACTTAACCCTCTTACAGCACAGGACAAAGAATTGCTCCTGTGGTTTCATAGAGATAC 2057

Qy   941 ValLeuValIleGlyValAspArgHisIleAsnAspAsnIleMetIleSerGluThrGlyGlnLeu 960
Db  3138 GTTCTTGGAAATAGGGCACAGGACAATATTATGATACCAGAGACCAGGAAACCTA 3197
Qy   581 GluSerLeuLysAspProLysAlaLysLysTyrProLysLysPheSerSerValLysSerValLysSerTrpGlyGln 600
Qy  2058 GAAAGCCTTAAGGACCCAAAAGCATCCAAAAGCATATTAGCTAATTATTAGTCATTTGAAAAATGGGGCAGAG 2117

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGluGlyIleAsnLys 980
Db  3198 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTCCTGGGCATTAATAAA 3257
Qy   601 GlnGluIleGluValAlaLysThrTyrGlnGlnLeuValLeuAlaLeuAlaArgGlyLyValTrpAspGlnSer 620
Qy  2118 CAAGAAATTGTGGCCAAAAACATACCAATTGTTGGCACGAAGGGAAGTCTGGGATCAAAGT 2177

Qy   981 GluAlaArgValProPheLeuAspSerProPheLeuValMetGlyTyrSerGlyLyLys 1000
Db  3258 GAGGAGAGTGCCATTTGTCGAACCCCTGACTTCCCTTTGTGATGGGAACTTCTGGAAAG 3317
Qy   621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuLeuAspCysLysAsnPheSerAspSerAsnVal 640
Qy  2178 GCTTTGGATGTTGGTTTAACAATGCAGCTCTGACTTCTCAGATGAAAAATGTA 2237

Qy  1001 LysThrSerLeuHisPheGlnLysAspGlnLysAspAspAspLysLysTyrLeuValAlaLeu 1020
Db  3318 AAGACAAGCCCACACTTCCAGAAATTTCAGGACATCTGTGTTAAGGCTTATCTCAGCCCCTT 3377
Qy   641 ArgAlaIleAlaValGlnLysLysGlnLeuSerLeuGlnGluLeuLeuGlnLysAspAspAlaAspValHisTyrLeu 660
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Qy   1021 ArgHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3378 CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC 3437

Qy   1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
          |||||||||||||||||||||||||||||||||||||||||||||||||||| :::  :::
Db   3438 CAGTTAACAAGCAAAGAGACAATTGAATATATCCGGAGATGCCCTCACAGTGGGGAAAAAT 3497

Qy   1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCys-ArgAspLysGlyTyr 1080
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   3498 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGGCAGAGACAAAAGGATG 3557

Qy   1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyLysGlyLysHi 1100
          |||||||||||||||||||||||||||||||||||||||||||||||||:::::::::::::
Db   3558 GACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAGGAGGAGAAACA 3617

Qy   1100 sSerAla 1102
          |||||||
Db   3618 TTCAGCC 3624


RESULT 10
AAQ57012
ID   AAQ57012 standard; cDNA to mRNA; 3498 BP.
XX
AC   AAQ57012;
XX
DT   25-MAR-2003  (updated)
DT   31-AUG-1994  (first entry)
XX
DE   PtdIns 3-kinase 110 kD catalytic subnit cDNA.
XX
KW   110 kD catalytic subunit; phosphatidyl inositol 3-kinase;
KW   transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;
KW   PtdIns 3-kinase; assay; detection; cell growth; regulation; cancer;
KW   blood vessel plaques; ss.
XX
OS   Bos taurus.
XX
FH   Key         Location/Qualifiers
FT   CDS         1..3207
FT               /*tag= a
FT               /product= P110
XX
PN   WO9403609-A1.
XX
PD   17-FEB-1994.
XX
PF   05-AUG-1993;  93WO-GB01651.
XX
PR   05-AUG-1992;  92GB-0016654.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Gode NT,  Nurse PM,  Parker PUJ,  Waterfield MD;
XX
DR   WPI; 1994-065697/08.
DR   P-PSDB; AAR46294.
XX
PT   Eukaryotic cells transformed with mammalian phospholipid or
PT   protein kinase DNA - useful in assays for compounds involved in
PT   cell growth regulation and for treating cancers
XX
PS   Disclosure; Fig 1; 71pp; English.
XX
CC   This sequence encodes the 110 kD catalytic subunit of the phosphatidyl
CC   inositol (PtdIns) 3-kinase.  This sequence was transformed into
CC   Schizosaccharomyces pombe cells under the regulatory control of the
CC   nmt promoter in an embodiment of the invention.  In the presence of
CC   thiamine the promoter is inactive and the cells carrying the PtdIns
CC   catalytic subunit plasmid grow as the parental strain.  In the absence
CC   of thiamine the nmt promoter function and the PtdIns 3-kinase
CC   catalytic subunit in induced.  PtdIns activity is substantially
```

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CC   increased under these conditions.  Cells containing constructs such as
CC   this, are useful in assays for detecting compounds involved in cell
CC   growth regulation.  It is also used as the basis for detecting
CC   compounds for treating cancers and the formation of blood vessel
CC   plaques.
XX   (Updated on 25-MAR-2003 to correct PN field.)
SQ   Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T; 0 other;
```

```
Alignment Scores:
Pred. No.:                     2.44e-129          Length:             3498
Score:                         1467.50            Matches:            382
Percent Similarity:            51.49%             Conservative:       205
Best Local Similarity:         33.51%             Mismatches:         404
Query Match:                   25.35%             Indels:             149
DB:                            15                 Gaps:               39
```

```
US-09-974-573-1 (1-1102)  x AAQ57012 (1-3498)

Qy    23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIlePro---------- 39
          :::                         ::::::::::::::::::::::::
Db     1 ATGCCTCCAAGACCATCATCAGGTGACTGTGGGGCATCCACCTTGTCCCCAAGAATC 60

Qy    40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
             :::||| :::::::|||||||
Db    61 CTAGTAGAATGTTTACTACCAAATGGATGATAGTGACT------------------------ 99

Qy    59 LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla 78
          |||                  :::  ::::::::|
Db   100 TTAGAATGCCCCGTGAGGCTACGTTAATACGATAAAAGCATGACTATTTAAAGAAGCA 159

Qy    79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
          :::
Db   160 AGAAAATACCCTCTC-----------------CATCAACTTCTTCAAGATGAAATCTTCTTAC 204

Qy    99 LeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValGlnThr 118
          ::::::                  :::
Db   205 ATTTTCGTAAGTGTACCCAAGAAGCAGAAAGGAAGAAGATTTTTGATGAAACAGACGA 264

Qy   119 LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal 138
          ::::::                          :::  |||
Db   265 CTTTGTGACCCTCGGCTTTTTCAACCCTTT-----------------TTAAAAGTAATT 306

Qy   139 GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIle 158
          :::|||                ---CTCAATCGAGAAATTGGTTTTGCTATC
Db   307 GAACCAGTAGGCAACCGTGAAGAAAGATC---CTCAATCGAGAAATTGGTTTTGCTATC 363

Qy   159 GlyTyrAspValThrArgSerAsnValHisAspArgGlnLeuGluPheThrArgArg 178
          |||                :::
Db   364 GGCATGCCAGTGTGCAAATTCGATATGGTTAAAGATCCAGAAGTACAGGACTTCCGAAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGluValAlaGlyArgAsp--------------- 192
          :::::
Db   424 AATATTCTCAATGTTTGTAAAGAAGCTGTGAATCTTGGGATCTTAATTCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu 211
          :::                          :::::::::::
Db   484 AGAGCAATGTATGTTTATCCTCAAATGAGAATCTTCACCAGAACTGCAAAGCACATA 543

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleVal Ile---------------His 225
          |||:::                :::  ::|||||||
Db   544 TATAAAAAATTGGATAAAGGGCAAATAAATAGTGGTAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrSerGlnThrIleLysValSerAlaAspThrProGlyThrIleLeu 245
          :::                ::::::
Db   604 AATGACAAACAGAAGTATACTCTGAAAATCAACCATGACTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSer-PhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer--- 264
          |||:::                :::||||||
Db   664 GCTGAAGCAATCAGGAAA-----AAAACTCGAAGTATGTTGCTATCATCTGAACACTA 717

Qy   265 ---------GlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGlu 279
          ::::                :::::::::|||||
```

```
Qy  606  LysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspValGly  625
              :::       |||
Db 1744  CAGATGTACTGCTTG--------------GTAAAAGATTGGCCTCCAATCAACCCTGAA  1788

Qy  626  LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaVal  645
Db 1789  CAGGGCTATGGAGCTTGGACTGCAATACCCAGATCCTATGGTTGGAGGTTTGCTGTT     1848

Qy  646  GlnLysLeuGluSer---LeuGluAspAspValLeuHisTyrLeuLeuGlnLeuVal     664
              :::                      |||
Db 1849  CCGTGCTTAGAAAAATATTAACAGATGACAAACTTTCTAGTACCTAATCAGTAGTA    1908

Qy  665  GlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLysArg  684
              :::|||:::||                    |||:::
Db 1909  CAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAA  1968

Qy  685  GlyLeuArgAsnLysArgIleGlyHisThrPheLeuLeuArgSerGluIleAla       704
Db 1969  GGCGTTAACTAATCAAAGGATCGGTCACTTTTCTTTGGCATTTAAAATCTGAGATG---  2025

Qy  705  GlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluGlyAlaTyrLeuArgGlyCys  724
              :::
Db 2026  CACAATAAAAACAGTTAGTCAGAGGTTTGGCCTTGGAGTCCGTATTGGCGTGCATGT   2085

Qy  725  GlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspMetLeuGlnLys  744
              :::
Db 2086  GGGATGTATCTGAAGCAC---CTTAATAGGCAAGTTGAGGCTGGAGAAAAGTCATTAAC  2142

Qy  745  ValThrIleAspIleLysSerLeuSerAlaGluLysTyrArgAspValSerGlnValIle  764
              :::|||
Db 2143  TTGACT---GACATT------CTCAACAACAAGAGAAGGATGAAACACAAAAGGTA---  2190

Qy  765  SerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsn---------LeuAsnLeuProGln  781
              |||:::
Db 2191  ---CAGATGAAGTTTTAGTTGAGCAAATGCGGGCGGACCAGATTCATGGATGCTCCCAG  2247

Qy  782  SerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuLeuGluGluLysCys  801
Db 2248  GGCTTTCTGTCTCCCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAGTGT  2307

Qy  802  LysValMetAlaSerLysLysTrpLeuTrpProLeuPheLysCysAlaAspProThr     821
              :::
Db 2308  CGAATTATGTGCTTCTCGCAAAAAGGCCACTGTGGTTGAATTGGGAG---AACCCAGAC  2361

Qy  822  AlaLeuSer-----------------------------AsnGluThrIleGlyIleIlePheLysHisGly  835
              :::                                    ||||
Db 2362  ATCATGTCAGAATTACACTTTCAGAGACAATGAG---------ATCATCTTTAAAAATGGG  2412

Qy  836  AspAspLeuArgGlnAspArgMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrp  855
              ||||
Db 2413  GATGATTTACGGCAAGATATGCTAACCCTTCAGATTATTCGCATATGGAAAATATCTGG  2472

Qy  856  GluThrGluSerLeuAspLeuCysLeuLysProTyrGlyCysIleSerThrGlyAspLys  875
              :::
Db 2473  CAAAATCAAGGTCTTGATCTTCGAAATGTTACCTTATGGATGTCTGTCATGGTGACTGT  2532

Qy  876  IleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleGluGlnSerThr     895
              :::
Db 2533  GTGGGACTTATCGGAGTGGTGGTGAAGAAATTCTCACACTATAATGCAGATT---CAGTGTAAA  2589

Qy  896  ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLysGlu     913
Db 2590  GGAGGGCCTGAAAGGTGCACTGCAGTTAACAGCCACCATCCATGCTGCTCAAAGAC     2649

Qy  914  LysCysProIleGluGluPheGlnAlaAlaValGluPheValTyrSerCysAla       933
              :::
Db 2650  AAGAACAAG--GGGAAAATATGATGGCGGCCATCGATTTGTTTACAAGGATCATGTGCT  2706

Qy  934  GlyTyrCysValAlaThrPheValLeuGlyIleIleGlyArgHisAsnAspAsnIleMet  953
              :::
Db 2707  GGATATTGTGTTGCCACCTTCATTTTGGGATTGGGAATTGGGAGATCGTCACATAGTAATCATG  2766
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```
Db  718  AAACTCTGTGTTTAGAATATCAGGCAAGTATATTTAAAAGTGTGTGGATGTGATGAA     777
Qy  280  TyrLeuValGlyGluThrProIleLeuLysAsnPheGlnAsnTrpValArgGlnCysLeuLysAsn  299
              :::       |||:::
Db  778  TACTTCCTAGAAAAATATCCTCGAGTCAGTATATAGTATATAAGAAGCTGTATAATGCTT  837

Qy  300  GlyGluGluIleHisLeuValLeuAspLeuAspCysThrProProAlaAlaLeuAspGluValArg  319
              |||:::|||
Db  838  GGGAGGAATGCCCAATTTGATGCTG------ATGGGTAAAGAAAGGCCTC             879

Qy  320  LysGluGluTrpProLeuValAlaAspCysAspCysThrGlyValThrGlyValTyrHisGluGlnLeu  339
              :::       |||:::                    :::::::
Db  880  TATTCTCAACTGCCAATG-----GACTGTTTTACAAATGCCATCATATTCCAGACGCATC  933

Qy  340  Thr---------IleHisGlyTyrIleLysAspHisGluSerValPheThrValSerLeu  354
              :::       |||:::
Db  934  TCCACAGCTACGCCATAATGAATGGAGAA-----------ACATCTACAAAATCCCTT    981

Qy  355  TrpAspCysAspArgLysPheArgValLys                                364
              :::
Db  982  TGGGTTAAATAGTGCACTCAGAATAAAAATCTTGTGCAACCTATGTGAATGTAAAT     1041

Qy  365  IleArgGlyIleLeuAspIleProValLeuProArgThrLeuAspLeuThrAlaAspLeuThrValPheValGlu  384
              :::::
Db 1042  ATTTGAGACATTGAC-----------------------AAGATTTATGTTCGA       1071

Qy  385  AlaAsnIleGlnIleTyrGlyValGlnGlnValLeuCysGlnInArgArgThrSerProLysProPhe  404
              :::       ||||
Db 1072  ACAGGTATCTACCATGGAGGAGAACCCTTATGTGATATGTGAACACTCAAAGAGTACCT  1131

Qy  405  ThrGluGlnValLeuTrpAspAsnValTrpLeuGluTrpPheSerIleLeuLysIleLysAspLeuPro  424
              ||||
Db 1132  TGTTCCAATCCCAGGTGGAATGGATGGCTGAATTACGATATATACAATTCCTGATCTTCCT  1191

Qy  425  LysGlyAlaAlaLeuLeuAsnLeuAsnLeuGlnIleIleTyrCysGlyLysLysAlaProAlaLeuSerGlyLysLys  444
              :::       ||||
Db 1192  CGTTGCAGCTCGACTTGCCTTTGCATT---TGT------------TCTGTTAAAGGCCGA  1236

Qy  445  ThrSerAlaGluMetProSerProGluSerGlyLysLysGlyAlaGlnLeuLeuTyrTyrVal  464
              ||||
Db 1237  AAGGGTGCT----------AAAGAGGAACACTGTCCATTGGCCTGGGGA             1275

Qy  465  AsnLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisIleMet  484
              :::
Db 1276  AATATAAAACTGTTTGATTACACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTT  1335

Qy  485  TrpGlnLeuSerGlyLysGlyGlyLeuAspAspGlnGlySerPheAsnAlaAspLysLeuThrSer  504
              ||||
Db 1336  TGGCCAGTACCTCATGGACTAGAAGAT---TTGCTGAACCCTATGGTGTTACT--       1386

Qy  505  AlaThrArgAsnProAspLysGluGlnAsnSerMetSerIleSer-IleLeuLeuLeuAspAsnTyrCys  524
              :::
Db 1387  GGATCAAATCCAAATAAAGAA---ACTTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGC  1443

Qy  525  HisProIleAlaGluProLysHisProAspProThrProProGluGlyArgVal---    543
              :::
Db 1444  AGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATGGTCTGTATCC  1503

Qy  544  -----------------------ArgAlaAlaGluMetProAsn                 549
              ||||
Db 1504  CGTGAAGCAGGAGGATTTAGTTATTCCCATGGACTGAGTGAACAGAACTAGAGACAAT   1563

Qy  550  GlnLeuArg----------LysGlnLeuGluAlaIleAlaIleAlaThrAspProLeuAsn  565
              :::|||:::
Db 1564  GAATTAAGAGAAATGATAAAGAACAGCTCCGAGACAATTGTACACGAGATCCTCTATCT  1623

Qy  566  ProLeuThrAlaGluAspLysAspLysPheArgTyrGluSerLeuLysAsp           585
              :::|||:::
Db 1624  GGAATCAAATCCAGAGCAAGAGAAAGAGTTTTCTGTGGAGCCACCAGACTACTATTGTTAACTATC  1683

Qy  586  ProLysAlaTyrProLysPheSerSerValLysTrpProGlyGlnGlnIleLeuValAla  605
              :::|||:::
Db 1684  CCCGAAATTCATCTACCCAAAATTGCTTCGTCGTCTTCGTCGTGTAAATGAACCTAGAGATGAAGTAGCT  1743
```

```
CC   polymer is located at a predetermined position on the solid support, and
CC   the array comprises nucleic acid polymers which are specific for less
CC   than 100 genes other than the selected genes. The method is useful for
CC   determining tumour characteristics in a tissue sample taken from a
CC   patient. The present sequence represents a human lipid-associated gene
CC   related cDNA sequence, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;
```

```
Alignment Scores:
Pred. No.:                                      Length:          3424
Score:                      2.95e-129           Matches:          387
Percent Similarity:         1466.50             Conservative:     206
Best Local Similarity:      51.52%              Mismatches:       396
Query Match:                33.62%              Indels:           163
DB:                         25.33%              Gaps:              40
                            24
```

```
US-09-974-573-1 (1-1102) x ABL59523 (1-3424)

Qy    19  ArgArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetLysLeuIle      38
          |||  :| :||  ::: |  ||        |||          ::: ::::::
Db     1  AGGATCAGAACAATGCCTCCAAGACCATCATCAGTGAACTGTGGGCATCCACTGATG      60

Qy    39  Pro--------IleGluPheValLeuProThrSerGlnArgAsnThrLysThrPro      54
          :::          ::  || :|| :|  ||   :
Db    61  CCCCCAGAATCCTAGTGACAATGTTTACTACCAAATGGATGATAGTGACT--------    111

Qy    55  GluThrAlaLeuLeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnVal   74
          :   |:    |||     :::
Db   112  --------------TTAGAATGCCTCCGTGAGGCTACCATTAGTAACTATAAAGCATGAACTA  159

Qy    75  TrpLeuArgAlaLeuGluThrSerValSerAlaAlaAspPheTyrHisArgLeuGlyProAsp  94
          ||| :::  |
Db   160  TTTAAAGAAGCAAGAAAAATACCCTC------CATCAACTTCTTCAAGAT             204

Qy    95  HisPheLeuLeuTyrArgLysLysLeuTyrGlyGlnIleArgTyrGluIleTyrGln     114
          :::
Db   205  GAATCTTCTTACATTTCGTAAGTGTACCCCAAGAACAGAAGAGCCAGAAAGGGAAGAATTTTTGAT  264

Qy   115  ValValGlnThrLeuAspCysLeuArgTyrLeuTrpLysValLeuHisArgSerProGlyGln  134
          ||||
Db   265  GAAACAAGACGACTTTGTGATCTTGGCTTTTCAACCATT------               306

Qy   135  IleHisValValGlnArgHisAlaProSerGluGluThrGluValAlaPheGlnArgGlnLeu  154
          :::  ::::::
Db   307  TTAAAGTAATTGAACCAGTAGGCCAACCGTGAAGAAAGATC---CTCAATGCAGAGAAATT    363

Qy   155  AsnAlaLeuLeuGlyTyrAspTyrAspValSerAsnValHisAspAspProGluLeuGlu    174
          :::   ::|
Db   364  GGTTTTGCTATCGGCATGCCAGTGCCAGTTGCGAATTGATATGGTTAAAGATCCTGAAGTACAG  423

Qy   175  PheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaGlyAsp------  192
          :::::
Db   424  GACTTCCGAACAGAAAATTCTTAATGTTGTAAAGAAGCGTGAAGTCTTAGGGATCTTAAT     483

Qy   193  --------ProLysLeuTyrAlaMetHisProValThrSerLysLysPro----Leu      207
          :::::
Db   484  TCACCTCATAGTAGAGCAAATGATGTCTATCGCCACATGGCCACCAGAGAATCTTCACCAGAGCTG  543

Qy   208  ProGluTyrLeuLeuLysLysIleThrAsnAsnCysValPheValIle-----------    224
          |||  :::       |||
Db   544  CCAAGCACCATATATAATAATTGATAGAGGCCAAATATAGTGGTTGGTAATA          603

Qy   225  --------HisArgSerThrThrSerGlnThrIleLeuValSerAlaSerAlaAspAspThrPro  241
          :::   :::::
Db   604  GTTTCTCCAAATAATGACAAGACAGAGTATCTCGAAAATCACCATGACTGTGTGCCA         663

Qy   242  GlyThrIleLeuGlnSerPhePheThrLysMetAlaLysSerLeuMetCysIle         261
          :::
Db   664  GAACAAGTAATTGCTGAAGCAATACGGAAA-----AAAACTAGAAGTATGTTGCTATCA      717

Qy   262  ProGluSer---------GlnAsnGluArgPheValLeuArgValCys               275
```

```
Qy   954  IleSerGluThrGlyLysAsnLeuPheHisIleAspPheGlyHisIleLeuGlyGlyAsnTyrLys  973
          :::   :::
Db  2767  GTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGATCACAAGAAG                2826

Qy   974  SerPheLeuGlyIleAsnLysGluArgValProPheValThrProPheLeuPhe          993
          |||        :::||
Db  2827  AAAAAATTGGTTATAAACGAGAGCGGCGTGCCGTTTGTTTGACACAAGATTCTTAATA        2886

Qy   994  ValMetGlyThrSerGlyLysLys------ThrSerLeuHisPheGlnLysPheGlnAsp    1011
          ||| :::
Db  2887  GTGATTAGTAAAGGAGGAGCCCAGAATGCACAAGAATGCACAAGAGACAAGAGAAGAATTTGAGAGGTTTCAGGAG  2946

Qy  1012  ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuIleLeuIleLeuPhe    1031
          :::|||       |||
Db  2947  GAAAAGACCCTAGCTTTAGATAAAACTGAGCAAGGCTTTGGAGTATTTCATGAAACAA      3006

Qy  1032  SerMetMetLeuThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIle       1051
          :::|||||||
Db  3007  TCAATGATGCTTGGCTCTGGAATGCCAGAACCTGCAATCTTTTGATGATATTGCATACATT    3066

Qy  1052  ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysLysTyrPheLeuAspGln    1071
          |||       |:: |  ||
Db  3067  CGAAAAGACCCTAGCTTTAGATAAAACTGAGCAAGGCTTTGGAGTATTTCATGAAACAA     3126

Qy  1072  IleGluValCysArgAspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal    1091
          :::    :::
Db  3127  ATGAATGATGCACCACATGGTGGCTGGACAACAAAATGGATTGGATCTTCCACACAATT     3186
```

```
RESULT 11
ABL59523
ID   ABL59523 standard; cDNA; 3424 BP.
XX
AC   ABL59523;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW   Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme;
KW   tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW   chromosome 3q26.3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO20227028-A1.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US30366.
XX
PR   28-SEP-2000; 2000US-0676052.
XX
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI   Skinner MK, Patton JL, Chaudhary J;
XX
DR   WPI; 2002-402054/43.
XX
PT   Identifying tumor characteristics in a tissue sample taken from a
PT   patient, involves determining the copy number or expression level of
PT   genes associated with lipid metabolism, synthesis or action -
XX
PS   Example 1; Page 82-83; 111pp; English.
XX
CC   The present invention describes a method for identifying tumour
CC   characteristics, comprising measuring a copy number or expression level
CC   of at least two genes associated with lipid metabolism, synthesis, or
CC   action in cells from a patient tissue sample, and comparing the results
CC   with a copy number or expression level of the genes in a normal cell.
CC   Also described is an array of nucleic acid polymers immobilised on a
CC   solid support, comprising a solid support, at least two different nucleic
CC   acid polymers which are each specific for a different gene associated
CC   with lipid metabolism, synthesis or action, where each nucleic acid
```

```
Db  1665  ATGGAGTCACAGACACTATTGTCTAACTCCCGAAATTCACCCAAATTGCTTCTGTC  1724
          ::: |||  ::::::|||||||||
Db   718  TCTGAACAATTAAAACTCTGTGTTTAGAGATATCACGGGCAAGTACATTTAAAAGTGTGT  777

Qy   595  rValLysTrpGlyGlnGlnIleValIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGl  615
          ||||| |||      :|||||    :: |||:||
Qy   276  GlyArgAspGluTyrLeuValGlyGluThrProIleLeuTyrProIleLysGluAsnPheGlnIleTrpValArgGln  295

Db  1725  TGTTAAATGGAATTCTAGAGATCGAAGTAGCCCAGATGTATTGCTTG---------  1770
          ||||||| :: ||||   : |||:|||||
Db   778  GGATGTGATGAATAATCCTCTGAGTCAGTATAAGTATATAAGAGAGC  837

Qy   615  uValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPh  635
          ::: |||
Qy   296  CysLeuLysAsnGlyGluGluHisIleLeuLeuValLeuValAspThrProProAspProAlaLeu  315

Db  1771  -GTAAAAGATTGGCCTCCAATCAAACCTATGGAACTTCTGGACTGTAATTA  1829
          |||  :: |||
Db   838  TGTATAATGCTGTGGGAGGATG-----CCCAATTG  867

Qy   635  eSerAspGluAsnValArgAlaIleAlaValAlaGlnLysLeuGluSer-----LeuGluAspAs  654
          ||| ::: |||||
Qy   316  AspGluValArgLysGlu-----GluTrpProLeuValAspAspCysThrGly  331

Db  1830  CCCAGATCCTATGTTCGAGGTTTGCTGTCGGTGCTGGAAAAATATTTAACAGATGA  1889
          |||:||     :::||
Db   868  AAGATGATGCTAAAGAAAGCCCTTATTCTCAACTGCCAATG-----GACTGTTTTACA  921

Qy   654  pAspValLeuHisTyrLeuLeuLeuLeuGlnLeuValGlnAlaValLysPheGlnProTyrHisAs  674
          ::: |||
Qy   332  ValThrGlyTyrHisGlyGlnLeuThr-----IleHisGlyLysAspHis  346

Db  1890  CAAACTTTCTCAGTATTTAATTCAGTACGTACCTGCCTCCTAAAATATGAACATATTTGGA  1949
          |||:||| :::
Db   922  ATGCCATCTTATTCCAGACCGCCATTTCCACAGCTACCACCATATATGAATGGAGAA-----  975

Qy   674  pSerAlaLeuLeuAlaArgPheLeuLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPh  694
          ::: |||||||
Qy   347  GluSerValPheThrValSerLeuTrpAspCysAspArgLysPheArgValLys-----  364

Db  1950  TAACTTGCTTGTGAGATTTTACTGAAGAAAGCATTGACTAACTCAAAGGATTGGGCACTT  2009
          :::||||
Db   976  -----ACATCTACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTT  1029

Qy   694  eLeuPheTrpPheLeuArgSerGlyIleAlaGlnSerArgHisTyrGlnGlnArgPheAl  714
          ::: ||||
Qy   365  -----IleArgGlyIleIleAspIleProValLeuProArgThr  376

Db  2010  TTTCTTTTGGCATTTAAAAATCTGAATG---CACAATAAAACAGTAGCCAGAGGTTTGG  2066
          :::||||
Db  1030  TGTGCAACCTACGTGAATCTAAATATTAAATATTCGAGACAATTGAC  1068

Qy   714  aVallleLeuGluAlaTyrLeuArgCysGlyCysGlyThrAlaMetLeuHisAspPheThrGl  734
          ::::::: |||||
Qy   377  AlaAspLeuThrValPheValGluAlaAsnIleGlnThrTyrGlyGlnGlnValLeuCysGln  396

Db  2067  CCTGCTTTGGAGTCCTATTGTCGTGCGATGGATGTATTGAAGCAC---CTGAATAG  2123
          ::: :::
Db  1069  -----AAGATTTATGTTCGAACAGGTATCTACCATGGAGGAACCCTTATGTGAC  1119

Qy   734  nGlnValGlnValIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerAl  754
          :::||||||
Qy   397  ArgArgThrSerProLysProPheThrGluThrGluValLeuTrpAsnValTrpLeuGluPhe  416

Db  2124  GCAAGTGCAGGCAATGAAAAGTCATTAACTTAACT---GACATT-----CTCAAACA  2174
          |||
Db  1120  AATGTTGAAACACTCAAAGAGTACCTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTAT  1179

Qy   754  aGluLysTyrAspValSerSerGlnValIleSerGlnLeuLysGlnLeuGluAsnLe  774
          :::||||
Qy   417  SerIleLysIleIleAspLeuTrpAspCysAspLysAlaLeuLeuAsnLeuGlnIleLeuTyrCysGly  436

Db  2175  GGAGGAAGGATGAAACACAAAGGTA---------CAGATGAAGTTTTAGTTGAGCAAAT  2228
          |||
Db  1180  GATATATACATTCCTGATCTTCCTCGCTGCTCGCGACTTTGCCTTTCCATT----TGC---  1233

Qy   774  uGlnAsn----------LeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLyLe  791
          :::
Qy   437  LysAlaProAlaLeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGly  456

Db  2229  GAGGCGACCAGATTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCA  2288
          |||
Db  1234  ----------TCTGTTAAAGGCCGAAAGGGTGCT-----  AAAGAG  1263

Qy   791  uLysAlaGlyAlaLeuValIleGluLysValMetAlaSerArgLysLysProLe  811
          :::||||
Qy   457  LysAlaAlaGlnLeuLeuLeuTyrTyrValAsnLeuLeuIleLeuIleAspHisArgPheLeuLeuArg  476

Db  2289  TCAACTAGGAAAACCTCAGCTTAAAGAGTGTGAATTATGTTCTTCTGCAAAAGGCCACT  2348
          ::: :::
Db  1264  GAACACTGTCCATTGGCATGGGAAAATAACTGTTGATTACACAGACACTCTAGTA  1323

Qy   811  uTrpLeuGluPheLysCysAlaAspProThrAlaLeuSer----------As  825
          ||||| |||
Qy   477  HisGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySer  496

Db  2349  GTGGTTGAATTGGGAG-----AACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAA  2402
          |||||
Db  1324  TCTGGAAAAATGGCTTGAATCTTTGGCCAGTACCTCCATGGAGTAGGAAGAT------TTG  1377

Qy   825  nGluThrArgLeuTyrIleIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuIleLeLe  845
          |||
Qy   497  PheAsnAlaAspLysAspLeuLysLeuTrpLeuThrSerAlaThrAspGlyGluAsn----------  512

Db  2403  TGAG---ATCATCTTTAAAAATGGGGATGATGATTTACGGCAAGATATGCTAACACT  2453
          |||
Db  1378  CTGAACCCATTGGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAG  1434

Qy   845  nGlnIleLeuGluArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuGlu  865
          |||||| :::
Qy   513  ----------SerMetSerIleSerIleLeu----------  519

Db  2454  TCAAATTATTCGTATTATGGAAAAATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTT  2513
          ||||| :::
Db  1435  TTGGAGTTTGACTGGTTCAGCAGTGGTAAAGTTCCAGATATGTCAGTG----  1485

Qy   865  uProThrGlyGlyIleSerThrGlyAspLysGlyMetIleGlyValMetLysLysAspAl  885
          |||||| :::
Qy   520  LeuAspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGlu  539

Db  2514  ACCTTATGGTGTTCGTCAATCGGTGACTGCTGTGGGACTTATTGAGGTGGTGCGAAATTC  2573
          :::||
Db  1486  ATTGAAGAGCA---TGCCAATTGGTCTCTGTATCCCGAAGCAGGATTAGCTAGTCATTCCCACGC  1544

Qy   885  aThrThrIleAlaLysIleGlnSerThrValGlyAsnThrGlyVal Ala----------PheLyAla  903
          :::||||| |||
Qy   540  -GlyAspArgValArgAlaAlaGluMetProAsnGlnLeuArg----------LysGlnLe  555

Db  2574  TCACACTATTATGCAAATT--CAGTGCAAAGCGCGGTTGAAAGGTGCACTGCAGTCAA  2630
          |||||
Db  1545  AGGACTGAGTAACAGACAGAGATTAAGGGAAAATGACAAAGAACAGCT  1604

Qy   903  sAspGluValLeuSerHisTrpLeuLysTrpLeuLysCysProIleGlyGluLysPheGlnIleA  923
          |||||| :::
Qy   555  uGluAlaIleIleAlaThrArgAspProLeuThrAlaAspAsnProLeuAsnIleCactCACGAGAACACT  575

Db  2631  CAGCCACCACACTACATCAGTGGCTCAAGACAAGAACAAA---GGAGAAATATGATGC  2687
          |||||| :::
Db  1605  CAAAGCAATTTCTACAGCAGATCCCTCTCGAAATCACTCACCTGAGCCAGGAAAGAGATTTTCT  1664

Qy   923  aAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGl  943
          |||||
Qy   575  uTrpHisPheArgTyrGluSerLeuLysAspProLysAlaTyrProLysLysSerPheSerSe  595

Db  2688  AGCCATTGACCTGTTTACACGTTCATGTGCTGGATCGTGTAGCTACTTGTGTGGCCACTTCATTTTGGG  2747
```

```
Qy    943  YIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIl  963
           |||||||||||||||||        :::  ::: |||||||||||||||||||||||
Db   2748  AATTGGAGATCGTCACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATAT  2807

Qy    963  eAspPheGlyHisIleLeuLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgVa  983
           :|||||||||||||||||||         ::: :|||||||||||||||||::||||
Db   2808  AGATTTTGGACACTTTTGGATCACAAGAAGAGAAAAAATTTGGTTATAAACGAGAAGGTGT  2867

Qy    983  lProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLys-----  1001
           |||||||||||||||||||||           :::::
Db   2868  GCCATTTGTTTTGACACAGGATTTCTTAATAGTGATTAGTAAAGGAGCCCAAGAATGCAC  2927

Qy   1002  -ThrSerLeuHisPheGlnLysAspValCysValLysAlaTyrLeuAlaLeuAr  1021
            :::|||||||||||||||||::::||||||||||||||||||||||
Db   2928  AAAGACAAGAGAATTTGAGAGGTTCAGAGATGTGTTACAAGGCTTATCTAGCTATTCG  2987

Qy   1021  gHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGl  1041
           |||||||||||||||||||||||||            ||||||||
Db   2988  ACAGCATGCCAATCTCTTCATAAATCTTTTCCAATAAGCTGGCTCTGGAATGCCAGA  3047

Qy   1041  nLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGl  1061
           :|||     :::|||||||   :::||| |||    ::: |||||
Db   3048  ACTACAATCTTTTGATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAAACTGA  3107

Qy   1061  uGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpTh  1081
           :::|||     |:::|||||   |||||||||||||||||||||
Db   3108  GCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGACACATCATGGTGGCTGGAC  3167

Qy   1081  rValGlnPheAsnTrpPheLeuHisLeuVal  1091
           ||| ::: |||||||
Db   3168  AACAAAAATGGATTGGATCTTCCACACAATT  3198
```

```
RESULT 12
AAS14365
ID   AAS14365 standard; cDNA; 3424 BP.
XX
AC   AAS14365;
XX
DT   12-MAR-2002  (first entry)
XX
DE   cDNA encoding human p110alpha isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform;
KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          13..3219
FT                /*tag= a
FT                /product= "p110alpha isoform of PI3-kinase"
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US15065.
XX
PR   10-MAY-2000; 2000US-203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   P-PSDB; AAU09687.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3
PT   domain-containing polypeptides e.g. LASP-1, comprising allowing the
PT   binding partners to interact in the presence and absence of a test
```

```
PT   compound -
XX
PS   Example 1; Page 55-60; 85pp; English.
XX
CC   The present invention relates to identifying a modulator of the
CC   phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC   the catalytic subunit via a SH3 domain-containing polypeptide such as
CC   LASP-1. Also described are methods of assaying the specific binding
CC   affinity of the PI3-kinase binding partner. Such modulators are useful
CC   for the treatment of diseases characterised by the undesirable or
CC   excessive activity of PI3Kdelta. For example the modulators can be used
CC   for inhibiting the growth or proliferation of cancer cells
CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC   system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC   and Type I diabetes mellitus. The present sequence encodes for human
CC   p110alpha isoform of PI3k.
XX
SQ   Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;
```

```
Alignment Scores:
Pred. No.:                          3424
Score:               2.95e-129      Matches:           1466.50
Percent Similarity:  51.52%         Conservative:       387
Best Local Similarity: 33.62%       Mismatches:         206
Query Match:         25.33%         Indels:             396
DB:                                 Gaps:               163
                                                         40
                                                         24
```

```
US-09-974-573-1 (1-1102) x AAS14365 (1-3424)

Qy     19  ArgArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIle  38
           |||||||||||||||||||||||||||  |||::::|||||||
Db      1  AGGATCAGAGAACAATGCCTCAAGACCATCATCAGGTGAACTGTGGGCATCCACTTGATG  60

Qy     39  Pro-------------IleGluPheValLeuProThrSerGlnArgAsnThrLysThrPro  54
               :::|||:::||||||||:::||||
Db     61  CCCCCAGAATCCTAGTGGGAATGTTTACTACCAAATGGAATGATAGTGACT-------  111

Qy     55  GluThrAlaLeuLeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnVal  74
                                :::        ||
Db    112  -------------TTAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTA  159

Qy     75  TrpLeuArgAlaLeuGluThrSerValSerLeuAlaAspPheTyrHisArgLeuGlyProAsp  94
           |||              :::
Db    160  TTTAAAGAAGCAAGAAAATACCCTCTC------------CATCAACTTCTTCAAGAT  204

Qy     95  HisPheLeuLeuLeuTyrGlnLysLysGlyGlnThrTyrGluIleTyrArgAspLysTyrGln  114
                    :::::
Db    205  GAATCTTCTTACATTCGTAAGTGTACCCAAGAAGCAGAAGGAGAAGAGAATTTTTTGAT  264

Qy    115  ValValGlnPheLeuLysCysLeuArgTyrTrpLysTrpLysValHisArgSerProGlyGln  134
                           ||||
Db    265  GAAACAAGACCAGCACTTTGTGATCTTCCGGCTTTTCACCCATT------------  306

Qy    135  IleHisValValGlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeu  154
           |||:::|||||||      |||:::||||
Db    307  TTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAAGATC---CTCAATCGAGAAATT  363

Qy    155  AsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAspAspGluLeuGlu  174
                                  ::: |||
Db    364  GGTTTTGCTATCCGCACCATGCCACGTGTGCCAATTGAATATGGTTAAAGATCCTGAAGTACAG  423

Qy    175  PheThrArgArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaGlyArgAsp------  192
           |:::|||||||||||||:::
Db    424  GACTTCCGAAGAAAATATTCTTAATGTTTGTAAAGAAGCTGTGAATCTTAGGGATCTTAAT  483

Qy    193  ------------ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---Leu  207
                       |||:::|||:::
Db    484  TCACCTCATAGTAGAGCAATGTATGTCTATCCGCCACCATGTAGGAATCTTACACCAGAGCTG  543
```

```
Qy    520 LeuAspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGlu 539
          |||:::||||||||||            :::  |||||||||||||||||:::|||||
Db   1486 ATTGAACAGCA--TGCCAATTGTCTCGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGC 1544

Qy    540 -GlyAspArgValAlaGluMetProAsnGlnLeuArg-------------------- LysGlnLe 555
           :::|||                 :||||||  ||||||
Db   1545 AGGACTGAGTAACAGACAGCTAGCTAGAGACAAATGAATTAAGGAGAAAATGACAAAGAACAGCT 1604

Qy    555 uGluAlaIleIleAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLe 575
          |||||||||||||||:::|||       |||||||||:::||||||||||||||||||||
Db   1605 CAAAGCAATTTCTACACGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCT 1664

Qy    575 uTrpHisPheArgTyrGluSerLeuLysAspProLysLysAspProLysLeuPheSerSe 595
          ||||  :::       :::
Db   1665 ATGGAGTCACAGACACTATTGTCAACTATCCCGAAATTCTACCCAAATTGCTTCTGTC 1724

Qy    595 rValLysTrpGlyGlnGlnIleLeuGluThrGlnInLeuAlaLysThrTyrGlnLeuLeuAlaLysArgGl 615
          |||       |||           :::|||||||||
Db   1725 TGTTAAATGGAATTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG----------- 1770

Qy    615 uValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuLeuLysCysAsnPh 635
          ||||||                        :::|||:::||||||||||
Db   1771 -GTAAAAGATTGGCCTCCAATCAAACCTGACACGGCTATGGAACTTCTGACTGTAATTA 1829

Qy    635 eSerAspGluAsnValArgAlaIleAlaValAlaValGlnLysLeuGluser--- LeuGluAspAs 654
          |||       |||||||:::|||||||||||            :::
Db   1830 CCCAGATCCTATGGTTTGCGAGTTTCGGTGCTTGGAAAAATATTAACAGATGA 1889

Qy    654 pAspValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHisAs 674
          |||       ||||||                    |||||||||||||||
Db   1890 CAAACTTTCTCAGTATTTAATTCAGGTACTAGTACAGGTCCTAAAATATGAACAATATTTGGA 1949

Qy    674 pSerAlaLeuAlaArgPheLeuLeuLysSerGlyLeuArgAsnArgAlaArgIleGlyHisPh 694
          |||       :::|||||||||||||              ::::::||||||:::
Db   1950 TAACTTGCTTGTGAGATTTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGGCACTT 2009

Qy    694 eLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAl 714
          :::           |||||||||||            :::
Db   2010 TTTCTTTTGGCATTTAAAATCTGAGATG-- CACATAAAACAGTTAGCCAGAGGTTTGG 2066

Qy    714 aValIleLeuGluAlaTyrLeuArgGlyGlyGlyThrAlaMetLeuHisAspPheThrGl 734
          |||                    :::
Db   2067 CCTGCTTTGGAGTCCTATTGTCGTGCATGTGGATGTATTTGAAGCAC--- CTGAATAG 2123

Qy    734 nGlnValGlnIleValIleAspMetLeuGlnLysValThrIleAspProIleLysSerLeuSerAl 754
          :::                    :::
Db   2124 GCAAGTCGAGGCAATGAAAAGCTCATTAACTTAACT--------- GACATT----- CTCAAACA 2174

Qy    754 aGluLysTyrAspValSerSerGlnValIleSerGlnInLeuLysGlnLeuGluAsnLe 774
          |||                    :::
Db   2175 GGAGAGGAAGGATGAAACACAAAGGTA----------- CAGATGAAGTTTTTAGTGAGCAAAT 2228

Qy    774 uGlnAsn---------- LeuAsnLeuProSerPheArgValProTyrAspProGlyLe 791
          :::       :::
Db   2229 GAGGCGACCAGATTTCATGGATGCCCTACAGGGCTTGCTGTCTCCTAAACCCTGCTCA 2288

Qy    791 uLysAlaGlyAlaLeuValIleGluLysCysLysValMetAlaSerLysLysProLe 811
          :::       :::
Db   2289 TCAACTAGGAAACCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACT 2348

Qy    811 uTrpLeuGluPheLysCysLysAspProThrAlaLeuSer---------- As 825
          |||:::
Db   2349 GTGGTTGAATTGGGAG------ AACCCAGACATCATGTCAGAGTTACTGTTCAGAAACAA 2402

Qy    825 nGluThrIleGlyIleIlePheLysHisGlyAspLeuHisGlnAspMetLeuIleIle 845
          |||:::       :::
Db   2403 TGAG-- ATCACTTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACT 2453

Qy    845 uGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLe 865
          |||       :::
Db   2454 TCAAATTATTCGTATTATGGAAAATCTGCAAAATACAAGGTCTTGATCTTCGAATGTT 2513

Qy    865 uProTyrGlyCysIleSerThrGlyMetIleGlyLeuIleGluValLysAspAl 885
```

```
Qy    208 ProGluTyrLeuLeuLysLysIleThrAsnAsnCysValPheIleValIle----- 224
          ||||||:::|||            :::
Db    544 CCAAAGCACATATATAAATTGGATAAGAATAATAGTGGTGATTTGGGTAATA 603

Qy    225 ---------- HisArgSerThrSerGlnThrIleLeuLysValSerAlaAspAspThrPro 241
                    :::
Db    604 GTTTCTCCAAATAATGACAAGCAGAAGTATATCTCTGAAAATCAACCATGACTGTGTGCCA 663

Qy    242 GlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIle 261
          :::
Db    664 GAACAAGTAATTGCTGAAGCAATCAGGAA------- AAAACTAGAAGTATGTTGCTATCA 717

Qy    262 ProGluSer---------- GlnAsnGluArgGlyAspPheValLeuArgValCys 275
          :::
Db    718 TCTGAACAATTAAAACTCTGTGTTTAGATATCAGGGCAAGTACATTTTAAAAGTGTGT 777

Qy    276 GlyArgAspGluTyrLeuValGlyValGlyGluThrProIleLeuLysAsnPheGlnInTrpValArgGln 295
          :::
Db    778 GGATGTGATGAATTACTTCCTAGAAAAAATATCCTTCGAGTCAGTATAAGTATATAAAGAAGC 837

Qy    296 CysLeuLeuLysAsnGlyGluGlnIleLeuHisLeuValLeuAspThrProProAspProAlaLeu 315
          :::
Db    838 TGTATAAATGCTTGGAGGATG---------- CCCAATTTG 867

Qy    316 AspGluValArgLysGlu---------- GluTrpProLeuValAspAspCysThrGly 331
          :::
Db    868 AAGATGATGGCTAAAGAAAAGCCCTTATTCTCAACTGCCAATG------ GACTGTTTTACA 921

Qy    332 ValThrArgGlyTyrArgHisGluGlnLeuThr---------- IleHisGlyLysAspHis 346
          :::
Db    922 ATGGCCATCTCATTCCAGACGCCATTCCACAGCTACCACCCATATATGGAATGGAGAA 975

Qy    347 GluSerValPheThrValSerLeuTrpAspCysAspPheArgLysPheArgValLys----- 364
          :::
Db    976 -ACATCTACAAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTT 1029

Qy    365 ---------- IleArgGlyIleAspIleProValLeuProArgThr 376
          :::
Db   1030 TGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC- 1068

Qy    377 AlaAspLeuThrValPheValGluAlaAsnIleGlnInTyrGlnInValLeuCysGlnGln 396
          :::
Db   1069 -----AAGATTTATGTTCGAACAGGTATCCTACCATGGAGGAGGAGAACCCCTTATGTGAC 1119

Qy    397 ArgArgThrSerProLysProPheThrGluGlyValTrpGluValTrpPheLeuuTrpLeuGluPhe 416
          :::
Db   1120 AATGTGAAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAATGGCTGAATTAT 1179

Qy    417 SerIleLysIleLysAspArgAspTyrLysAlaLeuAlaLeuAsnLeuGlnInIleTyrCysGly 436
          :::
Db   1180 GATATAATATACATTCCTGATCTTCCTGGTGGTGCTGCTTGGCTTCCATT---TGC- 1233

Qy    437 LysAlaProAlaLeuSerGlyLysLysThrSerArgAlaGluMetProSerProGluSerLysGly 456
          :::
Db   1234 ---------- TCTGTTAAAGGGCCCGAAAAGGGTGCT------ AAAGAG 1263

Qy    457 LysAlaGlnInLeuTyrTyrValAsnLeuLeuLeuLeuLeuAspHisArgPheLeuArg 476
          :::
Db   1264 GAACACTGTCCATTGGCATGGGAAAATAAACTTGTTTGATTACACAGACACTCCAGTA 1323

Qy    477 HisGlyGluTyrValLeuHisMetTrpGlnInLeuSerGlyLysGlyLysAspGlnInGlySer 496
          :::
Db   1324 TCTGGAAAAATGGCTTTGAATCTTTGGCCAGTACCTCCATGGATTAGAAGAT---- TTG 1377

Qy    497 PheAsnAlaAspLysLysGluThrSerAlaThrAsnProAspLysGluAsn----- 512
          :::
Db   1378 CTGAACCCTATTGGTGTTACT-- GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAA 1434

Qy    513 ---------- SerMetSerIleSerIleLeu 519
          :::
Db   1435 TTGGGAGTTTGACTGGTTCAGCAGTGTCGTGTAAAGTTCCCAGATATGTCAGTG------ 1485
```

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Db    2514  ||||||||||||||||  :::||||||||  |||||||      :::|||||||||||||||  2573
            ACCTTATGGTGTCTGCAATCGGTGACTGTTGTGGGACTTATTGAGGTGGTGCGAAATTC

Qy    885   aThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGlyAla-----PheLy  903
            ||| ::||||      :::|||      :: |||||||||
Db    2574  TCACACTATTATGCAAATT---CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAA  2630

Qy    903   sAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLysPheGlnAl  923
            ||||              |||||||::||||  |||
Db    2631  CAGCCACCACACTACATCAGTGGCTCAAAGACAAGAACAAA---GGAGAAATATATGATGC  2687

Qy    923   aAlaValGluArgPheValTyr-SerCysAlaGlyTyrCysValAlaThrPheValLeuGl  943
            |||::::::   |||      ::|||||||||:|||||||::||||||
Db    2688  AGCCATTGACCTGTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGG   2747

Qy    943   yIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIl  963
            :::||||      ::||||  :::  |||          :::||||
Db    2748  AATTGGAGATCGTCACAATAGTAACATCATGATGAAAGACGATGGACAACTGTTTCATAT  2807

Qy    963   eAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgVa  983
            ||| :::||||      :::
Db    2808  AGATTTTGGACACTTTTGGATCAACAAGAAGAAAATTGGTTATAAACGAGAACGTGT   2867

Qy    983   lProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLys-----  1001
            ||||||||||      :::|||
Db    2868  GCCATTTGTTTTGACACAGGATTTCTAAATGTGATTAGTAGAAAGAGCCCAAGAATGCAC  2927

Qy    1002  -ThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeuAr  1021
            ::: ||::::::|||||||||      |||||||:::|||
Db    2928  AAAGACAAGAAGATTTGAGAGGTTTCAGGAGATGTGTTACACAGGCTTATCTAGCTATTCG  2987

Qy    1021  gHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGl  1041
            ||||||||      :::||||||
Db    2988  ACAGCCATGCCAATCTCTTCATAAATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGA  3047

Qy    1041  nLeuThrSerLysGluGluTyrIleArgAspAlaLeuThrArgLeuLysGlyLysSerGl  1061
            :::      |||||||      :::
Db    3048  ACTACAACTCTTTGATGATGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGA  3107

Qy    1061  uGluAspAlaLysLysTyrPheLeuAspLysProGlnIleGluValLysGlyTrpTh  1081
            :::||||      ||| |||||
Db    3108  GCAAGAGGCTTTGAAGTATTTCATGAAACAAATGAATGAGGTGCACATCATGTGGCTCGAC  3167

Qy    1081  rValGlnPheAsnTrpPheLeuGlyVal 1091
            ||| |||
Db    3168  AACAAAAATGGATTGGATCTTCCACACAATT 3198
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```
RESULT 13
AAQ51155
ID   AAQ51155 standard; cDNA; 3207 BP.
XX
AC   AAQ51155;
XX
DT   25-MAR-2003 (updated)
DT   09-JAN-2003 (updated)
DT   12-APR-1994 (first entry)
XX
DE   p110 cDNA.
XX
KW   Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW   antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW   platelets; neutrophil activity; 3-phosphorylated phosphoinositides;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3207
FT                   /*tag= a
FT                   /note= "PI3- kinase p110"
XX
PN   WO9321328-A1.
XX
```

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PD   28-OCT-1993.
XX
PF   13-APR-1993;   93WO-GB00761.
XX
PR   13-APR-1992;   92GB-0008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI   Panayotou G, Volinia S, Gout I;
XX
DR   WPI; 1993-351738/44.
DR   P-PSDB; AAR43341.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 7; Fig 9; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a. Positive clones were sequenced to give the human
CC   PI3 kinase p110 sequence shown. This sequence has 95 percent
CC   homology with the bovine sequence. The domain encoding residues 19-
CC   100 of human p110 is sufficient to encode the kinase which will
CC   associate with the p85 kinase subunit. The gene may be used to
CC   provide a protein with PI3 kinase activity, and is useful for
CC   screening for (ant)agonists of PI3 kinase activity which could be
CC   useful for stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy. Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAQ51156, AAQ59012-23 and AAQ57522-3.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 3207 BP; 1028 A; 581 C; 680 G; 918 T; 0 other;
XX

Alignment Scores:
Pred. No.:                           3.33e-129      Length:         3207
Score:                               1465.50        Matches:        382
Percent Similarity:                  51.40%         Conservative:   204
Best Local Similarity:               33.51%         Mismatches:     405
Query Match:                         25.31%         Indels:         149
DB:                                                 Gaps:           39

US-09-974-573-1 (1-1102) x AAQ51155 (1-3207)

Qy    23   MetLysProArgSerThrAlaAlaSerLeuSerMetGluIlePro----------- 39
           |||              :::||| |||||
Db    1    ATGCCTCCAAGACCATCACCAGGTGAACTCGTGGGGCATCCACTTGATGCGCCCCAAGAATC 60

Qy    40   ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
           ||| |||
Db    61   CTAGTAGAATGTTTACTACCAAATGGGATGATAGTGACT--------------------- 99

Qy    59   LeuHisValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgArgAla 78
           |||              :: :::||||||
Db    100  TTAGAATGCCTCCGTGGAGGTACGTTAATAACGATAAAGCATGAACTATTTAAAGAAGCA 159

Qy    79   LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
           ||| |||
Db    160  AGAAAATACCCTC--------------CATCAACTTCTTCAAGATGAATCTTCTTAC 204

Qy    99   LeuTyrGlnLysLysGlnThrTyrGluIleTyrArgAspTyrLysTyrGlnValGlnThr 118
           ||| :::
Db    205  ATTTTCGTAAGTGTTACCCAAGAACGAGAAAGGGAAGAATTTTTGATGAAACAAGACGA 264

Qy    119  LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal 138
           |||  ::: :::
Db    265  CTTTGTGACCTTCGGCTTTTTCAACCCTTT------------TTAAAAAGTAATT 306
```

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Qy   139 GlnArgHisAlaProSerGluThrLeuAlaPheGlnLeuAsnAlaLeuIle 158
             :::              |||             |||:::  |||
Db   307 GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATGGTTTGCTATC 363

Qy   159 GlyTyrAspValThrArgMetAlaHisAspGluLeuGluPheThrArgArg 178
             |||               |||   :::               |||:::
Db   364 GGCATGCCAGTGTGTGAATTCGATATGGTTAAAGATACCAGGACTACCGAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGlyMetAlaGlyValAla---------Asp 192
             |||               |||  :::|||:::|||
Db   424 AATATTCTCAATGTTGTAAAGAGAGCTGGGGATCTTAGGGGATCTTAATCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLys---LeuProGluTyrLeu 211
             :::|||               |||  |||:::|||
Db   484 AGAGCAAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCCAGAACTGCCAAAGCACATA 543

Qy   212 LeuLysLysIleThrArgAsnCysValPheIleValIle----------His 225
             |||               ---|||:::              :::
Db   544 TATAATAAATTGGATAAACGGCAAATAATATAGTGGTAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspThrProGlyThrIleLeu 245
             :::|||               |||:::|||               |||
Db   604 AATGACAAACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGluSer--- 264
             |||               :::|||               |||:::
Db   664 GCTGAAGCAATCAGGAAA-----AAACTCGAAGTATGTTGCTATCATCTGAACAACTA 717

Qy   265 --------GlnAsnGluArgAspPheValLeuValArgValCysGlyArgAspGlu 279
                   |||               :::|||               |||
Db   718 AAACTCTGTGTTTTAGAATATCACGGGCAAGTATATTTTAAAGTGTGTGGATGATGAA 777

Qy   280 TyrLeuValGlyValGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsn 299
             |||               :::              |||:::
Db   778 TACTTCCTAGAAAAAATATCCTGAGTCAGTCAGTATATAAGATATAAGAAGCTGTATAAATGCTT 837

Qy   300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg 319
             |||               :::|||               |||
Db   838 GGGAGGATGCCCAATTGATGCTG---------------ATGGCTAAAGAAAGGCTC 879

Qy   320 LysGluGluTrpProLeuValAspAspCysThrGlyTyrValThrArgGlyTyrHisGluGlnLeu 339
             |||               ---|||:::|||               |||
Db   880 TATTCTCAACTGCCAATG-----GACTGTTTTACAATGGCCATCATATTCCAGACGCCATC 933

Qy   340 Thr-------IleHisGlyLysLysAspHisGluSerValPheThrValSerLeu 354
             :::              ---|||
Db   934 TCCCAGCTACGCGCCATATATGAATGGGAGAA------ACATCTACAAAATCCCTT 981

Qy   355 TrpAspCysAspArgCysLysPheArgValLys--------- 364
             |||               :::
Db   982 TGGGTTATAAATAGTGCACTCAGAATAAAAAATTCTTTGTGCAACCTATGTGAATGTAAAT 1041

Qy   365 IleArgGlyIleLeuAspIleProValLeuProArgThrArgAspLeuThrPheValGlu 384
             |||               :::|||               :::::
Db   1042 ATTCGAGACATTGAC-----------------AAGATTTATGTTCGA 1071

Qy   385 AlaAsnIleGlnTyrGlyGlyGlnInValCysGlnArgThrSerProLysProPhe 404
             |||               :::
Db   1072 ACAGGTATCTCCAAGGTGGAGGAGACCCCTATGTGATAATGTGAACACACAAAGGTA 1131

Qy   405 ThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysLysAspLeuPro 424
             |||               :::|||
Db   1132 TGTTCCAATCCCAGGTGAATTACGTGAATTACGATATATACATTCCTGATCTTCCT 1191

Qy   425 LysGlyAlaLeuAsnLeuAsnLeuGlnInIleTyrCysGlyLysAlaProAlaLeuSerGlyLys 444
             |||  :::              |||:::              |||
Db   1192 CGGTGCTGCTCGACTTTGCCTTTCCATT--TGT----TCTGTTAAAGGCGGA 1236

Qy   445 ThrSerAlaGluMetProSerProGluSerProGluSerLysLysGlyAlaGlnLeuLeuLeuTyrTyrVal 464
             |||               :::|||
Db   1237 AAGGGTGCT----------------------AAAGAGGAACACTGTCCATTGGCCTGGGGA 1275

Qy   465 AsnLeuLeuIleLeuAspHisArgArgPheLeuLeuArgHisGlyGluThrTyrGluHisMet 484
             |||:::|||
Db      (continued) 
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Db   1276 AATATAAACTTGTTTGAGATTACCACAGATACTCTAGTATCTGAAAAATGGCTTGAATCTT 1335

Qy   485 TrpGlnLeuSerGlyLysGlyGluAspProGlySerPheAsnAlaAspLysLeuThrSer 504
             :::|||               |||
Db   1336 TGGCTGCAGTACCTCATGGACTAGAAGAT-----TTGCTGAACCCTATTGGTGTGTACT--- 1386

Qy   505 AlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeuLeuAspLysAsnTyrCys 524
             |||  :::|||               :::
Db   1387 GGATCAAATCCCAAATAAAGA---ACTCCATGTTTAGAGTTGGAGTTGACTGGTTCAGC 1443

Qy   525 HisProIleAlaLeuProLysHisArgProThrProAspProGluGlyGlyAspArgVal--- 543
             |||               :::|||               |||
Db   1444 AGTGTGGTAAAGTTTCCAGATATGTCAGTATGTCAGTGATGAAGAGCATGCCAATGGTCTGTATCC 1503

Qy   544 --------ArgAlaGluMetProAsn 549
             ---|||
Db   1504 CGTGAAGCAGGATTAGTTATTCCATGCACAGGACTGCGAGTAACAGACACTAGCTGAGAGACAAT 1563

Qy   550 GlnLeuArg----------LysGlnLeuGluAlaIleIleAlaThrAspProLeuAsn 565
             :::              |||
Db   1564 GAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAATTGTACACGAGATCCTCATCT 1623

Qy   566 ProLeuThrAlaGluAspLysGluLeuLeuTrpHisProAsnPheArgTyrGluSerLeuLysAsp 585
             |||:::|||               |||
Db   1624 GAAATCACTGAGCACAAGAAAGATTTTCTGTGGACCCACAGACACTATTGTAACTATC 1683

Qy   586 ProLysAlaTyrProLysPheSerSerValLysTrpGlyGlnGlnIleGlnIleValAla 605
             :::|||               |||:::|||               |||
Db   1684 CCCGAAATTTCACCCAAATTGCTTCGTCGTCTGTTAAATGGAACTCTAGAGATGAAGTAGCT 1743

Qy   606 LysThrTyrGlnLeuLeuLeuAlaLysGluValValTrpAspGlnSerAlaLeuAspValGly 625
             |||               ---|||
Db   1744 CAGATGTACTGCTTG---------------GTAAAAGATTGGCCTCCAATCAAGCCTGAA 1788

Qy   626 LeuThrMetGlnLeuLeuAspLysCysAsnPheSerAspGluAsnValAlaIleAlaIleAlaVal 645
             :::|||               |||:::
Db   1789 CAGGGCCATGGAGCTTCTGGACTGGCAATTACCCAGATCCTATGGTCCGAGGTTTGTGTT 1848

Qy   646 GlnLysLeuGluSer---LeuGluAspAspAspValLeuHisTyrLeuLeuGlnLeuVal 664
             |||  :::              |||:::
Db   1849 CGGTGCTTAGAAAAAATATTTAACAGATGACAAACTTTCTCAGTACTAATTCAGCTAGTA 1908

Qy   665 GlnAlaValValLysPheGluThrGlnInValAspSerAlaLeuAlaArgPheLeuLeuLysArg 684
             |||:::|||               |||
Db   1909 CAGGGTACTAAAATATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTTACTCAAAAA 1968

Qy   685 GlyLeuArgAsnLysArgIleGlyHisProPheLeuGluArgSerGluIleAla 704
             |||               :::
Db   1969 GCGTTAACTATCAAAGGATCGGTCACTTTTCTTTTGGCATTTAAAATCTGAATG--- 2025

Qy   705 GlnSerArgHisTyrGlnInArgPheAlaValIleLeuGluAlaThrLeuArgGlyCys 724
             |||               :::
Db   2026 CACAATAAAAACAGTAGTCAGAGGTTTGGCGTGTTTGGAGTCCTATTGCCGTGCATGT 2085

Qy   725 GlyThrAlaMetLeuHisAspPheThrArgGlnInValGlnLysValSerSerGlnInLys 744
             :::              |||:::
Db   2086 GGGTATCTGAAGCAC---CTTAATAGGCAGAGTTGAGGCTATGGAAAAGCTCATTAAC 2142

Qy   745 ValThrIleAspLysSerSerLeuSerGlnArgThrLysTyrAspValSerGlnValIle 764
             :::|||               :::
Db   2143 TTGACT-----GACATT--CTCAAACAAGAGAGAAGGGATGAAACACAAAGGTA--- 2190

Qy   765 LeuAsnLeuProGln 781
             :::
Db   2191 ---CAGATGAAGTTTTTAGTTGAGCAAATGCGGCCACCAGATTCCATGGATGCTCTCCAG 2247

Qy   782 SerPheArgValProTyrArgAspTyrValTyrGlyLeuLysProLeuTrpLeuProGlyLysCys 801
             :::              :::
Db   2248 GGCTTTCTGCTCGTCCCTCTAAACCTCTCATCAGCTGGAAATCTCAGGCTGGGAAATCTCCAG 2307

Qy   802 LysValMetAlaSerLysLysProLeuPheLysGluLysGlyGluThr 821
             :::::|||
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```
Db  2308 CGAATTATGTCTTCTGCAAAAAGGCCACTGTGTTGAATTGGGAG------AACCCAGAC 2361
Qy   822 AlaLeuSer------------AsnGluThrIleGlyIleIlePheLysHisGly         835
Db  2362 ATCATGTCAGAATTACTCTTCAGAACAGAG------ATCACTTTAAAAATGGG        2412
          :::::||

Qy   836 AspAspLeuArgGlnAsnMetLeuIleLeuGlnIleIleArgIleMetGluSerIleTrp   855
Db  2413 GATGATTTACGGCAAGATATGCTAACCCTTCAGATTATTCGCATATGGAAAATATCTGG   2472

Qy   856 GluThrGluSerLeuAspLeuCysLeuLeuProTyrArgGlyCysIleSerThrGlyAspLys 875
Db  2473 CAAAATCAAGGTGTTACCTTCGAATGTACCTTATGGATGTCGTCAATCGGTGACTGT      2532

Qy   876 IleGlyMetIleGluIleValLysAspAlaThrThrIleAlaLysIleGlnInSerThr    895
Db  2533 GTGGGGACTTATCCAGGTGGTGGGAGAAATTCTCACACTATAATGCAGATT---CAGTGTAAA 2589

Qy   896 ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLeuLysGlu    913
Db  2590 GGAGGCCCTGAAAGGTGCACTGCAGTTTAACAGCCACCACTCCATCAGTGGCTCAAAGAC   2649

Qy   914 LysCysProIleGluGluLysPheGlnAlaAlaAlaValGluArgPheValTyrSerCysAla 933
Db  2650 AAGAACAAG--GGGAAATATATGATGGGGCCATCGATTTGTTTACACGATCATGTGCT     2706

Qy   934 GlyTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMet    953
Db  2707 GGATATTGTGTTGCCACCTTCATTTTGGGAGATCGTCACAATGACAATATCATG        2766

Qy   954 IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys    973
Db  2767 GTTAAAGATGAATGGACAACGTTTCATATAGATTTTGGACACACTTTTGGATCACAAGAAG  2826

Qy   974 SerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProAspPheLeuPhe    993
Db  2827 AAAAAAATTTGGTTATAAACGAGACGCGTCCCGTTTGTTTTGACACAAGATTTCTTAATA   2886

Qy   994 ValMetGlyThrSerGlyLysLys------ThrSerLeuHisPheGlnLysPheGlnAsp   1011
Db  2887 GTGATTAGTAAAGAGCCCAAGAATGCACAAGACCAAGAGAATTTGAGAGGTTTCAGGAG    2946

Qy  1012 ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleIleLeuPhe   1031
Db  2947 ATGTTTTACAAGGCTTATCTAGCTATTCGGCAGCATGCCAATCTTCTCATAAAATCTTTTC  3006

Qy  1032 SerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluThrSerLysGluTyrIle 1051
Db  3007 TCAATGATGCTTGGCTCTGGAATGCCACAACTGACACTTTGATGATTATTGCCATACATT   3066

Qy  1052 ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysTyrPheLeuAspGln      1071
Db  3067 CGAAAGAGCCCTAGCTTAGATAAAACTGAGCAAGAGGCTTGGAGTATTTCATGAAACAA    3126

Qy  1072 IleGluLeuValCysArgAspLysSerGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal 1091
Db  3127 ATGAATGATGCACACACATGGTGGCTGGAACACAAAAATGGATTGGATCTTCCACACATT   3186
```

```
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1..3207
FT                    /tag= a
FT                    /note= "PI3- kinase p110"
XX
PN   WO9321328-A1.
XX
PD   28-OCT-1993.
XX
PF   13-APR-1993;  93WO-GB00761.
XX
PR   13-APR-1992;  92GB-0008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI   Panayotou G, Volinia S, Gout I;
XX
DR   WPI; 1993-351738/44.
DR   P-PSDB; AAR43342.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 7; Fig 16; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a.  Positive clones were sequenced to give the human
CC   PI3 kinase p110 sequence shown.  This sequence has 95 percent
CC   homology with the bovine sequence. The domain encoding residues 19-
CC   100 of human p110 is sufficient to encode the kinase which will
CC   associate with the p85 kinase subunit. The gene may be used to
CC   provide a protein with PI3 kinase activity, and is useful for
CC   screening for (ant)agonists of PI3 kinase activity which could be
CC   useful for stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy.  Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAQ51155 and AAQ57522-3.
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 3412 BP; 1128 A; 616 C; 706 G; 962 T; 0 other;
```

Alignment Scores:
Pred. No.:   39
Score: 1.1e-128   Length: 3412
                         1460.50   Matches: 385
Percent Similarity: 51.53%   Conservative: 206
Best Local Similarity: 33.57%   Mismatches: 394
Query Match: 25.22%   Indels: 163
DB: Gaps: 40

US-09-974-573-1 (1-1102) x AAQ51156 (1-3412)

```
Qy   23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluIleIlePro---------  39
Db    1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCCACCTTGATGCCCCAAGAATC 60

Qy   40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu   58
Db   61 CTAGTGGAATGTGTTACTTACCAAAATGGAATGGATAGTGACT---------------    99

Qy   59 LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgArgAla 78
Db  100 TTAGAATGCTCCGTGAGGCTACATTAGTAACTATAAAGCACTATTTAAAAGAAGCA      159

Qy   79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspPheHisPheLeuLeu 98
Db  160 AGAAAAATACCCCTC------CATCAACTTCTTCAAGAGATGAATTCTTCTTAC        204
```

```
RESULT 14
AAQ51156
ID   AAQ51156 standard; cDNA; 3412 BP.
XX
AC   AAQ51156;
XX
DT   25-MAR-2003  (updated)
DT   12-APR-1994  (first entry)
XX
DE   Human p110 cDNA.
XX
KW   Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW   antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW   platelets; neutrophil activity; 3-phosphorylated phosphoinositides;
KW   ds.
```

```
Qy   99  LeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThr   118
                :  : :
Db  205  ATTTTCGTAAGTGTACCCAAGAACAGAAGAAGGGAGAAGAATTTTTGATGAAACAAGACGA   264

Qy  119  LeuAspCysLeuArgTyrTrpLysTrpLysValLeuHisArgSerProGlyGlnIleHisValVal   138
              :  : :
Db  265  CTTTGTGATCTTCGGCTCTTTTCAACCATTT-----------TTAAAAGTAATT   306

Qy  139  GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgLeuAsnAlaLeuIle   158
                              :  :::
Db  307  GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCCGAGAAAATTGGTTTGCTATC   363

Qy  159  GlyTyrAspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArg   178
Db  364  GGCATGCCAGTGTGCCAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGA   423

Qy  179  ArgLeuValThrProArgMetAlaGluMetAlaGlyValAlaGlyValAlaGlyAsp   192
              : ::::::
Db  424  AATATTCTTAATGTTGTAAAGAGAGCCGTGGATCTTAATTCACCTCATAGT   483

Qy  193  ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu   211
              ::::::::::  ::::::::::
Db  484  AGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGTCTGCCAAAGCACATA   543

Qy  212  LeuLysLysIleThrAsnAsnCysValPheIleValIle-------------His   225
Db  544  TATAATAAATTGGATAGAGCGCCAAATAATAAGTGGTAATATAGTTTCTCCAAAT   603

Qy  226  ArgSerThrSerGlnThrIleLysValSerAlaSerAspThrProGlyThrIleLeu   245
                 :::::::::  :::::::
Db  604  AATGACAACAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT   663

Qy  246  GlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGlySer--   264
              :::
Db  664  GCTGAAGCAATCAGGAAA------AAAACTAGAAGTATGTTGCTATCATCTGAACAATTA   717

Qy  265  ---------GlnAsnGluArgAspPheValLeuArgValCysGlyValCysGlyValValArgAspGlu   279
              : :::
Db  718  AAACTCTGTGTTTTAGAATATCAGGGCAAGTAACATTTTAAAGTGTGTGGATGATGAA   777

Qy  280  TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpValArgValGlnCysLeuLysAsn   299
              : :::  :::
Db  778  TACTTCCTAGAAAAAATATCTCTGAGTCAGTATGAGTATATAAGAAGGTGTATAATGCTT   837

Qy  300  GlyGluGluIleHisLeuValLeuValLeuAspThrProProAspAlaLeuAspGluValAlaArg   319
Db  838  ------------CCCAATTTGAAGATGATGGCT   867

Qy  320  LysGlu---------GluTrpProLeuValAspAspCysThrGlyValThrGlyTyr   335
              : :::
Db  868  ACAAAATCCCTTTGGGTTATAAATAGAGACACTCAGAATAAAATTCTTTGTGCAACCTAC   921

Qy  336  HisGluLeuHisThr------------IleHisGlyLysAspHisGluSerValPhe   350
              :::
Db  922  TCCAGACGCATTCCACAGTCACCATATGAATGGGAGAA------ACATCT   969

Qy  351  ThrValSerLeuTrpAspTrpCysAspAspAspLysPheArgGlyValLys   364
              :::
Db  970  ACAAAATCCCTTTGGGTTATAAATAGAGACACTCAGAATAAAATTCTTTGTGCAACCTAC   1029

Qy  365  ---------IleArgGlyIleLysAspIleProValLeuProArgThrAlaAspLeuThr   380
              :::
Db 1030  GTGAATCTAAATAATTCGAGACATTGAC------------AAG   1059

Qy  381  ValPheValGluAlaAsnIleGlnTyrGlyGlnInValLeuGlnInValLeuGlnInLeu   400
              ::::  ::  :::
Db 1060  ATTTATGTTCGAACAGGTATCTCACCATGGAGGAGAACCCTTATGTGACAATGTGAACACT   1119

Qy  401  ProLysProPheThrGluGluValLeuTyrAsnValTrpLeuGluPheSerIleLysIle   420
              :::  :::
Db 1120  CAAAGAGTACCTTGTTCCAATCCCAGGTGCATGGAATGAATGGCTGAATTATGATATATACATT   1179


Qy  421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla   440
              ||||||||  :::  ||||||||||
Db 1180  CCTGATCTTCCTCGTGCTGCTGACTTTTGCCTTTGCCTTCCATT---TCT   1224

Qy  441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysGlyAlaGlnLeu   460
              : ::  ::::
Db 1225  GTTAAAGGCGGAAAGGGTGCT------AAAGAGGACAACACTGTCCA   1263

Qy  461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisHisGlyGluTyr   480
              ||||||
Db 1264  TTGGCATGGGAAATATAAACTTGTTTGATTACCAGACACTCTAGTATCTGGAAAAATG   1323

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlyLeuGlyGluAspGlnLySerPheAsnAlaAsp   500
              |||||||
Db 1324  GCTTTGAATCTTTGGCCAGTACCTACGTAGGATTAGAAGAT------TTGCTGAACCCTATT   1377

Qy  501  LysLeuThrSerAlaThrAsnProAspLysGluAsn   512
              :  :::
Db 1378  GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGAC   1434

Qy  513  ---------------SerMetSerIleSerIleLeuLeuAspAsnTyr   523
                       :  :::
Db 1435  TGGTTCAGCAGTGTGGGTAAAGTTCCCAGATATGTCAGTG---------ATTGAAGAGCA   1484

Qy  524  CysHisProIleAlaLeuProLysHisArgProThrProAspProGlu--GlyAspArgArgVa   543
              :  :::  :::  |||
Db 1485  TGCCAATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTAGTCCACGCAGACTGAGTAA   1544

Qy  543  lArgAlaGluMetProAsnGlnLeuArg---------   559
              :::  :::  |||
Db 1545  CAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGAGACAGCTCAAAGCAATTTC   1604

Qy  559  eAlaThrAspProLeuAsnProLeuThrAlaGluAsnProLysLeuLeuLeuTrpHisProAr   579
              :  :  :::
Db 1605  TACACGAGATCCTCTCTCTGAAATCACTCACTGAGCGAGGAGAAAGATTTTTCTATGGAGTCACAG   1664

Qy  579  gTyrGluSerLeuLeuAspProLysAlaTyrProLysSerLeuPheSerSerValLysTrpGl   599
              :::  :::  |||
Db 1665  ACACTATTGTGTAACTATCCCGGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAA   1724

Qy  599  yGlnGlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysAsnArgGluValTrpAspGl   619
              ::::::  :::
Db 1725  TTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG------GTAAAAGATTG   1769

Qy  619  nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerArgSerGluAs   639
              :::
Db 1770  GCCTCCAATCAAACCTGAACAGGCTATGAACGTTCTGGAACTTCTGGAACTGTAATTACCCAGATCCTAT   1829

Qy  639  aArgPheLeuLysArgGlyLeuArgAsnLysArgIleGlyIleTyrHisSerPheLeuTrpPh   658
              :::
Db 1830  GAGATTTTTACTGAAGAAGACATTGACTAATCAAAAGATTGGCACTTTTCTTTTGGCA   1889

Qy  658  sTyrLeuGlnLeuValGlnAlaValLysPheGluLysProTyrArgHisAspSerSerAlaLeuAl   678
              ||||
Db 1890  GTATTTAATTCAGCTAGTACAGGTCCTAAAATATGAACAATAATTGGATAACTTGCTTGT   1949

Qy  678  IleAspMetLeuGlnInValLeuValThrIleGluLysSerLeuSerLeuLysLysTyrAs   698
              :::
Db 1950  GAGCTGAAAAGCTCATTAACTTAACT------CTCAAACAGGAGGAGAAGGA   2009

Qy  698  eLeuArgSerGluIleAlaGlnInSerArgHisTyrGlnInArgHisPheAlaValIleLeuGl   718
              :::
Db 2010  TTTAAAATCTGAGATG---CACAATAAAACAGTTAGCCAGAGGTTTGGCTGCTTTTTGGA   2066

Qy  718  uAlaTyrLeuArgGlyTyrCysGlyTyrArgHisAlaMetLeuHisAspPheArgHisGlnInValGln   738
              ||||::::  ::::
Db 2067  GTCCTATTGTGTCGTGCATGTGGGATGATTGAAGCAC---CTGAATAGGCAAGTGCAGGC   2123

Qy  738  lIleAspMetLeuGlnInValTrpAsnValTrpLeuGluPheSerIleLysTyrAs   758
              :  :::
Db 2124  AATGGAAAAGCTCATTAACTTAACT------GACATT   2174

Qy  758  pValSerSerGlnInValIleSerGlnInLeuLysGlnInLeuAsnLeuGlnInAsn------   776
```

```
ID   AAC65690 standard; DNA; 3213 BP.
XX
AC   AAC65690;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Human PI3 kinase p110beta DNA.
XX
KW   Human; pI3 kinase P110 beta; antisense inhibition; primer; cytostatic;
KW   antiinflammatory; antiinfective; ds.
XX
OS   Homo sapiens.
XX
PN   US6133032-A.
XX
PD   17-OCT-2000.
XX
PF   09-SEP-1999;   99US-0392350.
XX
PR   09-SEP-1999;   99US-0392350.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowsert LM;
XX
DR   WPI; 2000-686014/67.
DR   P-PSDB; AAB11124.
XX
PT   Antisense compound 8-30 nucleobases in length targeted to a start codon
PT   of the coding region of human PI3 kinase p110beta, useful for
PT   inhibiting the expression of the human polynucleotide -
XX
PS   Example 1; Column 43-50; 34pp; English.
XX
CC   This invention describes a novel antisense compound (I) 8-30 nucleobases
CC   in length targeted to a start codon or nucleobases 4-3174 of the coding
CC   region of human PI3 kinase p110beta (II), in which (I) specifically
CC   hybridizes with and inhibits the expression of (II). The products of the
CC   invention have cytostatic, antiinflammatory and antiinfective activity.
CC   (I) is useful for inhibiting the expression of (II) in human cells or
CC   tissues. The antisense compound can be utilized for diagnostics,
CC   therapeutics, prophylaxis and as research reagents and kits. The
CC   antisense compounds may also be useful prophylactically, e.g. to prevent
CC   or delay infection, inflammation or tumor formation. The antisense
CC   compounds are useful for research and diagnostics, because these
CC   compounds hybridize to nucleic acids encoding (II).
XX
SQ   Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

Alignment Scores:
Pred. No.:                               Length:              3213
Score:              1.32e-118            Matches:             1354.50
Percent Similarity:  49.60%             Conservative:        361
Best Local Similarity: 31.81%           Mismatches:          202
Query Match:        23.39%             Indels:              407
Db:                 21                   Gaps:                165
                                                             37

US-09-974-573-1 (1-1102) x AAC65690 (1-3213)
```

```
Qy    30 AlaSerLeuSerSerMetGluLeuIleProIleGluProValLeuProThrSerGlnArg   49
         :::::::::::::::::::::
Db    64 TCACAGATAGCATCTGATGGCTCCATCCTGGGATTTCCTTTGCCACTCGG------      117

Qy    50 AsnThrLysThrProGluThrAlaLeuLeuHisValAlaGlyHisAspValGluGln      69
                                                     ::: |||||||
Db   118 ------ATTTATATCCAGTTGGAGGTACCTCGGGAAGCTACCATTCTTAT         162

Qy    70 MetLysAlaGlnValTrpLeuArgAlaLeuGluGluThrSerValSerAlaAspPheTyrHis    89
         :::  ::  |||  ::
Db   163 ATTAAGCAGATGTTATGGAAGCAAGTTCACAATTACCCAATG------         204

Qy    90 ArgLeuGlyProAspHisPheLeuLeuTyrGlnLysGlyGlnTrpTyrGluIle    109
```

```
RESULT 15
AAC65690
```

(The left portion of the page contains a series of nucleotide/amino acid sequence alignments labeled Db and Qy with position numbers, e.g.:)

```
Db  2175  ...CAGATGAGTTTTAGTTGAGCAAATGAGGCGACCAGA  2228
Qy   777  ---LeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAl  795
Db  2229  TTTCATGGATGCCCTACAGGGCTTGCTGCTCCTCTAAACCCTGCTCATCAACTAGGAAA  2288
Qy   795  aLeuValIleGluLysCysLysValMetAlaSerLysLysLysLysProLeuTrpLeuGluPh  815
Db  2289  CCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTG  2348
Qy   815  eLysCysAlaAspProThrAlaLeuSer---------AsnGluThrIleGl  829
Db  2349  GGAG------AACCCAGACATCATGTCAGAGTTACTGTTTCAGAACAATGAG------  2394
Qy   829  yIleIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArg  849
Db  2395  -ATCATCTTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCG  2453
Qy   849  gIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy  869
Db  2454  TATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTG  2513
Qy   869  sIleSerThrGlyAspLysIleGlyMetIleGluValLysAspAlaThrThrIleAl  889
Db  2514  TCTGTCAATGGTACTGTGTGGGACTTATTGGAGGTGGTGCGAAATTCTCACACTATTAT  2573
Qy   889  aLysIleGlnGlnSerThrValGlyAsnThrGlyAla------PheLysAspGluValLe  907
Db  2574  GCAAATT---CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACT  2630
Qy   907  uSerHisIleTrpLeuLysGluGluProIleGluGluLeuPheGlnIleAlaAlaValGluAr  927
Db  2631  ACATCCAGTGGCTCAAAGACAAGAACAAA--GGAGAAATATATGATGCAGCCATTGACCT  2687
Qy   927  gPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIleGlyAspAr  947
Db  2688  GTTACACGTTCATGTGCGCTGCTAGACTGCGTGGTAGCTACCTTCATTTTGGGAATTGGAGATCG  2747
Qy   947  gHisAsnAspAsnIleSerGluGluThrHisGlyAsnLeuPheHisIleAspPheGlyHi  967
Db  2748  TCACAATAGTAACATCATCGGTGAAAGACGATGGCAACTGTTTCATATAATGATTTGGACA  2807
Qy   967  sIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgValProPheValLe  987
Db  2808  CTTTTGGATCACAAGAAGAAGAAAAATTGGTTATAAACAGAGAACGTGTGCCATTTGTTTT  2867
Qy   987  uThrProAspPheLeuProPheValMetGlyThrSerGlyLysLys------ThrSerLeuHi 1005
Db  2868  GACACCAGGATTTCTTAATAGTGATTAGTAAGTAAAAGAGCCCAAGAATGCACAAAGACAAGAGA 2927
Qy  1005  sPheGlnLysPheGlnLeuAspVallCysValLysValAlaTyrLeuAlaLeuArgHisHisThrAs 1025
Db  2928  ATTTGAGAGGTTTCAGGAGTGTTTACAAGGCTTATCTAGCTATTCGACAGCCATGCCAA  2987
Qy  1025  nLeuLeuIleLeuIleGluSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLy 1045
Db  2988  TCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAAATCTTT 3047
Qy  1045  sGluAspIleGluTyrIleGluArgAspAlaLeuThrValGlyLysSerGluGlyAspAlaLy 1065
Db  3048  TGATGACATTGCATCATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTT 3107
Qy  1065  sLysTyrPheLeuLysAspGlnIleGluValLysArgArgAspGlyGlyTrpThrValGlnPheAs 1085
Db  3108  GGAGTATTTCATGAAACAAAACAAATGAATGAGTCGACACATCATGGGCTGGCAACAACAAAATGGA 3167
Qy  1085  nTrpPheLeuHisLeuVal 1091
Db  3168  TTGGATCTTCCACACAATT 3186
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```
Qy   433 IleTyrCysGlyLysGlyAlaProAlaLeuSerGlyLysThrSerAlaGluMetProSerPro 452
             :::|||
Db  1210 GTTTAT--GCAGTTTGGATAAGAGTAAAACGAGAAATCAACGAAAACTATTAATCCC 1266

Qy   453 ------GluSerLysGlyLysAlaGlnLeuTyrTyr---------------ValAsn 465
             :::::
Db  1267 TCTAAATATCAGACACCATCAGGAAAGCTGGAAAAGTGCATTATCCTGTAGCGTGGGTAAAT 1326

Qy   466 LeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyTyrValGluHisMetTrp 485
             ::::::|
Db  1327 ACGATGGTTTTGACTTAAAGGACAATTGAGAACTGGACACATAATATTACACAGCTGG 1386

Qy   486 GlnLeuSerGlyLysGlyGlyGluAspGlnGlySerPheAsnAlaAspLysLeu--- 502
             |||||||
Db  1387 TCTTCATTT---CCTGATGAACTCGAAGAAATG 1416

Qy   503 ---------ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSer 517
Db  1417 TTGAATCCAATGGGAACTGTTCAAACAAATCCATATACTGAAAATGCAACAGCTTTGCAT 1476

Qy   518 IleLeuLeu--AspAsnTyrCysHisProIleAlaLeuPro--------------- 530
             :::|||
Db  1477 GTTAAAATTCCAGAGAATAAAAAACAACCTTATTATTACCCTCCTTCGATAAGATTATT 1536

Qy   531 ---LysHisArgProThrProGluGlyValArgValArgAlaGluMetProAsn 549
                ||||||
Db  1537 GAAAAGGCAGCTGAGATTGCAAGCAGTAGTGCTAATGTGTCAAGCTTCGAGGTGGAAAA 1596

Qy   550 GlnLeuArgLysGlnLeuLeuValAlaIleIleAlaThrAspAsnProLeuAsnProLeuThrAla 569
             :::
Db  1597 AAGTTCTTCCTGTATTGAAAGAAATCTTGGACAGGATCCCTTGTCTCAACTGTGTGAA 1656

Qy   570 GluAspLysGluLeuLeuTrpHisPheArgTyrGluSerLeuLys--AspProLysAla 588
             :::
Db  1657 AATGAAATGGATCTTATTTGGACTTTGCGACAAGAGCTGCCGAGAGATTTCCCACAATCA 1716

Qy   589 TyrProLysPheSerSerValLysTrpGlyValGlnGlnIleValAlaLysThrTyr 608
             |||
Db  1717 CTGCCAAAATTACTGCTGTCAATCAAGTGGAATAAACTTGAGGATGTTGCT------- 1767

Qy   609 GlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMet 628
             |||||
Db  1768 CAGCTTCAGGCGCGTGCTTCAGATTTGGCCTAAA-----CTGCCCCCGGGAGGCCCTA 1821

Qy   629 GlnLeuLeuAspCysAsnPheSerGluAsnValArgAlaIleAlaValGlnLysLeu 648
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Db  1822 GAGCTTCTGGATTTCAACTATCCAGACCAGTACGGTCGAGAATATGCTGGTCGCCTG 1881

Qy   649 GluSerLeuGluAspAspAspValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLys 668
             :::|:::
Db  1882 CGACAGATGAGTGATGAAGAACTTTCTCAATATCTTTACAACTGGTGCAAGTGTTAAAA 1941

Qy   669 PheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLysArgGlyLeuArgAsn 688
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Qy   689 LysArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHis 708
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Db  2002 CGGAGGATAGGCCAGTTCTATTTTGGCATCTTAGGTCAGAAGTG---------CAC 2049

Qy   709 ------------TyrGlnIleArgPheAlaValIleIleLeuGluAlaTyrLeuArgGlyCysGly 725
Db  2050 ATTCCTGCTGCTCCAGTACAATTTGGTGTCATCCTTGAGCATCTGCCGGGA---AGT 2106

Qy   726 ThrAlaMetLeuHisAspPheThrGlnValIleLeuAspMetLeuGlnLysVal 745
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Db  2107 GTGGGGCACATGAAAGTGCTTTCAAGCAGTTGAAGCACTCAATAAGTTAAAACTTTA 2166

Qy   746 Thr--------IleAspIleLeuSerLeuSerLeuAlaGluLysTyrArgAspValSerSerGlnVal 763
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Db  2167 AATAGTTTAATCAAACTGAATGCCTGAAGTAAACAGAGCCAAAGGAAGGAGGCCATG 2226
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Db   205 ----------TTCAACCTCCTATGATAATGACTCCTATATGTTTGCATGT 246

Qy   110 TyrAspLysTyrGlnValValGlnThrLeuAsp----------Cys------ 121
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Db   247 GTGAATCAGACTGCTGTATATGAGGAGCTTGAACAGATGAAACACGAAGACTCTGATGTC 306

Qy   122 ------LeuArgTyrTrpLysValLeuHisArgSer-----ProGlyGlnIleHis 136
             ||||||
Db   307 AGACCTTTTCTTCCAGTTCCAAATTAGTGACAAGAAGTGTGACCCAGGGGA------ 360

Qy   137 ValValGlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAla 156
             :::::
Db   361 ------------AAATTAGACTCAAAAATTGGAGTC 384

Qy   157 LeuIleGlyTyrArgAspValThrAspValSerAsnValHisAspAspGluLeu---GluPhe 175
             |||||||
Db   385 CTTATAGGGAAAAGTCTGCATGAATTTGATTCCTTGAAGGATCCTGAAGTAAATGAATTT 444

Qy   176 ThrArg------ArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaGlyLysArgAsp--- 192
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Db   445 CGAAGAAAAATGCGGCAAAATGCCGGAGGAAAAAATCCGTCACTGTGGGATGTCTTGG 504

Qy   193 ---ProLysLeuTyrAlaMetHisProTrpProValThrSerLysGlyProGluProGluTyrLeu 211
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Db   505 ATGGACTGGCTAAAACAAACATATCCACCAGAGCCATGAACCATCCCTGAAAACTTA 564

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIleHisArgSerThrThrSerGln 231
             :::   :::   :::|:::
Db   565 GAAGATAAACTTTTATGGGGAAAGCTCATCGTAGCTGTTCATTTGAAAACTGCCAGGAC 624

Qy   232 ------ThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerPhePhe 249
             :::   :::
Db   625 GTGTTAGTTCAAGTGTCTCCTAATAGAATCCTATCAAAGTAAATGAA-------- 675

Qy   250 ThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp 269
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Db   676 TTGCAATCCAAAAACGTTTGACTATTCATGGGAAGAAGATGAAGTTAGCCCCTATGAT 735

Qy   270 PheValLeuArgValCysGlyValArgAspGluTyrLeuValGlyTyrLeuGlyThrProIleLeuLysAsn 289
             :::|||::::::
Db   736 TATGTGTTGCAAGTCAGCGGAGGAGTAGAATATGTTTTTGGTGTAGATCATCCACTAATTCAG 795

Qy   290 PheGlnTrpValGlnCysLeuLysAsnGlyGluGluIleHisLeuValLeuAspThr--- 309
             :::|:::|||:::
Db   796 TTCCAGTATATCCCGGAACTGTGTGATGAACAGAGCCCTGCCCCATTTTATACTT--- 849

Qy   310 ProProAspProLeuAlaLeuAspArgLysGlyGluGluTrpProLeuValAspAspCys 329
Db   850 ----------GTGGAATGC 858

Qy   330 ThrGlyValThrGlyTyrHisGln-----LeuThrIleHisGlyHisGlu 347
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Db   859 TGCAAGGATCAAGAAAATGTATGACACAAGAAAATGATTGCCATAGAGGTGCCATAAATCGA 918

Qy   348 SerValPheThrValSerLeu------------------ 354
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Db   919 AATTCATCTAAATCTTCCTTCCATTACCACCAAAGAAAAACACGAATTATTCTCTGTT 978

Qy   355 TrpAspCysAspArgLysPheArg--ValLysIleArgGlyIleAspIleProValLeu 373
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Db   979 TGGGAAAATAACAACACCCTTTCCAAATTGTCTTGGTTAAGGGA-----AATAAACTT 1029

Qy   374 ProArgThrAlaAspLeuThrValPheValGluAlaAsnIleGlnTyrGlyValGlnValVal 393
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Db  1030 AACACAGAGGAAACTTCCTTCCTTCCATTACCACCAAAGAAAAACACGAATTATTCTCTGTT 1089

Qy   394 LeuCysGlnLysArgThrSerProLys---ProPheThrGluGluValAlaLeuAsnLeuGln 412
             :::
Db  1090 CTGTGTAAAACCATCGTAAGCTCAGGTATCAGGAGGTATCAGGAAAAAATGATCATATTTGGAATGAA 1149

Qy   413 TrpLeuPheSerIleLeuLysProLeuAspLeuAspLysProLysGlyAlaLeuAsnLeuGln 432
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Db  1150 CCACTGGAATTTGATATTAATATTTGGACTTACCAAGAATGGCTCCGATTATGTTTTGCT 1209
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Qy     764  IleSerGlnLeuLysGlnLys----------------LeuGluAsnLeuGlnAsnLeuAsn  778
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Db    2227  CATACCTGTTTAAAACAGAGTGCTTACCGGGAAGCCCTTCTGACCTGCAGTCA------  2280

Qy     779  LeuProGlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIle  798
                                   |||   :::            |||   :::
Db    2281  ----------CCCCTGAACCCATGTTATCCTCCAGAACTCATGTT  2319

Qy     799  GluLysCysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLeuLysCysAla  818
                 |||||||||||             :::
Db    2320  GAAAAGTGCAAATACATGGATTCCAAAATGAAGCCTTTGTGGCTGGTATAC--------  2370

Qy     819  AspProThrAlaLeuSerAsnGluThrIleGlyTyrIleIlePheLysHisGlyAspAspLeu  838
                 :::            :::::::||||||||:::||||||            |||
Db    2371  AATAACAAGGTATTTGGTGAGGATTCAGTTGGAGTGATTTTTAAAAATGGTGATGATTTA  2430

Qy     839  ArgGlnAspMetLeuLleGlnIleLeuArgIleMetGluSerIleTrpGluThrGlu  858
                 |||||:::            |||:::||||||            :::
Db    2431  CGACAGGATATGTTGACACTCCAAATGTTGCGTTGAGGATTACTCTGGAAGAAGCT  2490

Qy     859  SerLeuAspLeuCysLeuProTyrGlyCysIleSerGlyThrGlyAspLysIleGlyMet  878
                 |||||||||:::            |||:::||||||            :::
Db    2491  GGTTTGGATCTTCGGATGTGCCTTATGTTGCGTTGACAACAGGAGATCGCTCTGGCCTC  2550

Qy     879  IleGluIleValLysAspAlaThrThrIleAlaLysIleGln------GlnSerThrVal  896
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Qy     897  GlyAsnThrGlyAlaPheLysAspGluValLeuSerHisTrpLeuTyrSerGluLysCysPro  916
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Db    2611  GCTCCTGCAGCAGCCTTCAACAAAGATGCCCTTCGAACTGGCTTAAAGATACAACTCT  2670

Qy     917  IleGluGluLysPheGlnAlaAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCys  936
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Db    2671  GGGGATGAC---CTGGACCGAGCCATTGGAGAATTACACTGTCCTGCTGGCTACTGT  2727

Qy     937  ValAlaThrPheValGlyTyrIleGluTyrAspGlyAspAspHisAsnAspAspIleSerGlu  956
                 |||||||:::            :::||||||            :::
Db    2728  GTAGCTTCTTATGTCCTTGGGAGTTGGTGACAGACATCATGTCAAAAAA  2787

Qy     957  ThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeu  976
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Db    2788  ACTGGCCAGCTCTTCCACATTGACTTTGGACATATTCTTGGAAATTCAAATCTAAGTTT  2847

Qy     977  GlyIleGluLysGluArgValProPheValLeuThrProAspPheLeuPheValMetGly  996
                 ||||||            :::|||            ::::::
Db    2848  GGCATTAAAAAGGGAGCCGGAGTGCCCTTTATTCTTACCCATGATTTCATCCATGTCATTCAA  2907

Qy     997  ThrSerGlyLysThrSerLeuHisPheGlnLysHisPheGluAsnLeuLeuIleLeuLeuPheSerMetMetLeuMet  1016
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Db    2908  CAAGGAAAAACAGGAAATACAGAAAAGTTTGGCCGGTTCCGGCCAGTGTTGTGAGGATGCA  2967

Qy    1017  TyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMet  1036
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Db    2968  TATCTGATTTTACGACACGGCATGGAAATCTCTTCATCACTCTTTGCGCTGATGTTGACT  3027

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Db    3028  GCAGGGGCTTCCTGAACTCACATCACATCAGTCAAAGATATACAGTATCTTAAGGACTCCTCTTGCA  3087

Qy    1057  ValGlyLysSerGluGluLysAspAlaLysTyrPheLeuAspGlnIleGluValCysArg  1076
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Db    3088  TTAGGGAAGAGTGAAGAAGAGCACTCAAACAGTTAAGCAAAAATTTGATGAGGCGCTC  3147

Qy    1077  AspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal  1091
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Search completed: February 15, 2004, 02:33:38
Job time : 987 secs

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                       GenCore version 5.1.6
           Copyright   (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     February 15, 2004, 02:16:17 ; Search time 148 Seconds
                                        (without alignments)
                               3286.515 Million cell updates/sec

Title:          US-09-974-573-1
Perfect score:  5790
Sequence:       1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:  BLOSUM62
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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:    569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:    1139956

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09974573/runat_11022004_180015_18126/app_query.fasta_1.1287
-DB=Issued_Patents_NA  -QMT=fastap -SUFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -NORM=ext  -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -CUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974573 @CGN_1_1_71 @runat_11022004_180015_18126 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :    Issued_Patents_NA:*
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         6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	98.9	3808	2	US-08-916-917-3	Sequence 3, Appli
2	5726	98.9	3808	2	US-08-972-631-3	Sequence 3, Appli
3	5726	98.9	3808	2	US-08-972-629-3	Sequence 3, Appli
4	5726	98.9	3808	2	US-08-972-630-3	Sequence 3, Appli
5	5726	98.9	3808	2	US-08-672-211-3	Sequence 3, Appli
6	5534	95.6	3808	3	US-09-225-170-3	Sequence 3, Appli
7	5534	95.6	5162	3	US-08-916-917-13	Sequence 13, Appl
8	5534	95.6	5162	3	US-09-225-170-13	Sequence 13, Appl
9	5499.5	95.0	4137	2	US-08-817-090B-3	Sequence 3, Appli
10	5440	94.0	4134	2	US-08-817-090B-1	Sequence 1, Appli
11	1465.5	25.3	3207	1	US-08-162-081B-35	Sequence 35, Appl
12	1465.5	25.3	3207	2	US-08-780-872-35	Sequence 35, Appl
13	1465.5	25.3	3207	3	US-09-085-957-35	Sequence 35, Appl
14	1460.5	25.2	3240	1	US-08-162-081B-34	Sequence 34, Appl
15	1460.5	25.2	3240	2	US-08-780-872-34	Sequence 34, Appl
16	1460.5	25.2	3240	3	US-09-085-957-34	Sequence 34, Appl
17	1460.5	25.2	3412	1	US-08-162-081B-32	Sequence 32, Appl
18	1460.5	25.2	3412	2	US-08-780-872-32	Sequence 32, Appl
19	1460.5	25.2	3412	3	US-09-085-957-32	Sequence 32, Appl
20	1354.5	23.4	3213	3	US-09-392-350-1	Sequence 1, Appli
21	1352.5	23.4	5220	2	US-08-777-405A-1	Sequence 1, Appli
22	1352.5	23.4	5220	2	US-08-977-871A-1	Sequence 1, Appli
23	1352.5	23.4	5220	2	US-09-225-951-1	Sequence 1, Appli
24	1352.5	23.4	5220	3	US-09-84-341-1	Sequence 1, Appli
25	1350.5	23.3	3868	3	US-09-357-070-1	Sequence 1, Appli
26	1349.5	23.3	3387	4	US-09-194-640A-2	Sequence 2, Appli
27	1076.5	18.6	5285	3	US-08-609-049A-29	Sequence 29, Appl
28	1076.5	18.6	5285	3	US-09-170-996-29	Sequence 29, Appl
29	1074	18.5	5061	4	US-09-355-160D-1	Sequence 1, Appli
30	1034	17.9	3504	3	US-08-857-076-47	Sequence 47, Appl
31	874	15.1	6831	2	US-08-609-049A-27	Sequence 27, Appl
32	874	15.1	6831	3	US-09-170-996-27	Sequence 27, Appl
33	709.5	12.3	3063	3	US-09-620-312D-474	Sequence 474, App
34	690.5	11.9	3252	3	US-09-118-442-1	Sequence 1, Appli
35	690.5	11.9	3252	2	US-09-677-064-1	Sequence 1, Appli
36	382.5	6.6	393	1	US-08-162-081B-40	Sequence 40, Appl
37	382.5	6.6	393	2	US-08-780-872-40	Sequence 40, Appl
38	382.5	6.6	393	3	US-09-085-957-40	Sequence 40, Appl
39	322.5	5.6	2451	2	US-08-820-170A-29	Sequence 29, Appl
40	322.5	5.6	2451	3	US-09-055-699-29	Sequence 29, Appl
41	322.5	5.6	2451	4	US-09-273-565-29	Sequence 29, Appl
42	322.5	5.6	2451	4	US-09-565-538-29	Sequence 29, Appl
43	322.5	5.6	2451	4	US-09-661-468-29	Sequence 29, Appl
44	322.5	5.6	2451	2	US-09-976-165-29	Sequence 29, Appl
45	322.5	5.6	2487	2	US-08-820-170A-32	Sequence 32, Appl

ALIGNMENTS

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US-08-916-917-3
; Sequence 3, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/916,917
;   FILING DATE: 15-AUG-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Abrams, Samuel B
;   REGISTRATION NUMBER: 30,605
;   REFERENCE/DOCKET NUMBER: 8549-0006-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-493-4935
```

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;     TELEFAX:  650-493-5556
;     TELEX:    66141 PENNIE
; INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3808 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-916-917-3

Alignment Scores:
Pred. No.:           0          Length:       3808
Score:           5726.00        Matches:      1090
Percent Similarity:  99.46%     Conservative:    6
Best Local Similarity:  98.91%  Mismatches:      6
Query Match:         98.89%     Indels:          0
DB:                             Gaps:            2

US-09-974-573-1 (1-1102) x US-08-916-917-3 (1-3808)
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Qy     1 MetGluLeuAsnTyrGluGlnProValValArgGluAspAsnArgArgArgArg  20
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Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
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Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
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Qy    61 ValAlaGlyHisGlyAsnValGluGluMetLysGlyValTrpLeuArgAlaLeuGlu  80
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Qy   101 GlnLysLysGlyGlnTrpTyrTyrGlyLysAspLysTyrAspAspGlyGlnIleThrLeuAsp 120
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Qy   161 AspValThrAspValSerAsnValHisAspAspAspValTyrArgArgLeu 180
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Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspLysLysLeuTyrAlaMetHisPro 200
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Qy   221 PheGluValIleHisArgSerThrThrGlnIleThrLysValSerValSerArgAlaAspAspThr 240
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Db   809 CCAGGGACCATCCTCCTTTTACCCAGAGTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGlnArgAspPheAspPheValLeuArgValCysGlyArgAspGluTyr 280
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Qy   281 LeuValGlyGluThrProIleLysAspPheAsnPheGlnTrpValArgGlnCysLeuGluLeuLysAsnGly 300
           |||||||||||||||||||||||||||||||||||||||||||
Db   929 CTGGTGGGTGAGACGCCCATCAAAGATTTCAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy   301 GlyIleHisLeuValLeuAspThrProProAlaLeuAspGluValAlaArgLys 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   989 GGAGGAGATTCACCTGTGCTGGACACTCCTCCAGCACCCGACGAGGTGGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyValTyrHisGlyLeuLeuThr 340
           ||||||||||||||||||||||||||||||||||||||||||
Db  1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGCTGACC 1108

Qy   341 IleHisGlyLysAspHisGluSerValPheThrLeuSerLeuTrpAspCysAspArgLys 360
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1109 ATCCACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy   361 PheArgValLysIleArgGlyIleGluAspIleProValLeuProArgThrAlaAspLeuThr 380
           |||||||||||||||||||||||||||||||||||||||
Db  1169 TTCAGGGTGAAAATCAGAGGCATTGAATATCCCGTCCTGCCCCGGACCGCTGACCTCACG 1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnGlnValLeuCysGlnAsnArgThrSer 400
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGGCAGCAAGTCCCTTTGCCAAAGAACCAGC 1288

Qy   401 ProLysProPheThrGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
           ||||||||||||||||||||||||||||||||||||||||||||
Db  1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLeuGlyLysAlaProAla 440
           |||||||||||||||||||||||||||||||||||||||||||
Db  1349 AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProLysSerGlyLysAlaGlnLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||
Db  1409 CTGTCCGGCAAGACCTCTGCAGAGATGCCCAGTCCCAAGAGTGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
           ||||:||||||||||||||||||||||||||||||||||||||||
Db  1469 CTGTACTATGTCAACCTATTGCTCGATAGACACCGCTTCCTCCTGCGCCATGGCGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGluAspPheAsnAlaAsp 500
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysAsnSerMetSerIleSerLeuLeu 520
           ||||||||||||||||||:::||||||||||||||||||||||||||||||
Db  1589 AAGCTCACGTCGGCAACCAACCCCGACAAGAAGAGCATGTCCATCTCCATTCTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProGluGly 540
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1649 GACAATTACTGCCACCCCATAGCTTTGCCTAAGCATCGGCCTACCCCTGACCCAGAAGGG 1708

Qy   541 AspArgValArgAlaGluMetProAsnLeuArgLysGlnLeuGluAlaIleIleAla 560
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTCGGAGGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuTrpHisProPheArgTyr 580
           ||||||||||||||||||||||||||||||||||||||||||||
Db  1769 ACGGATCCCCTTAACCCACTCACAGCTGAAGACAAAGAACTGCTCTGGCATCCATTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysLysAlaTyrProLysLeuPheSerSerValValTrpGlyGln 600
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1829 GAAAGCCTGAAGGATCCCAAAGCGTAATCCTAAGCTCTTTAGCTCGGTGAAATGGGACAG 1888

Qy   601 GlnLysIleValAlaLysAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspTrpGlnSer 620
           |||||||||||||||||||||||||||||||||||||||||||||
Db  1889 CAAGAAATTGTGGCCAAAGCCAAGACCTACCAATTATTAGCCAAGAGGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuGluLeuLeuAsnAspCysAsnPheSerAspGluAspAsnVal 640
           ||||||||||||||||||||||||||||||||||||||||||
```

```
Db  1949  GCTTTGGATGTGGGGTTAACCATGATGCAGCTCCTGACTGCAACTTCTCGATGAAAACGTG  2008
                                                                              
Qy   641  ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspValLeuHisTyrLeu   660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2009  AGAGCCATTGCAGTCCAGAAACTCGAGAGAGCTTGGAGGATGATGACGTGCTCCATTACCTG  2068

Qy   661  LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaeuAlaArgPhe  680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2069  CTCCAGCTGGTCCAGGCTGTGAAATTTGAACATCAACGACAGACGTGCCCTAGCCAGATTT  2128

Qy   681  LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg  700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2129  CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGCTCACTTCTTGTTTTGGTTCTTGAGA  2188

Qy   701  SerGluIleAlaGlnSerArgHisTyrrGlnGlnIleArgPheAlaValIleLeuGluAlaTyr  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2189  AGTGAGATTGCCCAGTCCAGGCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC  2248

Qy   721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspAsp  740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2249  CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC  2308

Qy   741  MetLeuGlnLysValThrIleAspPheLysSerLeuSerAlaGluLysTyrAspValSer  760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2309  ATGTTACAAAAAGTCACCATTGACATTGACACATTAAATCGCTCCTCTGCTGAAAAGTATGACGTCAGT  2368

Qy   761  SerGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuLysAsnLeuAsnLeuAsnLeuPro  780
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Db  2369  TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAATTTGAATCCTCCC  2428

Qy   781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuAlaLeuValIleGluGlyLys  800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2429  CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAGCCGGGGCACTGTGCTGGATCGAAAAA  2488

Qy   801  CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheGluCysAlaAspPro  820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCCGATCCT  2548

Qy   821  ThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheLysHisGlyAspAspLeuArgGln  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2549  ACGGCTCTATCAAATGAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA  2608

Qy   841  AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2609  GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG  2668

Qy   861  AspLeuCysSerLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGluGlu  880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2669  GATCTGTGCTCCCTGCTACCATATGGCTGCATTGCACTGGTGACAAAATAGGAATGATCGAG  2728

Qy   881  IleValLysAspAlaThrIleAlaLysThrIleGlnSerThrValGlyAsnThrGly  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2729  ATCGTGAAGGACGCGCCACGGCAAATCGCCAAATTCAGCAAGCACAGTGGGCACACGGGT  2788

Qy   901  AlaPheLysAspPheGluValLeuSerHisTrpLeuLysGluLysLysProIleGluGluLys  920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2789  GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCATTGAAGAAAAG  2848

Qy   921  PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2849  TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT  2908

Qy   941  ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2909  GTTCTCGGAATAGGGGACAGAGGACAGACACATGACAATATTATGATCTCAGAAACAGGAAATCTA  2968

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2969  TTTCATATTGATTTCGGACACCATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA  3028

Qy   981  GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys  1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3029  GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTTGATGGGACTTCTGGAAAG  3088
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Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysSerValAlaTyrLeuAlaLeu  1020
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Db  3089  AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT  3148

Qy  1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetLeuMetThrGlyMetPro  1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3149  CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATCCTGATGACAGGAATGCCC  3208

Qy  1041  GlnLeuThrSerLysGluAspIleLeuArgAspAlaLeuThrValGlyTyrrValGlyLysSer  1060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3209  CAGTTAACCAGCAAAGAAGACATTGAATACATTGGGGATGCCCTCACAGTGGGCAAAAGT  3268

Qy  1061  GluGluAspAlaLysTyrPheAspLysLeuLeuAsnIleLysCysArgGlyAspAspLysGlyGlyTrp  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3269  GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG  3328

Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGlyLysHis  1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3329  ACCGTGCAGTTTAACTGGTTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT  3388

Qy  1101  SerAla  1102
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Db  3389  CCCGCA  3394
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RESULT 2
US-08-972-631-3
; Sequence 3, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/972,631
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3808 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
US-08-972-631-3

Alignment Scores:
Pred. No.:   Length: 3808
Score: 0   5726.00   Matches: 1090

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Percent Similarity:    99.46%        Conservative:  6
Best Local Similarity: 98.91%        Mismatches:    6
Query:                 98.89%        Indels:        0
DB:                    2             Gaps:          0

US-09-974-573-1 (1-1102) x US-08-972-631-3 (1-3808)

Qy     1 MetGluLeuAsnTyrGluGlnProValLeuArgGluArgAspAsnArgArgArgArg     20
Db    89 ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGCGAGAGAGACAACGCCGCAGGCGT    148

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluIleProIle       40
Db   149 CGGAGGATGAAGCCGCGCAGCACCGCAGCCAGCCTGTCCTCCATGGAGATCCCCATC    208

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
Db   209 GAGTTTGTTTTGCCCACATCACAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC 268

Qy    61 ValAlaGlyHisGlyAsnValGluGlnIleMetLysAlaGlnIleValTrpLeuArgAlaLeuGlu  80
Db   269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTTGTGGCTGCGCGCCCTGGAG    328

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
Db   329 ACGAGCGTTTCTTGGGACTTCTACCACCGGTTGGGCCCCGACCACTTCCTCCTGGTCTTC 388

Qy   101 GlnLysLysSerGlyGlnTrpTyrGluIleTyrArgAspLysTyrGlnValValGlnThrLeuAsp 120
Db   389 CAGAAGAAGGGGGAGTGGTACGAGATCTATAGAGACAAGTACCAGGTGGTACAGACCCTGGAC    448

Qy   121 CysLeuArgGlyTyrTyrGlnIleTyrGlyGlnIleLeuHisValValGlnArg           140
Db   449 TGCCTGCGCTACTGGGAGGTGTGCAGATCCAGTGGTGCACGTGGTCAGCGG             508

Qy   141 HisAlaProSerGluGluThrGlnLeuPheGlnInArgGlnLeuAlaAsnAlaLeuIleGlyLeuTyr 160
Db   509 CACGCGCCCTCGGAGGAGACCCAGCTGTTCCAGGCGCAGCTCAACGCGCTCATCGGTAC       568

Qy   161 AspValThrAspValSerAsnValHisAspAspGluPheThrArgArgArgLeu          180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGGAGTTCACGCGGCGCCTG       628

Qy   181 ValThrProArgMetAlaGlyValAlaGlyAlaGlyTyrArgAspProLysLeuTyrAlaMetHisPro 200
Db   629 GTCACCCCCAGGATGGCCGGAGGTGCCGGCGCCGGCTACCGCGACCCCAAGCTTTACGCCATGCACCCC 688

Qy   201 TrpValThrSerLysProGluProGluLeuProLysTyrLeuLysLysIleThrAsnAsnCysVal 220
Db   689 TGGGTGACATCCAAGCCCCCCGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC       748

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysSerValSerAlaAspAspThr 240
Db   749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCCGGCCGATGACACC    808

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp       260
Db   809 CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAGAATCTCTGATGAT    868

Qy   261 IleProGluSerGlnAsnGluArgAspPheValArgGlnCysLeuLysValArgAspGly   280
Db   869 ATCCCTGAAAGCCAGAACGAACAAGGGAGACTTGTGCGCCAGTGCCTCAAGAATGGG      928

Qy   281 LeuValGlyThrProIleLeuLysAsnPheGlnTrpLeuArgGlnCysLeuLysLysAsnGly 300
Db   929 CTGGTGGGTGGAGACGCCCCATCAAAATTTCCAGTGGGTAGGCAGTGCCTCAAGAAATGGG   988

Qy   301 GluGlnIleHisLeuValGlnAlaValPheGluLeuProAlaGluLeuAspGluValArgLys 320
Db   989 GAGGAGATTCACCTTGTCGTGGAGACTTCTCCAGCACCCCAGCCCGAGACGAGGTGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyLysTyrHisGlyValThrGlyHisGluGlnLeuThr 340
Db  1049 GAAGAGTGGCCGCTGGTGATGACTGCACGGGAGTCACTGGCTACCAGCAGCTGACC 1108

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
Db  1109 ATCCACGGCAAGGACCATGAAAGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
Db  1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCCGTCCTGCCCCGGACCGCTGACCTCACG 1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer 400
Db  1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGGTGCTGTGCCAAAGGAGAACCAGC 1288

Qy   401 ProLysProPheThrGluValLeuTrpAsnValTrpProGluThrAlaLeuLeuHis 420
Db  1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCCTGAGTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuIleTyrCysGlyLysAlaProAla 440
Db  1349 AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
Db  1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGTCCAAAGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
Db  1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCTGCGCCATGGGGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlnAspGlnGlySerPheAsnAlaAsp 500
Db  1529 GTGCTCCACATGTGGCAGTTATCCGGAAGGGGAAGACCAAGGAGACTTCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
Db  1589 AAGCTCACGTCGGAACCACCCGACAAGGAGAACTCAATGTCCATCTCCATTCTTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProGluGlyGly 540
Db  1649 GACAATTACTGCCACCCCATAGCCTTGCCCAAGCATCGGCCTACCCCTGACCCAGAAGGG 1708

Qy   541 AspArgArgAlaGlyMetAlaGluMetProAsnGlnLeuArgLysGluLeuTrpHisAla 560
Db  1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuTyrLysGluLysLeuTrpHisPheArgTyr 580
Db  1769 ACGGATCCCCTTAACCCACTCTACAAGGAGAAGCTGTGGCATTTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysProAlaTyrProLeuPheSerSerValLysTrpGlyGln 600
Db  1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy   601 GlnGluIleAlaAlaLysThrArgTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
Db  1889 CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTGCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
Db  1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaValGlnLysLeuSerLeuGluAspLysAspValHisTyrLeu 660
Db  2009 AGAGCCATTGCAGTCCAGAAACTGGAGAGCTTGGAGGATAAGGATGTGCTCCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaValPheGluLeuProTyrHisAspSerAlaLeuArgArgPhe 680
Db  2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy   681 LeuLeuLeuArgGlyLeuLysAsnLysArgIleGlyHisPheLeuTrpPheLeuArg 700
Db  2129 CTGCTGCTGAGGGGTGGTTAAGAAAACAAGAGAATTGGTCACTTCTTGTTTTGGTTCTTGAGA 2188
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Qy  1061 GluGluGluAlaLysTyrTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
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Db  3269 GAGGAGGATGCTAAAAGTATTTTCTTGGATCAGATGAAGTTGGAGAGACAAAGATGG 3328

Qy  1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyTyrIleLysGlnGluLysHis 1100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAGCAAGAGGAGAAGCAT 3388

Qy  1101 SerAla 1102
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Db  3389 CCCGCA 3394
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RESULT 3
US-08-972-629-3
; Sequence 3, Application US/08972629
; Patent No. 5859201
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/972,629
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hallwin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3808 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
US-08-972-629-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: Gaps: 0

US-09-974-573-1 (1-1102) x US-08-972-629-3 (1-3808)

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Qy    1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAsnArgArgArgArg 20
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Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGAGAGAGGAGAACCGCCAGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
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Db  3209 CAGTTAACCAGCAAAGAAGACATAAAGTACATCCGGGATGCCCTCACAGTGGGCAAAAGT 3268
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Qy  701 SerGluIleAlaGlnSerArgHisTyrArgGlnArgPheAlaValIleLeuGluAlaAlaTyr 720
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Db 2189 AGTGAGATTGCCCAGTCTCGGCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy  721 LeuArgGlyCysCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp 740
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Db 2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAGTAATTGAC 2308

Qy  741 MetLeuGlnLysValThrIleLysAspIleLysSerLeuSerGluSerAlaGluLysTyrAspValSer 760
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Db 2309 ATGTTACAAAAAGTCACCATTAAATCGCTCTCTGCTGAAAAGTATGACGTCAGT 2368

Qy  761 SerGlnValIleSerGlnLeuLysGlnLeuLysLeuGlnAsnLeuGlnAsnLeuAsnLeuPro 780
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Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAAATTTGAATCTCCC 2428

Qy  781 GlnSerPheArgValProTyrAspProGlyLeuLysSerAlaGlyValAlaLeuValIleGluGlyLys 800
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Db 2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAAGCGGGGCACTGGTGATCGAAAAA 2488

Qy  801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
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Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCCGACCCT 2548

Qy  821 ThrAlaLeuSerArgAsnGluThrIleGlyTyrIleGlyPheLysHisGlyAspAspLeuArgGln 840
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Db 2549 ACGGCTCTCATCAAATGAAACAATTGGAATTATCTTAAACACGGTGACGATCTGCGCCAA 2608

Qy  841 AspMetLeuIleLeuGlnIleLeuGlnArgIleMetGluSerIleTrpGluSerLeu 860
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Db 2609 GACATGCTTATTTTACAGATTCTACAGAGTCCCATTTGGGAGACCGAATCTTTG 2668

Qy  861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspAspLysIleGlyMetIleGlu 880
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Db 2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAAATAGGAATGATCGAG 2728

Qy  881 IleValLysAspAlaThrThrIleAlaAlaLysIleIleGlnGlnSerThrValGlyAsnThrGly 900
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Db 2729 ATCGTGAAGGACGGCCACGACACCAATCGCCAAAATTCAGCAAAGACCAGTGGGCAACACGGGT 2788

Qy  901 AlaPheLysGluValValLeuSerHisProLeuLysGlyGluLysLysCysProIleGluGluLys 920
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Db 2789 GCCTTTAAAGATGAAGTCGTGCTCAGCCATCCATTGAAGGGTCAAAGAAAATGCCCTATTGAAGAAAAG 2848

Qy  921 PheGlnAlaAlaValAlaValArgPheValAlaArgGlyTyrSerCysValAlaGlyTyrCysValAlaThrPhe 940
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Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTGCTCGTGGCTACTGTGTGCGCAACCTTT 2908

Qy  941 ValLeuGlyTyrIleGluGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
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Db 2909 GTTCTCGGAATAGGCGACAGACAGAACCAACAATATTATGATCTCAGAAACACAGGAAATCTA 2968

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2969 TTTCATATTGATTTCGGACACATCTTGGAATTACAAAAGTTCCTGGGCATTAATAAA 3028

Qy  981 GluArgValProPheValLeuProArgProAspPheProPheValMetGlyThrSerGlyLysLys 1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3029 GAGAGGGTTGCCATTTGTGCTAACCCCAGACTTCCTGTTGTTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerPheLeuHisPheGlnLeuLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTGAAGGCTTACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrAsnLeuIleLeuIleLeuPheSerMetMetLeuThrGlyMetPro 1040
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Db 3149 CGTCATCACACAAACCTACTGATCATCCTTTTTCCCATGATGCTGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspIleLysTyrIleArgAspAlaLeuThrValGlyLysSer 1060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3209 CAGTTAACCAGCAAAGAAGACATAAAGTACATCCGGGATGCCCTCACAGTGGGCAAAAGT 3268
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Qy  401  ProLysProPheThrGluValLeuTrpGluAsnValTrpLeuGluPheSerIleLysIle 420
         CCCAAACCCTTCACGGAGGAGGTGCTCTGGGAAAACGTGTGGCTTGAGTTCAGTATTAAAATC
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Db 1289                                                              1348

Qy  421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyValLysAlaProAla 440
         AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA
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Db 1349                                                              1408

Qy  441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
         CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCAGAGTCCAAAGGCAAAGCTCAGCTT
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1409                                                              1468

Qy  461  LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
         CTGTACTATGTCAACCTATTGCTAGATCACCGCTTCCTCCTGCGCCATGGCGAGTAT
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Db 1469                                                              1528

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyLysAspGlnGlySerPheAsnAlaAsp 500
         GTGCTCCACATGTGGCAGTTATCCGGGAAGGGAGGAGACCAAGGGAGCTTCAATGCCGAC
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Db 1529                                                              1588

Qy  501  LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
         AAGCTCACGTCGGGAACCAACCCGGACAAGGAGAACTCAATGTCCATCTCCATTCTTCTG
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Db 1589                                                              1648

Qy  521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
         GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCTACCCCTGACCCAGAAGGG
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Db 1649                                                              1708

Qy  541  AspArgAlaArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGlnLeuGluIleIleAla 560
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Db 1709                                                              1768

Qy  561  ThrAspProLeuAsnProLeuThrAlaGluLysProLysTrpHisPheArgTyr 580
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Db 1769                                                              1828

Qy  581  GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
         GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTAGCTCGGTGAAATGGGGACAG
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Db 1829                                                              1888

Qy  601  GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaAlaArgGluValTrpAspGlnSer 620
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Db 1889                                                              1948

Qy  621  AlaLeuAspAlaValGlyLeuThrMetGlnLeuLeuAsnLeuAspCysAsnPheSerGluAsnVal 640
         GCTTTGGATGCTGTGGGTTAACCAGCTCCTGAACCTTGACTGCAACTTCTCGGATGAAAACGTG
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Db 1949                                                              2008

Qy  641  ArgArgAlaIleGlnLysGluLeuGlnAsnProGlnAspAlaValIleLeuGluHisTyrLeu 660
         AGAGCCATTCAGTCCAGAAAACTGGAGAGGTTGGAGGATGATGACGTCCATTACCTG
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Db 2009                                                              2068

Qy  661  LeuGlnLeuValGlnAlaValLysProGluThrTyrHisSerAlaLeuAlaArgPhe 680
         CTCCAGCTGGTCCAGGCTGTGAAATTGAACCATACACAGTGCCCTAGCCAGATTT
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Db 2069                                                              2128

Qy  681  LeuLeuLeuArgGlyLeuArgAsnLeuValArgIleGlyHisPheLeuGlyHisPhePheLeuArg 700
         CTGCTGAAGCGTGGTTAAGAAACAAGAAATTGGTCACTTCTTGTTTGGTTCTTGAGA
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Db 2129                                                              2188

Qy  701  SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaTyr 720
         AGTGAGATTGCCCAGTCTCAGGCACTATCAGCAGAGGTTTGCAGTATCCTGGAAGCCTAC
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Db 2189                                                              2248

Qy  721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrArgGlnValIleValIleAsp 740
         CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTAATTGTGATTGAC
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Db 2249                                                              2308

Qy  741  MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluGlyLysTyrValSer 760
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Db 2309                                                              2368
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Db  149  CGGAGGATGAAGCCGGCGGCAGACGGCAGCCAGCCTGCCTGCCTCATCCCCATC  208

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         GAGTTTGTTTTGCCACCAGCCAGCGCAACACCAAGACCCCGAAACGGCACTGCTGCAC
Db  209                                                              268

Qy   61  ValAlaGlyLyHisGlyAlaAsnValGluGlnMetLysAlaGlnMetLysTrpLeuArgArgLeuGlu 80
         GTGGCCGGCCACGGCAATGTGGAAGAGATGAAGGCCCAGGTGTTGTTGCGGCGCTGGAG
Db  269                                                              328

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         ACGAGCGTTTCTTGGGACTTCTACCACCGGTTCGGCCCCGACCACTTCCTCCTGGTCTTC
Db  329                                                              388

Qy  101  GlnLeuLysSerGlyGlnThrTrpTyrGluLeuTyrGlnIleTyrArgAspLysTyrGlnIleTyrAsp 120
         CAGAAGAGGGGAGTGGTACAGAATTCATGACAAGTACCAAGGTGTGCAGACCCTGGAC
Db  389                                                              448

Qy  121  CysLeuArgArgTyrTrpLysValValLeuHisArgSerProGlyIleAsnIleHisValValGlnAsnArg 140
         TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCGGGGATCAATCACGTGGTCCAGCGCGG
Db  449                                                              508

Qy  141  HisAlaProSerGluThrGluArgLeuAlaPheGlnLeuArgGlnLeuAsnAlaLeuIleGlyTyr 160
         CACGCGCCCTCGGAGGAGACAGAGCGCCTCGCCTTCCAGCTCAACGCGCTCATCGGCTAC
Db  509                                                              568

Qy  161  AspAspValThrAspValSerArgSerAlaValHisAspAspGluLeuGluPheThrArgArgLeuGlu 180
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Db  569                                                              628

Qy  181  ValThrProArgMetAlaAlaGluGlyValValAlaGlyProLeuTyrArgAspGlyLeuTyrAlaMetHisPro 200
         GTCACCCCGCGCATGGCCGAGGTGGCCCGGCACCCCGGACGTTTACGCCCATGCACCCC
Db  629                                                              688

Qy  201  TrpValThrSerLysProGluLeuProGlyProGluTyrLeuLeuLysLysTyrIleIleThrAspAsnAsnCysVal 220
         TGGGTGACATCAAGCCCTCCGAGTACCTCCTGAAGAAGATACTAACAACTGCGTC
Db  689                                                              748

Qy  221  PheIleIleHisArgSerThrThrSerGlnThrIleLeuTyrLeuValSerAlaAspAspThr 240
         TTCATCGTCATTCACCGCAGTACCACCAGCCAAGGTGTCGGCCGATGACACC
Db  749                                                              808

Qy  241  ProGlyThrIleLeuGlnLeuAsnGlnArgGlyAspPheValLeuArgAspCysValCysGlyLysArgAspGluLysSerLeuMetAsp 260
         CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAGAAATCCTGATGGAT
Db  809                                                              868

Qy  261  IleProGluSerGlnLeuAsnGlnArgLeuArgLeuAspPheHisValCysTrpArgArgGluLeuValCysGlyLyArgGluGluTyr 280
         ATCCCTGAAAGCCAGAACGGAGAACCCAGACTTTGTTGTGTCGGCGCTGCCGGCGGATGAGTAC
Db  869                                                              928

Qy  281  LeuValGlyLysLysAspHisIleGluAsplLeuAspThrProLysSerLeuPheThrValPheLysGlnGlnCysLeuLysAsnGly 300
         CTGGTGGGGAAGAAGGACCGCATCCCCATCAAAAATTTCCAGTGGGGAGGCAGTGCTCTCAAGAATGGG
Db  929                                                              988

Qy  301  GluGluIleHisLeuValLeuAspAspThrProProAlaAlaLeuAspAspProGlnProLysValValArgLys 320
         GAGGAGATTCACCTTGTGCTGGACGACACTCCCTCCGCAGCCCTGGACGAGGTGAGGAAG
Db  989                                                              1048

Qy  321  GluGlnTrpProLeuAsnGlnArgLeuArgLeuAspAspPheValCysThrGlyVaLThrGlyTyrTyrHisGlyGlnLeuGlnLeuThr 340
         GAAGAGTGGCCGCTGGTGATGACAGCAAGCTCACTGGCTACCACCGAGCAGCTGACC
Db 1049                                                              1108

Qy  341  IleHisGlyLysLysAspHisGlySerValPheThrValPheThrProLysGlnSerLeuTrpAsnProCysTyrAspCysValAspArgLys 360
         ATCCACGGCAAGGACCACCATGAACGTGTTCACCCCTAAAGCAGAAAATGTCTGGGACTGTGACCGCAAG
Db 1109                                                              1168

Qy  361  PheArgValLysSerIleArgGlyIleIleAspTyrTyrIleleProProArgLeuProArgArgValProThrArgAlaAspLeuLeuThr 380
         TTCAGGGTCAAAATCAGGAGGGCCATTGAATATCCCTATCCTCCTCGGGTACCACCGTGCTGAGGACCTGACCTTCACG
Db 1169                                                              1228

Qy  381  ValPheValGluAlaAsnIleGluAspGlnIleTyrGlyGlnIleGlnValLeuCysGlnLeuValLeuGlnArgThrSer 400
         GTGTTTGTGGAGGCCAAACATCCAGTATGGGCCAAGGACGTCCTTTGCCAAGGGAACCAGC
Db 1229                                                              1288
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US-08-972-630-3
; Sequence 3, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds
;     STREET: 2730 Sand Hill Road
;     CITY: Menlo Park
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94025
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/972,630
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/672,211
;     FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Halluin, Albert P.
;     REGISTRATION NUMBER: 25,277
;     REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415)854-3660
;     TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 3808 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
US-08-972-630-3
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Alignment Scores:
Pred. No.:                   0              Length:          3808
Score:                    5726.00          Matches:         1090
Percent Similarity:        99.46%          Conservative:       6
Best Local Similarity:     98.91%          Mismatches:         6
Query Match:               98.89%          Indels:             0
DB:                           2            Gaps:               0
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US-09-974-573-1 (1-1102) x US-08-972-630-3 (1-3808)

Qy    1 MetGluLeuAsnTyrArgGluGlnProValValArgLeuArgGluAspAsnArgArgArgArg   20
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Db   89 ATGGAGCTGGAGAACTATAGAGAACAGCCCGTGGTGCTGAGGAGGACAACCGCCGCAGGCGT  148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerArgLeuSerSerMetGluSerIleProIle   40
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Db  149 CGGAGGATGAAGCCGCGCAGCACGGCAGCGTCCCGTCCTCCCATGGAGTCCATCCCCATC   208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis     60
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Db  209 GAGTTTGTTTTGCCCACCAGCCAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC   268

Qy   61 ValAlaGlyHisGlyAsnValGluGluMetLysAlaGlnValTrpLeuArgAlaLeuGlu     80
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Db  269 GTGGCCGGCCACGGCAATGTGGAAGAAATGAAGGCCCAGGTGTTGTGCGCGTGGAG       328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
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Db  329 ACGAGCGTTTCTGGGACTTCTACCACCGGTTCGGCCCCGACCACTTCCTCCTGGTCTTC   388
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Qy  761 SerGlnValIleSerGlnLeuLysGlnLeuLeuGluAsnLeuGlnAsnLeuAsnLeuPro    780
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Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAGCTTGAAAACCTACAGAATTTGAATCTCCCC   2428

Qy  781 GlnSerPheArgValProTyrAspProGlyLeuLeuLysAlaGlyValAlaLeuValIleGluLys  800
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2429 CAAAGCTTAGATGTTCCCTATGATCCTGGACTTGAAACGCCGGGCACTGGTGATCGAAAAA  2488

Qy  801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro    820
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Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAAATGTGCCGATCCT  2548

Qy  821 ThrAlaLeuSerAsnGluThrIleGlyTyrIleIleGlyHisGlyAspLeuArgGln      840
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Db 2549 ACGGCTCTATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA   2608

Qy  841 AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu   860
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTGGGAGACCGAATCTTTG   2668

Qy  861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu    880
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGTGACAAAATAGGAATGATCGAG   2728

Qy  881 IleValLysAspAlaThrThrIleAlaLysAsnIleGlnIleSerThrValGlyAsnThrGly  900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2729 ATCGTGAAGGACGCCACGACAATCGCACAAAATCAGCAAAGCACAGTGGGCAACACGGGT   2788

Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys    920
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Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG   2848

Qy  921 PheGlnAlaAlaValGlyArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe    940
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2849 TTTCAGGCAGCTGTGGGAAGATTTGTTTATTCCTGCGCCGGCTACTGTGTGGCAACCTTT   2908

Qy  941 ValLeuGlyTyrIleGlyTyrAspAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2909 GTTCTCGGAATAGGCGACAGACAAATGACAATTATGATCTTCAGAAAACAGGAAATCTA   2968

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys    980
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTTGGCATTAATAAA   3028

Qy  981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys   1000
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGAACTTCTGGAAAG   3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnIleAsnValCysValLysAlaTyrLeuAlaLeu 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGATGTCTCGCTCAAGGCTTACCTAGCCCTT   3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro     1040
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3149 CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC   3208

Qy 1041 GlnLeuThrSerLysGluAspPheIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3209 CAGTTAACCAGCAAAGAAGACATTATAGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT 3268

Qy 1061 GluGluAspAlaLeuLysLysTyrPheLeuAspLeuLeuAsnTrpGlnIleGluValCysArgArgAspGlyTrp 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAAGGATGG   3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLysGlyGluLysHis   1100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3329 ACCGTTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGGCATCAAAAAAGGGGAGAAGCAT   3388

Qy 1101 SerAla                                                         1102
        ||||||
Db 3389 CCCGCA                                                         3394
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RESULT 4

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Qy  101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
        CAGAAGAAGGGGGAGTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC
Db  389                                                               448

Qy  121 CysLeuArgTyrTrpLysValLeuValLeuHisValValGlnArg               140
        TGCCTGCGCTACTGGGAGGTGTTGCACGTGGTTCAGCGCGG
Db  449                                                               508

Qy  141 HisAlaProSerGluGluThrLeuGlnThrLeuAlaPheGluAsnLeuAsnAlaLeuIleGlyLysTyr  160
        CACGCGCCCTCGGAGGAGACCATTGGCCTTCCAGCGCGCAAGGCGCCCTCAACCGCCTCAACGGCTAC
Db  509                                                               568

Qy  161 AspValThrAspValSerAsnValHisAspAspProLysLysGluLeuGluPheThrArgArgLeu  180
        GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGGAGTTCACGCGGCGGCCGCTG
Db  569                                                               628

Qy  181 ValThrProArgMetAlaGluValValAlaAlaGlyArgAspProLysLeuTyrArgAlaMetHisPro  200
        GTCACCCCGCGCATGGCCGAGGTGGCCGCGGCAGGCCGCGACCCCAAGCTTTACCGCGCCATGCACCCC
Db  629                                                               688

Qy  201 TrpValThrSerLysTyrProGluProLeuTyrLeuValLeuLysLysLysIleThrAlaAsnCysSerVal  220
        TGGGTGACCAGCAAGTACCCCGAGCCCCTGTATCTGGTTCTGAAGAAGAAGATCACTAACACTGCGTC
Db  689                                                               748

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleThrLeuLysValSerAlaAspAspThr  240
        TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC
Db  749                                                               808

Qy  241 ProGlyThrIleLeuGlnSerPheThrPheLysMetAlaLysLysSerLeuMetAsp  260
        CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT
Db  809                                                               868

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValGlyTyrArgGlyGluTyr  280
        ATCCCTGAAAGCCAGAACGAACGAGGACTTTGTGCTCCGCGTCGGCTACCGCGGGGATGAGTAC
Db  869                                                               928

Qy  281 LeuValGlyGluThrProIleLysProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
        CTGGTGGGCGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG
Db  929                                                               988

Qy  301 GluGlnIleHisLeuValLeuValAspThrProAspProAlaLeuAspGluAspProLysGluLeuArgGlyLys  320
        GAGGAGATTCACCTTGGTGCTGGTCGACACTCCTGACCCTGCCCTGGGACGTGACGAGGAAG
Db  989                                                              1048

Qy  321 GluGluLeuProLeuValAlaAspCysGlyArgGlyThrGlyTyrValThrGlyTyrHisGluGlnLeuLeuThr  340
        GAAGAGTTGCCGTTGGTCGCTGGATGACTGTGGCGTACGTCACCGGCTACCATGGTGGTGAGCAGCTGGAGCT
Db  1049                                                             1108

Qy  341 IleHisGlyLysAspHisProGluSerValPheThrValPheThrLysSerValPheThrAspCysTrpArgLys  360
        ATCCACGGCAAGGACCATGGAGTCTGTTCCTTTCACCGTGTTTACCAAGAGTGTCTTTGGGGACTGCTGGAGG
Db  1109                                                             1168

Qy  361 PheArgValIleIleGlyValAspAspIleProValLeuProValLeuProArgAlaArgThrAlaAspLeuThr  380
        TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTCCCCGTCCTGCCGCGAGCACGCACCGCTGACCTCACG
Db  1169                                                             1228

Qy  381 ValPheGlnValGluLeuAlaAsnIleGlnTrpTyrGlyTyrGlnGlnValLeuCysGlnIleAsnArgThrSer  400
        GTGTTTGTTGGAGGTGGAGCTGGCCAACATCCAGTGGTATGGGCAGCAAGTCCTTTGCCAAAGGAACCAGC
Db  1229                                                             1288

Qy  401 ProLysProPheThrGluValGluLeuValAlaLeuSerTrpAsnValPheLeuGluProSerSerIleLeuIle  420
        CCCAAACCCTTCACCGAGGTGGAGCTGGTGGCCCTGTCCTGGAACGTGTTCCTAGAACCCTCATCCATATTAAATC
Db  1289                                                             1348

Qy  421 LysAspLeuProLysGlyLeuAlaLeuAsnLeuGlnAsnIleTyrCysGlyLysLysAlaProAla  440
        AAAGACTTACCCAAAGGGGCTCGCACTCAACCTCAACATCTACTGCGGCAAAGCTCCAGCA
Db  1349                                                             1408

Qy  441 LeuSerGlyLysValThrSerArgSerAlaGluMetProSerProLysGlySerLysLysGlyLysAlaGlnIleLeu  460
        CTGTCTGGGAAGAGTCACCTCTGCAGAGATGCCCAGCCCCAAAGGCTCCAAGAAAGGCAAAGCTCAGCTT
Db  1409                                                             1468


Qy  461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr            480
        CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCGCGCCATGGGCGAGTAT
Db 1469                                                              1528

Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyLeuAspGlnGlySerPheAsnAlaAsp      500
        GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC
Db 1529                                                              1588

Qy  501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu      520
        AAGTCACGTTCGGGAACCAACCCGGACAAGGAGACTCAATGTCCATTCCATTCTTCTG
Db 1589                                                              1648

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly      540
        GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCTACCCCCTGACCCAGAAGGG
Db 1649                                                              1708

Qy  541 AspArgValAlaGluMetProAsnGlnLeuArgLysGlnLeuGlnAlaIleIleAlaAla      560
        GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAATCATAGCC
Db 1709                                                              1768

Qy  561 ThrAspProLeuAsnProLeuThrAlaGluAspProLysGluLeuTrpHisPheArgTyr      580
        ACGGATCCGTTAAACCCACTCACAGCTGAAGACCAAAAGAACTGCTCTGGAAATGGGACAGT
Db 1769                                                              1828

Qy  581 GluSerLeuLysAspProLysLeuPheSerSerValLysTrpGlyGln                 600
        GAAAGCCTTAAGGATCCCAAAGGCGATCCCAAGCTCTTTAGCTCGGTGAAAATGGGACAG
Db 1829                                                              1888

Qy  601 GlnGluIleValGlyIleLysThrTyrGlnLeuLeuLeuAlaLysArgGluValIleTrpAspTrpGlnSer  620
        CAAGAAATTGTGGCAAAACATCACCAATTATTAGCCAAAAGGGAAGGGAGGTCTTGGGATCAGAGT
Db 1889                                                              1948

Qy  621 AlaLeuAspArgValGlyTyrLeuThrMetGlnLeuLeuAsnLeuAspProCysGlyAsnPheSerAspGluAsnVal  640
        GCTTTGGATGGGGTTAACCATGATGAGCAGTCCTGGACTGGAACTTCTCGGATGAAAACGTG
Db 1949                                                              2008

Qy  641 ArgAlaIleAlaValGlnLysValGlyLeuGluSerLeuGluAspLeuGlnHisTyrArgLeu            660
        AGAGCCATTGCAGTCGAGTCCGAGAAACTGGAGAGCTTGGAGGATGAGACTGTGCTCCATTACCTG
Db 2009                                                              2068

Qy  661 LeuGlnLeuValLeuAlaValLysPheGluHisProTyrHisAspSerAlaLeuAlaLeuArgPhe           680
        CTCCAGCTGGTGCAGGCTGTGAAATTTGAACCATGACAACCATGACAGTGCCCTAGCCAGCCAGATTT
Db 2069                                                              2128

Qy  681 LeuLeuLeuArgGlyTyrLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg             700
        CTGCTGGAGCGGGTGGTTTAAGAACAAGAGAATTGGTCACTTCTTGTTTTGGTTCTTGAGA
Db 2129                                                              2188

Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnLeuArgPheAlaValIleLeuGlnLeuAlaLeuTyr           720
        AGTGAGATTGCCCAGTCCAGTCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC
Db 2189                                                              2248

Qy  721 LeuArgGlyCysGlyTyrThrAlaMetLeuHisAspSerPheThrGlnGlnValIleGlnValIleAspAsp        740
        CTGAGGGGCTGTGGCTACACAGCCATGCTGCACGACTCGCGACTTCACCCCAGCAAGTTAATTGAC
Db 2249                                                              2308

Qy  741 MetLeuGlnLysValThrIleLysAspIleLysSerLeuSerArgAlaGluGlyLysTyrArgAspValSer        760
        ATGTTACAAAAAGTCACCATTAAAGACATTAAAAGTCTGTCTCGTGCTGAAAAGATGACGTCAGT
Db 2309                                                              2368

Qy  761 SerGlnValIleIleSerGlnAsnLysGlyLeuAsnGluGlnAsnLeuAsnLeuPro            780
        TCCCAAGTTATTTCCCAACTTAAGCAAAACAAAGGTTGAAAACCTACAGATTTGAAATCTCCCC
Db 2369                                                              2428

Qy  781 GlnSerPheArgValProTyrAspProValLeuTyrLeuAlaGlyTyrAlaLeuuValLysIleGluGluLys       800
        CAAAGCTTTAGAGTTCCCTATGAATCCTGTAGACCTGTATCTGGCTGGTTATGCCCTTGTTAAAATTGAGGAAAA
Db 2429                                                              2488

Qy  801 CysLysValMetAlaSerLysHisTrpLeuSerProLeuuTrpLeuLysPheCysAlaAspPro        820
        TGTAAAGTGATGGCCTCCAAGCACTGGCTTAGCCCTTTAAATGTGCCGATCCT
Db 2489                                                              2548

Qy  821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyIleAspAspLeuArgGln        840
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STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-672-211-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 2   Gaps: 0

US-09-974-573-1 (1-1102) x US-08-672-211-3 (1-3808)

Qy   1 MetGluLeuGluAsnTyrGluGlnProValLeuArgLeuArgGluAspAsnArgArgArgArg 20
Db   89 ATGGAGCTGGAGAACTACGAGCAGCCCGTGCTGCGTGCTGCGAGAGGAGGAGCAACCGCCGCAGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
Db   149 CGGAGGATGAAGCCGCGGTCGACACGGCAGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
Db   209 GAGTTTGTTTTGGCCACCAGCCAGCGGAACACCAAGACCCCGGAAACCGGCACTGCTGCAC 268

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
Db   269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTTGTTGCGCGGCCTGGAG 328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisArgLeuLeuLeuTyr 100
Db   329 ACGAGCGTTTCTTGGACTTCTACCACCGGTTCGGCCCCGACCACCTTCCTCCTGGTCTTC 388

Qy   101 GlnLysLysGlyGlnTrpTyrTyrGluIleTyrArgLysTyrArgGlnValValGlnThrLeuAsp 120
Db   389 CAGAAGAAGGGGGAGTGGTACGAGATCTATGACAAGTACCAGGTGTGCAGACCCTGGAC 448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisArgValGlnArg 140
Db   449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy   141 HisAlaProSerGluThrGluThrLeuAlaPheIleArgGlnLeuAsnAlaLeuIleGlyTyr 160
Db   509 CACGGCGCCCTGCAGGAGACAGATTGGCCTTCAAGCGCCCTCATCCGCTAC 568

Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluThrArgArgLeu 180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGAGCATGAGGTTCACGCGGCGCCCCTG 628

Db   2549 ACGGCTCATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACCATCTGCGCCAA 2608
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
Db   2609 GACATGCTTATTTTACAGATTCTACTACGAGATCATGAGTCCATTGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuLeuProTyrArgGlyCysIleSerThrGlyLysAspLysIleGlyMetIleGlu 880
Db   2669 GATCTGTGCCTCCTGCCATATGGCTGCATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaAlaIleAlaLysIleGlnInSerThrValGlyAsnThrGly 900
Db   2729 ATCGTGAAGGACGACGCCACGACCATCGCCAAAATTCAGCAAAGACAGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
Db   2789 GCCTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCATTGAAGAAAAG 2848

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysValAlaGlyTyrCysValAlaThrPhe 940
Db   2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGCGTGGCTACTGTGTGGCAACCTTT 2908

Qy   941 ValLeuGlyIleGlyLysAsnAspAsnIleMetIleSerGluThrGlyLeuAsnLeu 960
Db   2909 GTTCTCGGAATAGGCGACAGACCAATGACCAATTATGAATCTCAGAAACAGAAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db   2969 TTTCATATTGATTTCGGACACATTCTTGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db   3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy   1001 LysThrSerLeuHisPheGlnLysPheGlnInAspValCysValLysAlaTyrLeuAlaLeu 1020
Db   3089 AAGACAAGCTACACTTCCAGAAATTTCCAGAAGGATGCTCTGCGTGTCAAGGCTTACCTAGCCCTT 3148

Qy   1021 ArgHisHisThrAsnLeuLeuIleLeuIleLeuGluPheSerMetLeuMetThrGlyMetPro 1040
Db   3149 CGTCATCACCAACCTACTGATCATCCTTCTCCATGAGTCCATGCTGATGACAGGAATGCCC 3208

Qy   1041 GlnLeuThrSerLysGluAspSerIleGluTyrIleGluAspAlaAlaThrValGlyLysSer 1060
Db   3209 CAGTTAACCAGCAAAGAGAGACAGAGAGAATACAATCCGGAATGGCCCTACCAGTGGCAAAAGT 3268

Qy   1061 GluGluAlaAlaLysTyrPheLeuAspGlnIleGluValCysArgArgAspLysGlyTyrTrp 1080
Db   3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG 3328

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGlnGluLysHis 1100
Db   3329 ACCGTGCAGTTTAACTGGTTCTTACACCTGGTTCTTGGCATCAAAGGGACAGGGAGAAGCAT 3388

Qy   1101 SerAla 1102
          ||
Db   3389 CCCGCA 3394

RESULT 5
US-08-672-211-3
; Sequence 3, Application US/08672211
Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park

```
Qy  181  ValThrProArgMetAlaGluValAlaGlyValAlaGlyArgProLeuTyrAlaMetHisPro  200
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Db  629  GTCACCCCGCGCATGGCCGAGGTGGCCGGCGTGGCCGGACGCCCCCTGTACGCCATGCACCCC  688

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLysLysIleThrArgAsnCysVal  220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  689  TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC  748

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  749  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC  808

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrTyrLysMetAlaLysLysLysSerLeuMetAsp  260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  809  CCAGGCACCATCCTCCAGAGCTTCTTTACCTACAAGATGGCCAAGAAGAAATCTCTGATGGAT  868

Qy  261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValValGlyArgAspGluTyr  280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  869  ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTCGTGGGCCGGGATGAGTAC  928

Qy  281  LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnAsnCysLeuLysAsnGly  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  929  CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGAACTGCCTCAAGAATGGG  988

Qy  301  GluGluHisGluLeuValLeuAspThrProProAlaLeuAspGluValAlaArgGluValLys  320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  989  GAGGAGCATGAGTTGGTGCTGGACACTCCTCCAGCCCTGGACGAGGTGGCAAGGGAGGTGAAG 1048

Qy  321  GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyTyrHisGlyGlnLeuThr  340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1049  GAAGAGTGGCCGCTGGTTGCTGATGACTGTACACGGGAGTCACTGGCTACCACGAGCAGCTGACC 1108

Qy  341  IleHisSerGlyLysAspHisGluSerValPheThrValSerLeuSerTrpAspCysArgGly  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1109  ATCCACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGTCGGGACTGTGACCGGAAG 1168

Qy  361  PheArgValLysIleArgGlyTyrIleAspProIleProValLeuProArgThrAlaAspLeuThr  380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1169  TTCAGGGTCAAAATCAGAGGCTATATTGATCCTATCCCTGTCCTGCCCCGGACCGCTGACCTTCACG 1228

Qy  381  ValPheValGluValLeuAsnIleGlnTyrGlyValGlnIleValLeuCysGlnArgThrSer  400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1229  GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAAACCAGC 1288

Qy  401  ProLysProPheGluThrGluProGlnValLeuGluProThrAsnValTrpAsnValTrpPheLeuGluSerIleIle  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1289  CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGTGGCTTGGAGTTCAGTATTAAAAATC 1348

Qy  421  LysAspLeuProGlyGlyAlaLeuLeuLeuAsnLeuGlnIleLeuTyrCysTyrGlyLysAlaProAla  440
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Db 1349  AAAGACTTACCCAAAGGGGCTCTGCTACTCCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA 1408

Qy  441  LeuSerGlyLysLysThrSerAlaGluMetProSerProGluSerLysGlyGlyLysLysAlaGlnLeuArg  460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1409  CTGTCTGGCAAGAAGACCTCTGCAGAGATGCCCAGTCCCGAGAGCAAAGGCAAAGCCAAAGCTCAGCTT 1468

Qy  461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr  480
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Db 1469  CTGTACTATGTGAACCTATTGCTGATAGACCACCGCTTCCTCCTGCGGCATGGCGAGTAT 1528

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyGlyLysSerGlyGluAspGlnSerPheAsnAlaAsp  500
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Db 1529  GTGCTCCACATGTGGCAGTTATCCGGAGGAGGGGAAGGACCAGAGCTTCAATGGCGAC 1588

Qy  501  LysLeuThrSerAlaThrAsnProAspAspLysLysGluGlnInSerMetSerIleLeuSerLeuLeu  520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1589  AAGCTCACGTCGGCAACCAACCCAGACGACAAGAAAGAGCAGAATTCCATGTCCATTCTCTCTCTG 1648

Qy  521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGlyLy  540
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1649  GACAATTACTGCCACCCCATAGCCTTGCCTAAGCACCGGCCTACCCCTGACCCCAGAAGGGG 1708
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Qy  541  AspArgValAlaArgGlnLeuArgLysGlnLeuGluAlaIleIleAla  560
              ||||||||||||||||||||||||||||||||||||||||||||||
Db 1709  GACCGGGTTGCGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAACCATAGCC 1768

Qy  561  ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuTrpHisPheArgTyr  580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1769  ACGGATCCGCTTAACCCACTGACAGCTGAAGACAAAGAACTGCTCTGGCATTTCAGATAT 1828

Qy  581  GluSerLeuLysAspProLysLysPheSerSerValLysTrpGlyGln  600
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1829  GAAAGCCTGAAGGATCCCAAAAAGTTCTCTAGCGTGAAAATGGGGACAG 1888

Qy  601  GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaArgGluValTrpAspGlnSer  620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1889  CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAGGGAGGTCTGGGATCAGAGT 1948

Qy  621  AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1949  GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy  641  ArgAlaIleAlaAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2009  AGAGCCATTGCAGCTGTCCAGAAACTGGAGAGCTTGGAGGATGATGACGTGCTCCATTACCTG 2068

Qy  661  LeuGlnLeuValGlnAlaValLysPheGluGluProTyrHisAspSerAlaLeuAlaArgPhe  680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2069  CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGGTTT 2128

Qy  681  LeuLeuLeuLysArgGlyLeuLeuArgAsnLysArgIleGlyHisPheLeuPheTrpLeuArg  700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2129  CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTTGTTTTGGTTCTTGAGA 2188

Qy  701  SerGluIleAlaGlnSerArgHisTyrArgGlnAsnAlaValIleLeuGluAlaTyr  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2189  AGTGAGATTGCCCAGTCTAGGCACTATCAGCAGAATGCTGTCATCCTGGAAGCCTAC 2248

Qy  721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleLeuAsp  740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2249  CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTAATTCTGGAC 2308

Qy  741  MetLeuGlnLysValThrIleLysAspThrIleLysSerLeuSerGluAlaGluLysTyrAspValSer  760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2309  ATGTTACAAAAAGTCACCATTAAAGATACAATTAAATCGCTCTCTGAAGCTGAAAAGTATGACGTCAGT 2368

Qy  761  SerGlnValIleSerGlnLeuLysGlnLeuAsnLeuGlnAsnLeuGlnAsnLeuAsnLeuPro  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2369  TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACTTGAAATCTCCCC 2428

Qy  781  GlnSerPheArgValProTyrAspProGlyLeuLysProGlyLeuAlaGlyLysAlaLeuValIleLeuGluLys  800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2429  CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAGCCGGGCTGGCTGGCAAAGCCCTGGTGATCGAAAAA 2488

Qy  801  CysLysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro  820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCAGATCCT 2548

Qy  821  ThrAlaLeuSerAsnGluThrIleIleIleHisGlyLysHisGlyAspAspLeuArgGln  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2549  ACGGCTCTATCAAATGAAACCATTGGAATTATCTTTAAACGGGTGAGATCTGGCGACCAA 2608

Qy  841  AspMetLeuIleLeuGlnIleLeuLeuLeuArgIleMetGluSerIleTrpGluSerLeu  860
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Db 2609  GACATGCTTATTTACAGATTCTACGAATCATGGAGAGTCCATTGGGAGACCGAATTCTTTG 2668

Qy  861  AspLeuCysLeuLeuProTyrGlyCysIleSerSerThrGlyLysAspLysIleGlu  880
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Db 2669  GATCTGTGCCTTGCCATATGGCCTGCATTCAACTGGTGACAAAAAATAGGAATGATCGAG 2728

Qy  881  IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyLysAsnThrGly  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2729  ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGCAAGTCACACACGTGGGCAACACGGGT 2788

Qy  901  AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys  920
```

ATTORNEY/AGENT INFORMATION:
  NAME: Adrams, Samuel B
  REGISTRATION NUMBER: 30,605
  REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 650-493-4935
  TELEFAX: 650-493-5556
  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3808 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-09-225-170-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 3   Gaps: 0

US-09-974-573-1 (1-1102) x US-09-225-170-3 (1-3808)

Qy   1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGGAGGACAACCGCCGAGGCGT   148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle   40
Db   149 CGGAGGATGAAGCCGCGCAGCACGGCAGCCCAGCCTGTCCTCCATGGAGCTCATCCCCATC   208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
Db   209 GAGTTTGTTTTGCCACCAGCCAGCGCAACACCAAGACCCCGGAAACGGCACTGCTGCAC   268

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
Db   269 GTGGCCGGCCACGGCCAATGGGATGAGAAGATGAAGGCCCAGGTGTGTTGCGCGGCTGGAG   328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
Db   329 ACGAGCGTTCTTGGACTTCACCGGTTCGGCCCCGACCACTTCCTCCTGGTCTTC   388

Qy   101 GlnLysLysGlyGlnTrpTyrGlnIleTyrArgAspTyrGluIleTyrGlnValValGlnThrLeuAsp   120
Db   389 CAGAAGAAGGGGCAGTGGTACCAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC   448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg   140
Db   449 TGCCTGCGCTACTGGAGGTGTTGCACCGACGGATCCACGTGGTCCAGCGCGG   508

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaAlaLeuIleGlyTyr   160
Db   509 CACGCGCCCCTCCGAGGAGACATTGGCCTTCAACCGCCAGTCAACCCCCATCGCCTAC   568

Qy   161 AspValThrAspValSerAsnValHisAspAspSerCysLeuGluPheThrArgArgLeu   180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGGAGTTCACGCGGCGCCGCCTG   628

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro   200
Db   629 GTCACCCCGCGCATGGCCGAGGTGGCCGGCCGGGACCCTAAGCTTTACGCCATGCACCCC   688

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal   220
Db   689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC   748

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrLeuLysValSerAlaAspAspThr   240
Db   749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCCTCAAGGTCTCGGCCGATGACACC   808

Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTCGGCTCAAGAGAAAAATGCCCTATTGAAGAAAG   2848

Qy   921 PheGlnAlaAlaValAlaGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe   940
Db 2849 TTTCAGGCAGCTGTGGAGAGATTGTTTATTCCGTGCCCGGCTACTGTGTGGCAACCTTT   2908

Qy   941 ValLeuGlyValIleGlyAlaArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
Db 2909 GTTCTCGGAATAGGCGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA   2968

Qy   961 PheHisIleAspPheGlyHisHisLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys   980
Db 2969 TTTCATATTGATTTCGGACACCATTCTTGGGAATTACAAAAGTTCCTGGGCATTAATAAA   3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys   1000
Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGAACTTCTGGAAAG   3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu   1020
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT   3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro   1040
Db 3149 CGTCATCACACAAACCTACTGATCATCCTTCTTCCATGATGCTGATGACAGGAATGCCC   3208

Qy 1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer   1060
Db 3209 CAGTTAACCAGCAAAGAAGACATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT   3268

Qy 1061 GluGluAspAlaAlaLysLysTyrPheLeuAspLeuGlnAspTyrTrp   1080
Db 3269 GAGGAGGATGCCAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAAGGATGG   3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisValLeuValGlyIleLysGlnGluLysHis   1100
Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTGTTCTTGGCATCAAACAGGGGAGAAGCAT   3388

Qy 1101 SerAla 1102
Db 3389 CCCGCA 3394

RESULT 6
US-09-225-170-3
; Sequence 3, Application US/09225170
; Patent No. 6017763
GENERAL INFORMATION:
  APPLICANT: Stephens, Len
  APPLICANT: Hawkins, Phillip Thomas
  APPLICANT: Braselmann, Sylvia
  TITLE OF INVENTION: G-BETA-GAMMA REGULATED
  TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds, LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    STATE: NY
    COUNTRY: USA
    ZIP: 10036-2811
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: Windows
    SOFTWARE: FastSEQ for Windows Version 2.0b
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/225,170
    FILING DATE:
    CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/916,917
    FILING DATE: 15-AUG-1997

Left column

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Qy   241 ProGlyThrIleLeuGlnSerPheThrLysMetAlaLysLysSerLeuMetAsp 260
Db   809 CCAGGGACCACCATCCTCCAGAGCTTCTTTACCAAGATGATGGCCAAGAAGATCTCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluThrTyr 280
Db   869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTCTGCGGCCGGGATGAGTAC 928

Qy   281 LeuValGlyGluThrProIleLysAspPheAsnPheHisGlnTrpValArgGlnCysLeuLysLysAsnGly 300
Db   929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy   301 GluGlnIleHisLeuValLeuAspThrProProAspProLeuArgLeuAspGluValArgLys 320
Db   989 GAGGAGATTCACCTTGTCTGGACACTCCTCCAGACACCGGCCTGACGCGAGGTGGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
Db  1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGCTGACC 1108

Qy   341 IleHisGlyLysAspHisGlnSerValPheThrValSerLeuTrpAspAspCysAspArgLys 360
Db  1109 ATCCACGGCAAGGACCATCAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy   361 PheArgValLysIleArgGlyTyrIleAspProValLeuProValArgThrAlaAspLeuThr 380
Db  1169 TTCAGGGTCAAAATCAGAGGCTATATTGATCCTGTCCTGCCCCGGACACCGCTGACCTCACG 1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnAsnLeuCysGlyValLeuCysGlnArgThrSer 400
Db  1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAGGAGAACCAGC 1288

Qy   401 ProLysProPheThrGluGluLeuValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
Db  1289 CCCAAACCCTTCACGGAGGAGCTGGTCCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuLysProLysAspGlyAlaLeuLeuLeuAsnLeuGlnIleTyrCysGlyGlyLysGlyAlaProAla 440
Db  1349 AAAGACTTAAACCCAAAGGGCTCTGCTGACAACCTCACTGCGGCAAAGCTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaAlaGlnLeu 460
Db  1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGTCCAAAGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuIleAspPheHisArgPheLeuLeuArgHisGlyGluTyr 480
Db  1469 CTGTACTATGTCAACCTATTGCTAGATCAACCGTTCCTCCTGCGCCATGGCGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyValGlyAspGlnGlySerPheAsnAlaAsp 500
Db  1529 GTGCTCCACATGTGGCAGTTATCCGGAGAGGGGGAAGCAAGGGAGCTTCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeu 520
Db  1589 AAGCTCACGTCGGCAACCAACCCCGACAAGGAGAACTCCATGTCCATTTCCATTCTTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysAsnGluProThrProGluGly 540
Db  1649 GACAATTACTGCCATCCCATAGCCTTGCCTAAGAATGAGCCCACCCCTGAGGGG 1708

Qy   541 AspArgValArgAlaGluMetProLysAsnLeuArgLysGlnLeuGluGluAlaIleIleAla 560
Db  1709 GACCGGGTTCGGGCAGAAATGCCCATTAAGAACCTTCGGAAGCAACTGGAGGAGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysLysThrLeuGlnLeuLysLysPheSerArgTyr 580
Db  1769 ACGGATCCCGTTAACCCACTCACAGCTGAAGACAAAGAACTGCTCTGCATTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
Db  1829 GAAAGCCTGAAGGATCCCAAAGCCTATCCCAAGCTCTTTAGCTCGGTGAAATGGGGACAG 1888
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Right column

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Qy   601 GlnGluIleLeuGluValAlaLysArgGluTrpAspGlnSer 620
Db  1889 CAAGAAATTGTGGCCAAAACATACAATTATTATTAGCCAAAGGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
Db  1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTCGATTCGAACTTCTCGGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaLeuAlaThrAlaLysLysSerLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu 660
Db  2009 AGAGCCATTGCAGTCCAGAAACTGGAGAGCTTGGAGGATGATGACGTGCTCCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
Db  2069 CTCCAGCTGGTCCAGGCTGCAGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy   681 LeuLeuLeuArgGlyLeuArgAsnLysArgIleGlyGlyHisPheLeuPheGluTrpGlnLeuArg 700
Db  2129 CTGCTCGAAGCGCTGGTTTAAGAACAAGAGAATTGGTCACTTCTTGTTTGGTTCTTGAGA 2188

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgGluAlaValIleLeuGluAlaAlaTyr 720
Db  2189 AGTGAGATTGCCCAGTCTCAGGCACTATCAGCAGAGGTTTGCAGTTCAGTGGATCCTGGAAGCCTAC 2248

Qy   721 LeuArgCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnAsnIleGluAsp 740
Db  2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy   741 MetLeuGlnIleLysValThrIleGluAspAlaIleGluLysSerLeuSerArgAlaGluGlyLysTyrAspValSer 760
Db  2309 ATGTTACAAAAGTCACCATTGACATTGAATCGCTCTCTGCTGAAAGTATGACGTCAGT 2368

Qy   761 SerGlnIleValIleSerGlnLeuLysGlyLnLysGlnLeuGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro 780
Db  2369 TCCCAAGTTATTCCCAACTTAAGCAAAAGCTTGAAAAACTACACAGAATTTGAATCTCCCC 2428

Qy   781 GlnSerPheArgValProTyrLeuProGlyLeuLeuLysAlaGlyAlaLeuValIleGluLeuLys 800
Db  2429 CAAAGCTTTAGAGTTCCTATGATCCTGGACTTCTGAAGGCCGGGCACCTGGTGATCGAAAAA 2488

Qy   801 CysLysLysValMetAlaSerLysLysSerLysProLeuLeuTrpGluCysPheLysTrpLysSerAlaAspPro 820
Db  2489 TGTAAAGTGACATGGCCTCCAAGAAGAAGCCCCTGCTGGCTTAATTGTGGCCAAATGCCT 2548

Qy   821 ThrAlaLeuSerArgAsnGluThrIleGlyLysHisGlnIleLeuGlyLysHisGlyAspAspLeuArgArgGln 840
Db  2549 ACGGCCCTATCCAGAATGAAACAATTGGAATTAATCTTTAAACAGGTGAAGCATCTGCGGCGCCAA 2608

Qy   841 AspMetLeuLeuLeuGlnLeuAsnLeuIleLeuArgIleMetGluSerIleLeuTrpGluLeuThrGluSerLeu 860
Db  2609 GACATGCTTCTTCGACTTAACGTCGAATCCTCGATTCACGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuGlnProTyrGlyCysArgLeuSerGluThrArgGlyIleGlyLysMetIleGluGlu 880
Db  2669 GATCTGTGCCTCCTGCCCATATGGTGCCGCAAAATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleGluValLysAspAlaThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrArgGly 900
Db  2729 ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGCAAAGCACACGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluAlaValLeuSerHisTrpSerAlaGlyTyrSerValAlaAlaThrAla 920
Db  2789 GCCTTTAAAGATGAGGCAGTGCTGAGACATTGGTCTGCGGGCTACTCTGTGGCCGCGGGT 2848

Qy   921 PheGlnIleAlaAlaValGluLysAspAspAlaArgHisAsnAspAsnIleMetIleSerGluThrGlyValAlaThrPhe 940
Db  2849 TTTCAGGCAGTGGTGGAGAAGATTGTTATTCCTGGTGCGGGCTACTCTGTGGCCAACTTT 2908

Qy   941 ValLeuGlyIleIleGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db  2909 GTTCTCCGGAATAGGCGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
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                  STRANDEDNESS: single
              ;   TOPOLOGY: linear
              ;   US-08-916-917-13

                  Alignment Scores:
                  Pred. No.:              0                    Length:        5162
                  Score:                  5534.00              Matches:       1049
                  Percent Similarity:     97.10%               Conservative:  21
                  Best Local Similarity:  95.19%               Mismatches:    32
                  Query Match:            95.58%               Indels:        0
                  DB:                     2                    Gaps:          0

                  US-09-974-573-1 (1-1102) x US-08-916-917-13 (1-5162)

            Qy      1 MetGluLeuAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg  20
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            Db     84 ATGGAGCTGGAGAACTATAAACAGCCCGTGCTGCGAGAGGACAACTGCCGAGGGCGC 143

            Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    144 CGGAGGATGAAGCCCGCGAGTACGGCTGTGGGGCCAGCCTGTCCATGGAGCTCATCCCCATC 203

            Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
                      ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
            Db    204 GAGTTCGTGCTGCCCACCAGCCAGCGAAATGCAAGCGCCCGAAACGGGCGTGCTGCAC 263

            Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGTGGAG 323

            Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    324 ACCAGCGTGGGGGCCGGACTTCTACCACCGGCTGGGACCGCATCACTTCCTCCTGCTCTAT 383

            Qy    101 GlnLysGlyGlnThrTyrGlnIleTyrAspLysTyrGlnValGlnThrLeuAsp 120
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    384 CAGAAGAAGGGGCAGTCGTACCAGATCTACGACAAGTACCAGGTGCAGACTCTGGAC 443

            Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValGlnArg 140
                      ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
            Db    444 TGCCTGCGCTACTGGAAGGCCACCGGAGCCCGGGCCAGATCCACCTGGTGCAGCGG 503

            Qy    141 HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
                      ||||||||||||||||||||:::|||||||||||||||||||||||||||||
            Db    504 CACCCGCCCTCCGAGAGTCCCAAGCTTCCAGGCAGCTCACGGCGCTGATTGGCTAT 563

            Qy    161 AspValThrAspValSerAsnValHisAspAspSerProGluLeuGluPheThrArgArgLeu 180
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGTCACGGGAGCTGGAGTTCACGCGCCGTGGCTTG 623

            Qy    181 ValThrProArgMetAlaGluValAlaGlyTyrAlaArgAspProLysLeuTyrAlaMetHisPro 200
                      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    624 GTGACCCCGCGCATGGCCGAGGTGGCCGGCTACGCCCGAGACCCCAAGCTCTACGCCATGCACCCG 683

            Qy    201 TrpValThrSerLysProLeuProLeuTyrLeuLysLysIleThrAsnAsnCysVal 220
                      ||||||||||||||||||||||||||||||||||||||||||||||||::::
            Db    684 TGGGTGACGTCCAAGCCCCTGCCCCTCTACCTGAAGAAGATTCCAACAACTGCATC 743

            Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 803

            Qy    241 ProGlyThrIleLeuGlnSerProPheThrLysMetAlaLysLysLysSerLeuMetAsp 260
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    804 CCCGGGACCATCCTGCAGAGCCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 863

            Qy    261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValCysGluTyr 280
                      |||||||||||||||||||||||||||:|||||||||||||||||||||||||||
            Db    864 ATTCCCGAAAGCCAAAGCCAAGGACACAGGATTTTGTGCTGCGGGTCTGTGGGGATGAGTAC 923

            Qy    281 LeuValGlyThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Db    924 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA 983
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            Db   2969 TTTCATATTGATTCGGACACATCTTGGGAATTACAAAAGTTCCTCGGGCATTAATAAA 3028
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy    981 GluArgValProPheValLeuThrProAspPheLeuMetGlyThrSerGlyLys 1000

            Db   3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy   1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020

            Db   3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT 3148
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy   1021 ArgHisHisThrAsnLeuIleLeuIleArgHisHisSerMetLeuMetThrGlyMetPro 1040

            Db   3149 CGTCATCACACAAACCTACTGATCATCCTCCTTCTCCATGATGCTGATGACAGGAATGCCC 3208
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy   1041 GlnLeuThrSerLysGlyAspIleGluTyrIleGluArgAspAlaLeuThrValGlyLysSer 1060

            Db   3209 CAGTTAACCAGCAAGAGACATTGAATACATTCGGAGATCACTCCACAGTGGGCAAAAGT 3268
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy   1061 GluGluAspAlaAlaLysTyrPheLeuAspTyrPheLeuHisValCysArgAspLysLysGlyTrp 1080

            Db   3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            Qy   1081 ThrValGlnProHeAsnTrpPheLeuHisLeuValLeuGlyTyrIleLysGluGlyHis 1100

            Db   3329 ACCGTGGGAGTTTAACTGGTTCTTACACCTGGTTCTTGGCATCAAAGAAGGGGAAGCAT 3388
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            Qy   1101 SerAla 1102

            Db   3389 CCCGCA 3394
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            RESULT 7
            US-08-916-917-13
            ;   Sequence 13, Application US/08916917
            ;   Patent No. 5856132
            ;   GENERAL INFORMATION:
            ;      APPLICANT: Stephens, Len
            ;      APPLICANT: Hawkins, Phillip Thomas
            ;      APPLICANT: Braselmann, Sylvia
            ;      TITLE OF INVENTION: G-BETA-GAMMA REGULATED
            ;      TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
            ;      NUMBER OF SEQUENCES: 14
            ;      CORRESPONDENCE ADDRESS:
            ;         ADDRESSEE: Pennie & Edmonds, LLP
            ;         STREET: 1155 Avenue of the Americas
            ;         CITY: New York
            ;         STATE: NY
            ;         COUNTRY: USA
            ;         ZIP: 10036-2811
            ;      COMPUTER READABLE FORM:
            ;         MEDIUM TYPE: Diskette
            ;         COMPUTER: IBM Compatible
            ;         OPERATING SYSTEM: Windows
            ;         SOFTWARE: FastSEQ for Windows Version 2.0b
            ;      CURRENT APPLICATION DATA:
            ;         APPLICATION NUMBER: US/08/916,917
            ;         FILING DATE: 15-AUG-1997
            ;         CLASSIFICATION: 435
            ;      PRIOR APPLICATION DATA:
            ;         APPLICATION NUMBER: 08/672,211
            ;         FILING DATE: 27-JUN-1996
            ;      ATTORNEY/AGENT INFORMATION:
            ;         NAME: Abrams, Samuel B
            ;         REGISTRATION NUMBER: 30,605
            ;         REFERENCE/DOCKET NUMBER: 8549-0006-999
            ;      TELECOMMUNICATION INFORMATION:
            ;         TELEPHONE: 650-493-4935
            ;         TELEFAX: 650-493-5556
            ;         TELEX: 66141 PENNIE
            ;   INFORMATION FOR SEQ ID NO: 13:
            ;      SEQUENCE CHARACTERISTICS:
            ;         LENGTH: 5162 base pairs
            ;         TYPE: nucleic acid
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Qy  661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe    680
            ||||||||||||| ||| |||||||||  ||||||||||||
Db 2064 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATATAGCGCCCTTGCCAGATTT         2123

Qy  681 LeuLeuLysArgGlyLeuArgAsnLysArgLysValArgIleGlyHisPheLeuGluTrpPheLeuArg  700
            ||||||||||||||||||||||||||||||||||||||||||
Db 2124 CTGCTGAAGCGGGTTAAGAACAAAAGAAAGATTGGTCACTTTTTGTTTCTTGAGA        2183

Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnGlnAsnArgGlnAlaValIleAlaValAlaTyr    720
            |||||||||||||||||||||||||||||||||||||||||||
Db 2184 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGTTCGCTGTGATTCTGGAAGCCTAT     2243

Qy  721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValGlnValIleAsp      740
            |||||||||||||||||||||||||||||||||||::::
Db 2244 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAAGTCCAAGTAATCGAG      2303

Qy  741 MetLeuGlnLysValThrHisIleAspIleLysSerLeuSerAlaGluLysLysTyrAspValSer   760
            ||||||||||||||||||||||||||||||||||||||||||
Db 2304 ATGTTACAAAAAGTCACCCATATTGATATTAAATCGCTCTCGTGAAAAGTATGACGTCAGT   2363

Qy  761 SerGlnValIleSerGlnLeuLysGlyLeuLysLysGluAsnGlnAsnLeuGlnLysAsnLeuAsnLeuPro  780
            ||||||||||||||||||||||||||||||||||||||||||||
Db 2364 TCCCAAGTAATTTCACAACTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC    2423

Qy  781 GlnSerPheArgValProTyrArgAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys    800
            :::|||||||||||||||||||||||||||||||||||
Db 2424 GAAAGCTTTAGAGTTCCATATGAGGATCCTGGACTGAAAGCAGGAGCGCTGGCATTGAAAAA  2483

Qy  801 CysLysLysValMetAlaSerLysSerLysLysProLeuProLeuPheLysGluLysCysAlaAlaAspPro 820
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Db 2484 TGTAAAGTAATGGCCTCCAAGAAAAAAACACTATGGCTTGAGTTTAAAATGTGCCGATCCT   2543

Qy  821 ThrAlaLeuSerAsnGluThrGlyIleIleLeuArgIleMetGluSerIleThrGluTrpGluSerLeu   840
            |||||||||||||||||||||||||||||||||||||||
Db 2544 ACAGCCCTATCAAATGAAACAATGGAATTATCTTAAACATGGTGGAATGATCTGCGCCAA   2603

Qy  841 AspMetLeuLeuLeuGlnIleLeuLeuArgIleLeuTyrThrLysAspGluSerThrArgLeu     860
            ||||||||||||||||||||||||||||||||||||
Db 2604 GACATGCTTATTTTACAGATTCTACGAGTCTATTGGAGGACTGAATCTTTG          2663

Qy  861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerSerThrGlyLysAspLysLysSerMetIleGly  880
            |||||||||||||||||||||||||||||||||||||||||
Db 2664 GATCTATGCCTCCTGCCCATATGGTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG   2723

Qy  881 IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyLysAsnThrGly    900
            |||||||||||||||||||||||||||||:::|||||||||||
Db 2724 ATTGTGAAAGACGCCACGACGATAGCCAAAATTCAGCAAAGCACAGTGGGCAACACGCGGA   2783

Qy  901 AlaPheLysAspArgValLeuSerHisTrpLeuLysSerCysProIleGluGluLysLys     920
            |||||||||||||||||||||||||||||||||||||||||
Db 2784 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG    2843

Qy  921 PheGlnAlaAlaValGluArgPheValSerArgHisAsnAspAsnIleSerGluArgAlaAlaThrPhe  940
            :::|||||||||||||||||||||||||||||||||||
Db 2844 TTTCAGGCAGCAGTGGAGAGATTTGTTATTCCTCGGCAGCATAATGATCACCGGAGCAGCAAACCTTT 2903

Qy  941 ValLeuGlyIleIleGlyAspTyrArgHisAspAspAsnIleSerGluThrPheAsnLeu    960
            |||||||||||||||||||||||||||||||||||||
Db 2904 GTTCTTGGAATAGGGGACTATAGGCATGACGACAATATCACCGGAGACAGAAACCTA      2963

Qy  961 PheHisIleAspPhePheGlyLeuLeuHisGlyAsnTyrLysSerPheLeuGlyIleAsnLys   980
            |||||||||||||||||||||||||||||||||||||||
Db 2964 TTTCATATTGACTTCGGGCAACATTCTTGGGATTACAAAAGTTTCCTGGGCATTAATAAA   3023

Qy  981 GluArgValProPheGlnLysPheGlnAsnAspHisLysGluSerValLysLeu         1000
            |||||||||||||||||||||||||||||||||||
Db 3024 GAGAGAGTGCCCATTTCAGAAATTTCAGGACGACATGTGTCTAAGGCTTATCTT         3083

Qy 1001 LysThrSerLeuHisAspGlnLysGluSerLeuGlnAspAspSerValLeuHisTyrLeuLysLeuAlaLeu 1020
            ::|||||||||||||||||||||||||||||||||||
Db 3084 AAGACAAGCCCACACTTCCAGAAATTTCAGGACGACATGTGTAAGGCTTATCTTAAGCTTTAGTTCCCTT 3143

Qy 1021 ArgHisHisThrAsnLeuIleIleLeuLeuProheSerMetMetThrGlyMetPro       1040
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Qy  301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuLeuAspGluValArgLys   320
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Db  984 GAAGAGATTCACGTGGTACTGGACACGCCCTCCAGACCCCGGCCCTGCTGGACGAGGTGAGGAAG  1043

Qy  321 GluGluTrpProLeuValAspAspCysThrAspCysValThrGlyValThrHisGluGlnLeuThr  340
            |||||||||||||||||||||||:::|||||||||||||||||||||
Db 1044 GAAGAGTGGCCGCTGGTGGACGACTGCACGGACTGCGTCACCGGAGTCACCCACGAGCTTACC   1103

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys    360
            |||||||||||||||||||||||||||||||||||||||||
Db 1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGGAAG    1163

Qy  361 PheArgValIleArgGlyIleIleAspAspProValLeuProArgThrAlaAspLeuThr    380
            |||||||||||||||||||||||||||||||||||||||||
Db 1164 TTCAGGGTCAAGATCAGAGGCATTGAATCCCCGTCCCTGCCTCGGACCGCCGACCTCACA    1223

Qy  381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnGlnValLeuCysGlnArgArgThrSer    400
            |||||:::|||||||||||||||||||||||||||||||||||
Db 1224 GTTTTTGTAGAGGCAAACATCCAGTATGGCGTGCAGCAAGTCCTTTGCCAAAGGAGAACCAGC  1283

Qy  401 ProLysProPheThrGluValLeuTrpProAsnValTrpLeuGluProSerIleLeuLys    420
            ||||||||||||||||||||||||||||||||||:::|||||
Db 1284 CCCAAACCCTTCACAGAGGTGCTGTGGCCAAATGTGTGGCTTGAGCCTAGTATTCAAAATC   1343

Qy  421 LysAspLeuProLysGlyValAlaLeuLeuAsnLeuAsnIleTyrCysGlyLysAlaProAla    440
            ||||||||||||||||||||||||||||||||||||||||||||
Db 1344 AAAGACTTGCCCAAAGGGCTCTACTGAACCTCAGATCTACTGCGGTAAAGCTCCAGCA      1403

Qy  441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerGlyGlyLysAlaGlnLeu    460
            ||||||||||:::|||||||||||||||||||||||::|||||
Db 1404 CTGTCCAGCAAGACCTCTGCAGAGATGCCCAGTCCTGAGTCTGGTGGGAAAGCTCAGCTT    1463

Qy  461 LeuTyrTyrValAsnLeuLeuLeuIleAspArgHisArgLeuLeuArgPheGlyGluTyr    480
            |||||||||||||||||||||||||||||||||||||||||
Db 1464 CTCTATTATGTGAACCTGCTGCTCATAGACCGCCACAGGCTGCTCCGCTTCGGCGAGTAC    1523

Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyTyrGluAspGlnGlySerPheAsnAlaAsp   500
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Db 1524 GTCCTCCACATGTGGCAGATATCTGGAAGGGAGAAGACCAAGGAAGCTTCAATGCTGAC    1583

Qy  501 LysLeuThrSerAlaThrAsnProAspLysLysGluAsnSerMetSerIleLeuSerLeuLeu   520
            |||||||||||||||||||||||||||||||||||||||||
Db 1584 AAACTTCACGTCTGCAACTAACCCAGACAAGAAGGAGAACTCCATGTCCATTCTCTG      1643

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisProThrProAspProGluGly     540
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Db 1644 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCACCCCACCCCTGACCCGGAAGGG    1703

Qy  541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysIleuGlnLeuGluIleIleAla    560
            |||||||||||||||||||||||||||||||||||||||||
Db 1704 GACCGGGTTCGAGCAGAGATGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC    1763

Qy  561 ThrAspProLeuAsnProLeuThrAlaLysLeuAspAspLysLysGluLeuTrpHisPheArgTyr  580
            |||||||||||||||||||||||||||||||||||||||||||
Db 1764 ACTGATCCACTTAACCCTCTCACAGCGAAGCTTGATGACAAGAAAGAATTGTGGCATTTTAGATAC 1823

Qy  581 GluSerLeuLysAspProLysProLeuAlaTyrTyrProLysLeuGluPheSerSerValLysTrpGlyGln 600
            |||||||||||||||||||||||||||||||||||||||||
Db 1824 GAAAGCCTTAAGGACCCCAAAAAGCATACTACAAGCCTAAGCTAGAGTTCAGTAGTGTGAAATGGGGACAG 1883

Qy  601 GlnIleIleGluValAlaAlaValGlnLysLysThrTyrGlnLeuLeuAlaLysArgGluGlnTrpAspSerArgGlnSer 620
            |||||||||||||||||||||||||||||||||||||||||
Db 1884 CAAGAAATTGTGGCAGTTGCTGCAGGTCCAGAAGAAGACCTATCAGCTCCTGGCCAAAAGAGAGCAGTGGGATCAAAGT 1943

Qy  621 AlaLeuAspValGlyLeuThrMetGlnHisLeuAspCysPheSerSerAspGluAsnVal    640
            |||||||||||||||||||||||||||||||||||||||||
Db 1944 GCTTTGGATGTGGGTTTAACAATGCAGCATCTGGATTGTTTCTCAAGTGATGAAAATGTA    2003

Qy  641 ArgAlaAlaIleAlaValGlnLysLysGlnSerLeuGluSerLeuGlnAspAspSerVa.LeuHisTyrLeu  660
            |||||||||||||||||||||||||||||||||||||||||||
Db 2004 AGAGCAGCCATTGCAGTTCAGAAAAAGCAGAGCTTGGAGAGCTTGCAAGATGATTCTGTGTTACACTACCTT 2063
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Db    3144  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  3203
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Qy    1041  GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer  1060
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            CAGTTAACAGGACAAAGAAGAGACATTGAATATATCCCGGATGCCCTCACAGTTGGGAAAAAT

Qy    1061  GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp  1080
Db    3264  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  3323
            GAGGAGGATGCATAAAAGTATTTTCTGATCAGATCGAAGTTGCAGGACAAAGGATGG

Qy    1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyGlyLysGlnGlyGluLysHis  1100
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Qy    1101  SerAla  1102
Db    3384  ||||||  3389
            TCAGCC
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RESULT 8
US-09-225-170-13
; Sequence 13, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,170
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,917
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-225-170-13

Alignment Scores:
Pred. No.:   0   Length: 5162
Score: 5534.00   Matches: 1049
Percent Similarity: 97.10%   Conservative: 21
Best Local Similarity: 95.19%   Mismatches: 32
                         95.58%   Indels: 0
                                         Gaps: 0
Query Match: 3
DB:

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US-09-974-573-1 (1-1102) x US-09-225-170-13 (1-5162)

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           ATGGAGCTGGAGAACTATAAACAGCCCGGTGCTGGAGAGAGACAACTGCCGAAGGCGC

Qy     21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle   40
Db    144  |||||||||||||||||||||||||||||||||||||||||||||||||||||||  203
           CGGAGGATGAAGCCCGGCAGTGCTGCGGCCAGCCTGTCTCCATGGAGCTCATCCCCATC

Qy     41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
Db    204  |||||||||||||||| |||||||||||:|::|||||||||||||||||||||  263
           GAGTTCGTCCTGCCCACCAGCCAAATGCACCCCCGAAAGCGCCGCTGCTGAC

Qy     61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnInValTrpLeuAlaLeuGlu   80
Db    264  |||||||||||||||||||||||||||||||||||||||||||||||||  323
           GTGGCCGGCCACCGGCAACCTGGAGCAGATGAAGGCCCAGGTGTGGCTGGCAGCGCTGGAG

Qy     81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
Db    324  ||||||||:::|||||||||||||||||||||||||||||||||||||||  383
           ACCAGCGTGGCGGGCGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT

Qy    101  GlnLysLysGlyInTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
Db    384  |||||||||||||||||||||||||||||||||||||||||||||::||  443
           CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTCCAGACTCTGGAC

Qy    121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
Db    444  |||||||||||||||||||||||||||||||||||||||::||::|||  503
           TGCCTGCGCTACTGGAAGGCCACCGGAGCCCGGGCCAGGATCCACCTGGTGCAGGCGG

Qy    141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
Db    504  ||||||||||:::::||||||||||||||||||||||||||||||  563
           CACCCGCCCTCCGGAGGAGCCCCAGCCTTCCAGCGGCAGCTCAACGCGCTGATTGGCTAT

Qy    161  AspValThrAspValSerAsnValHisAspAspValAspAspArgAspArgArgLeu  180
Db    564  ||||||||||||||||||||||||||||||||||||||||||||  623
           GACGTCACTGACGTTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG

Qy    181  ValThrProArgMetAlaGluAlaAlaGlyLysArgAspLysTyrAlaMetHisPro  200
Db    624  ||||||||||||||||||||||||||||||||||||||||||||||  683
           GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGGCAGCTCACGCGCCAAGCTCACGCACCCG

Qy    201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleLeuThrAsnAsnCysVal  220
Db    684  ||||||||||||||:||||||||||||||||||||::|||:|:  743
           TGGGTGACGTCCAAGCCTCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC

Qy    221  PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr  240
Db    744  ||||||||||||||||||||||||||||||||||||||||  803
           TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC

Qy    241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp  260
Db    804  ||||||||||||||||||||||||||||||||||||||||  863
           CCCGGCCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGAT

Qy    261  IleProGluSerGlnAsnGluArgAspPheValLeuLeuArgValCysGlyValArgGluTyr  280
Db    864  |||||||||||||||||||||||||||||||||||||  923
           ATTCCCGAAAGCCAAAGCCAACAGGATTTGTTGCTGCGGGTCTGTGGCGGGATGAGTAC

Qy    281  LeuValGlyThrProIleLysGlnAsnPheGlnIleLysAsnGlyLeuLysLeuLysAsnGly  300
Db    924  ||||||||||||||||||||||||||||||||||||  983
           CTGGTGGGCACCCCTATCAAGCAGAACTTCCAGATGGGGCTGAGCGCACTGCCTCAAGAACGGA

Qy    301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluValArgLys  320
Db    984  ||||||||||:::|||||||||||||||||||||||||||  1043
           GAAGAGATTCACGTGGTACTGGACACGCCTCCAGCACCGGCCCTAGACGAGGTGAGAAAG

Qy    321  GluGluTrpProLeuValAspLysCysThrGlyValThrGlyValThrArgGlyTyrHisGluGlnLeuThr  340
Db   1044  |||||||||||||||||||||||||||||||||||  1103
           GAAGAGTGGCCGCTGGTGGACAAGTGCACGGGAGTCACGGGCTACCATGAGCAGTTACC

Qy    341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys  360
Db   1104  ||||||||||||||||||||||||||||||||||||||  1163
           ATCCACGGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGGAAG
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721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp  740
Qy       |||||||||||||||||||||||||||||||||||||   |||||||||| :::
2244 CTGAGGGGCTGTGGCACAGCCATGCTGCACCAGACTTTACCCAACAAGTCCAAGTAA:CGAG  2303

741  MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysCysTyrAspValSer  760
Qy       |||||||||||||||||| :::||||  |||||||||||||||| ||||||||||
2304 ATGTTACAAGAGGTCACCATCGATATCAAATCGCTCTGCTGAAAAGTATGACGTCAGT  2363

761  SerGlnValIleSerGlnLeuLysGlnLysLysGlnGluAsnLeuGlnAsnLeuAsnLeuPro  780
Qy       ||||||||||||||||||||||||  ||||||||||||||| |||||||||||
2364 TCCCAAGTVATTTCACAACTTAAACAAAAGAAGCAGAATTCTCCAACTCCC  2423

781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaAlaLeuValIleGluLys  800
Qy       :::||||||||||||||||||||||||||||||||||||||||| ||||||||
2424 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCCGCTGGCAATTGAAAAA  2483

801  CysLysValMetAlaSerLysLysProLeuTrpLeuGluLysProLeuLysCysAlaAspPro  820
Qy       |||||||| ||||||||||||||||||||||||||  ||||| |||||||||||
2484 TGTAAAGTAATGGCCCTCCAAGAAAAAACCACTATCTTTAAACATGGATGAAATGTGCCGATCCT  2543

821  ThrAlaLeuSerAsnGluThrIleGlyIleLeuIleLeuPheLysHisGlyAspLeuArgGln  840
Qy       ||||||||||||||||||||||||  |||||||||||||||||||||| ||||||||
2544 ACAGCCCTATCAAATGAAACAATTGGAATAATTCTTATTCTTAAAACATGGTGATTTGCGGCAA  2603

841  AspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
Qy       |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
2604 GACATGCTTATTTTACAGATTCTACGGATCATGGAGTCTATTTGGGAGACTGAATCTTTG  2663

861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspLysLysMetIleGlu  880
Qy       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
2664 GATCTATGCCTCTGCCCTTACGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG  2723

881  IleValLysAspAlaThrArgThrLeuGlnGlnIleSerPheLeuAlaLeuValGlyAsnThrGly  900
Qy       |||||||||||||||||||||||||||||||||||||||||||||||||||||||
2724 ATTGTGAAAGACGCCACGAGCATTGCCAAATTCAGCAAAGCACAGTGGGCAACACGGGA  2783

901  AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys  920
Qy       ::::||||||||||||||||||||||||||| |||||||||||||||||||||
2784 GCATTTAAAGATGAAGTGCCTGAAGCCAATTCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG  2843

921  PheGlnAlaAlaValGlyArgPheValTyrSerCysSerValAlaThrPhe  940
Qy       ||||||||||||||||||||||||||||||||||||||||||||
2844 TTTCAGGCAGCAGTGGAGAGATTTGTTATCCTGTGCAGGCTACTGTGTGGCAACCTTT  2903

941  ValLeuGlyIleGlyTyrAspAspArgHisAsnAspAsnIleMetIleSerGluGluThrGlyAsnLeu  960
Qy       ||||||||||||||||||| :::||||||||||||||||||||||||||||
2904 GTTCTTGGAATAGGCGACAGACATAATGAATATCACCGAGACACGAGAACCTA  2963

961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
2964 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA  3023

981  GluArgValProPheValProPheSerMetMetMetThrGlyMetProSerGlyLys  1000
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
3024 GAGAGAGTGCCATTTGTCCCATTTTCTATGATGATGACAGGAATGCCCAGTGGAAAG  3083

1001 LysThrSerLeuHisAspPheGlnLysPheGluLeuLeuIleLeuIleGluAlaAlaLeu  1020
Qy       ||||||||||| :::||||||||||||||||||||||||||||||||||||
3084 AAGACAAGCCCACACTTCCAGAAATTTCAGGAACATCGTGTTAAGGCTTATCTAGCCCTT  3143

1021 ArgHisHisThrAsnLeuLeuIleIleLeuIleSerLeuMetGlyGlyLysPhe  1040
Qy       ||||||||||||||||||||||||||||||||||||||||||||||||||||
3144 CGTCATCACACAAACCTACTGATCATCATCTCTTCCATGATGGGAGGAAATGCCC  3203

1041 GlnLeuThrSerLysSerGluAspIleGluTyrIleArgArgAlaLeuThrValGlyTyrLysSer  1060
Qy       ||||||||||||||| :::||||||||||||||||||||||||  :::
3204 CAGTTAACAAGCAAAGAGAGAAGATATTGATTATATCCGGGATGCCCTCCACAGTGGGAAAAAT  3263

1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleValCysArgGlyAspLysGlyTrp  1080
Qy       |||||||||||||||||||||||||||||||||||||||||||||
3264 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGCAGAGGGAGATGG  3323

1081 ThrValGlnPheAsnTrpPheHisAsnLeuValLeuLysIleLeuLysGlnGluLysHis  1100
Qy
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361  PheArgValLysIleArgAspIleProValLeuProArgThrAlaAspLeuThr  380
Qy       ||||||||||||||||||||||||||||||||||||||||||||||
1164 TTCAGGGTCAAGATCAGAGATATCCCCGTCCTGCCTCGGACAACCGACCTCACA  1223

381  ValPheValGluValAlaAsnIleGlnThrGlyArgGlnValCysGlnArgThrSer  400
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
1224 GTTTTTGTAGAGGGCAAACATCCAGCATGGGCAACAAGTCCTTTGCCAAGGAGAACCAGC  1283

401  ProLysProPheGluThrGluValLeuTrpAsnValTrpLeuGluPheLeuIleLysIle  420
Qy       ||||||||||||||||||||||||||||||||||||||||||||||||
1284 CCCAAACCCTTCGAGACAGAGGTGCTGTGGAATGTGTGGCTTGAGTTCCTTATCAAAATC  1343

421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuIleTyrCysGlyLysLysAlaProAla  440
Qy       |||||||||| |||||||||||||||||||||||||||||||||||||
1344 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCATCTACTGCGGTAAAGCTCCAGCA  1403

441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerProGlyLysLysAlaGlnIleLeu  460
Qy       ||||||||||||||||||||||||||||||||||||||||||
1404 CTGTCCAGCAAGGCCTTCTGCAGAGTCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT  1463

461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr  480
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
1464 CTCTATTATGTGAACCTGCTGCTCATAGACCACCGTTTCCTTCCGCGCCTGAGAATAC  1523

481  ValLeuHisIleMetTrpGlnLeuSerGlyGlyValGlnGlyLysSerPheAsnAlaAsp  500
Qy       ||||||||||| :::||||||||||||||||||||||||||||||||
1524 GTCCTCCACATGTGGCAGATATCTGGGAGGAGAAGAGCCAAGAGCTTCAATGCTGAC  1583

501  LysLeuThrSerAlaThrAsnProAspLysValAsnSerMetSerIleSerLeuLeu  520
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
1584 AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTCAATGTCCATCTCCATTCTCTG  1643

521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProAspProGluGly  540
Qy       |||||||||||||||||||||||||||||||||||||||||||||
1644 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCGACCCCGAAGGG  1703

541  AspArgValAlaArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluAlaIleIleAla  560
Qy       |||||||||||||||||||||||||||||||||||||||||||||||||||
1704 GACCGGGTTGCGAGAGCAGAGATGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC  1763

561  ThrAspProLeuAsnProLeuThrArgAlaGluLysAsnGluLeuTrpHisPheArgTyr  580
Qy       ||||||||||||||||||||||||||||||||||||||||||||||||
1764 ACTGATCCACTTAACCCTCTCACACGAGCAGAGAAGAATGAATTGTCTGGCATTTTTAGATAC  1823

581  GluSerLeuLysAspProLysLysGlnSerAlaTyrProLysLeuPheSerSerValLysTrpGlyGlyGln  600
Qy       |||||||||||||||||||||||||||||||||||||||||||||||||
1824 GAAAGCCTTAAGGCACCCAAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAC  1883

601  GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaArgGluValArgValArgTrpAspGlnSer  620
Qy       :::||||||||||||||||||||||||||||||||||||||||||||||
1884 CAAGAGAAAATTGTGGCCAAAACATACCAATTGTTGGCCAGAAGGGAAGTCTGGGATCAAAGT  1943

621  AlaLeuAsnValGlyValLeuLysMetGlnLeuLysAspCysAsnPheSerGluAspValAsnVal  640
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
1944 GCTTTGGATGTTGGGGTTCTTAAGAAATTGAACATGACGCACCGTTTGAACTTCCCAGGAGATATCC  2003

641  ArgAlaIleAspValTyrArgLeuThrValArgGluValArgAspAspAspValLeuHisTyrLeu  660
Qy       |||||||||||||||||||||||||||||||||||||||||||||||
2004 AGGACAAGCCCAAAATGTCCGTTTACCGTCTGACAGTTCGTGATGATGAGGATCAAAGT  2063

661  LeuLeuLysValGlnAlaValGlyLeuArgAsnLysArgIleGlyHisGlyPheLeuTrpGlyPheLeuLeuArg  680
Qy       ||||||||||||||||||||||||||||||||||||||||||||||
2064 CTACAATTGGTCCAGGCTGTGAAATTTGAACTGAAAAACAAAAGAGAATTGGTCACTTTTTGTTTGGTTCTTGGACAGA  2123

681  GluGluGlnIleGlnSerArgHisTyrArgGlnArgPheAlaValIleLeuGluValAlaTyr  700
Qy       ||||||||||||| :::||||||||||||||||||||||||||||||
2124 CTGCTGAAGCCTGAAACAAAGAGCCGACATTATCGGCAGCGTTTTGCAGTGATCCTGGAAGTTGCA  2183

701  SerGluIleGlnSerArgHisTyrArgGlnArgPheAlaValIleLeuGluValAlaTyr  720
Qy       ||||||||||||||||||||||||||||||||||||||||||||||
2184 AGTGAGATAGCCCAGTCCCAGACTATCAGCAGAGGTTCGCTGATCTGAAGCCTTAT  2243
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Db   3324 ACTGTGCAGTTAATTGGTTTCTACATCTGTTCTGGCATCAAACAAGGAGAGAGAAACAT 3383
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Qy   1101 SerAla 1102

Db   3384 TCAGCC 3389
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RESULT 9
US-08-817-090B-3

; Sequence 3, Application US/08817090B
; Patent No. 5885777
; GENERAL INFORMATION:
;   APPLICANT: Stoyanov, Borislav
;   APPLICANT: Hanck, Theodor
;   APPLICANT: Wetzker, Reinhard
;   TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF
;   TITLE OF INVENTION: A NEW FORM OF PHOSPHATIDYLINOSITOL-3-KINASE
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
;   STREET: 655 Fifteenth Street N.W. Suite 330
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005-5701
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/817,090B
;   FILING DATE: 11-APR-1997
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE P 44 36 696.5
;   FILING DATE: 13-OCT-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE P 44 45 562.3
;   FILING DATE: 20-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Berman, Richrd J.
;   REGISTRATION NUMBER: 39,107
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)638-5000
;   TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 4137 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 423..3572
US-08-817-090B-3

Alignment Scores:
Pred. No.:   0
Score: 5499.50
Percent Similarity: 96.92%
Best Local Similarity: 95.01%
Query Match: 94.98%

Length: 4137
Matches: 1048
Conservative: 21
Mismatches: 32
Indels: 2
Gaps: 1

US-09-974-573-1 (1-1102) x US-08-817-090B-3 (1-4137)
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Qy     1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluArgGluAspAsnArgArgArgArg 20
         |||||||||||||||||||||||||||:||::|||||||||||||||||
Db   324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTCCTGGTGGAGAGAGAGGACAACTGCCGAAGGCGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
         |||||||||||||||||||||||   |:|||||||||||||||||||||||||||||
Db   384 CGGAGGATGAAGCCGCGCAGT--GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 440

Qy    41 GluPheValLeuProThrSerGlnAsnThrLysThrProGluThrAlaLeuLeuHis 60
         ||||||||||||||||||||||||||||:|||::|||||||||
Db   441 GAGTTCGTCGTGCCACCAGCCCAAATCAAGAGCCCGAAACGGCGCTGCTGCAC 500

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuValArgAlaLeuGlu 80
         ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGGTGCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         ||||:|:|||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db   561 ACCAGCGTGGGCGGCGACTTCTACCACCGGCTGGGACCCCATCACTTCCTCCTGCTCTAT 620

Qy   101 GlnLysLysGlyGlnTrpTyrGlyIleTyrGluIleValValGlnThrLeuAsp 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 CAGAAGAAGGGCCAGTGTACGAGATCTACGAACAAGTACCAGGTGTGCAGACTCTGGAC 680

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleIleHisValValGlnArg 140
         ||||||||||||:|||||||||||||||||:|||||||::||||||||||||||
Db   681 TGCCTGCGCTACTGGAAGGCCCACCGCAGCCCAGATCCACCTGGTGCAGCGCGG 740

Qy   141 HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
         |||||||||||||||||||||:::|||
Db   741 CACCCGCCCTCCGAGACCCTGGCAGCTGCGGGCTGATTGGCTAT 800

Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   801 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG 860

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861 GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGCGACCCCCAAGCTCTACGCCATGCACCCG 920

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleLysLysThrAsnAsnCysVal 220
         |||||||||||||||||||||||||||||||||||||||||||:::|||
Db   921 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC 980

Qy   221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr 240
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Db   981 TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1040

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
         ||||::|||||||:::|||
Db  1041 CCCGGCGGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1100

Qy   261 IleProGluSerGlnAsnGluArgAspPhePheLysValLeuArgValCysGlyValArgAspGluTyr 280
         ||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db  1101 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCCTCTGTGGCCGGGATGAGTAC 1160

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
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Db  1161 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA 1220

Qy   301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluValArgGlyLys 320
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Db  1221 GAAGAGATTCACGTGGTACTGGACACGCCCCTCAGACCCGAGGCCCTAGACGAGGTGAGGAAG 1280

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluLeuLeuThr 340
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Db  1281 GAAGAGTGGCCCGCTGTGGACGACTGCACGGGAGTCACCGGCTACCATGAGCAGTTACC 1340

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspTrpAspCysAspArgLys 360
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  1341 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGGGATGAGTAC 1400

Qy   361 PheArgValLysIleArgGlyIleAspIleLeuProValLeuProArgThrAlaAspLeuThr 380
         |||||||||||||||||||::|||||||:||
Db  1401 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTCGGACACACGACCTCACA 1460
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Qy   2541 ||||||||||||||||||||||||||||||||::::||||||||||||||||||||||||||
           ATGTTACAAAAGTCACCCTGATATTAAATCGGCTCTCTGCTGAAAAGTATGACGTCAGT 2600

Db   761 SerGlnValIleSerGlnLeuLysGlnLeuGlnLysLeuGlnAsnLeuAsnLeuAsnLeuPro 780
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Db   2601 TCCCAAGTTATTTCACAACTTAAACAAAGCTTGAAAACCTGAGAATTCTCAACTCCCC 2660

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuValIleGluGluLys 800
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 GAAAGCTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGGCCTGGCAATTGAAAAA 2720

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpPheLysGluPheLysCysAlaAspPro 820
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Db   2721 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGCCGATCCT 2780

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheLysHisGlyAspLeuArgGln 840
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Db   2781 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTGATCTGCGCCAA 2840

Qy   841 AspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlySerLeu 860
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Db   2841 GACATGCTTATTTACAGATCTACGAATCATGGAGTCTATTGGGAGACTGAAATCTTTG 2900

Qy   861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2901 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2960

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGluGlnIleSerThrValGlyAsnThrGly 900
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Db   2961 ATTGTGAAAGACGCCACGACGATTGCCAAATTCAGCAAAGCAAGCACAGTGGGCAACACGGGA 3020

Qy   901 AlaPheLysAspArgGluValLeuSerHisTrpLeuLysGlyLysCysProIleGluGluLys 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3021 GCATTTAAAGATGAAGTCCTGGCTCACTGGCTCAAAGAAAAATCCCTACTGAAGAAGAAAG 3080

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   941 ValLeuGlyIleGlyAspSerArgHisAsnAspAsnIleMetIleSerGluThrGlyValAsnLeu 960
           ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db   3141 GTTCTTGGAATAGGCGACAGCAGACACATAATGACACCGGACACACCGAGAAACCTA 3200

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3201 TTTCATATTGACTTTGGGCACATTCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3260

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3261 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3320

Qy   1001 LysThrSerLeuHisPheGlnAspValCysValLysAlaValTyrLeuAlaLeu 1020
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3321 AAGACAAGCCCACACCTTCCAGAAATTTCAGGACATCTGTGTTAAGGCTGTTATCTAGCCCTT 3380

Qy   1021 ArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3381 CGTCATCACAACAACTTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC 3440

Qy   1041 GlnLeuThrSerLysGluGlnAspIleGluValTyrIleLeuArgAspAlaLeuThrValGlyLysSer 1060
           ||||||||||||||||||||||||||||||||::::||||||||||||||||||||:::
Db   3441 CAGTTAACAAGCAAAGAGCAAGATATCGAGGTGTATATCCTGGGATGGGGGCAAAAAT 3500

Qy   1061 GluGlnThrSerLysGlnAspIleGluLeuGluValCys-ArgAspLysGlyTyr 1080
           |||||||||||||||||||||||||||||||||||||||||||||||::::||||||
Db   3501 GAGGAGGATGCAAAAGCTAAAAAGTTATTTTCGAAGATCCGGGATGCCCACCAGTGGGGAGATG 3560

Qy   1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuIleLeuLysGlnIleGluLysHi 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3561 GACTGTGCAGTTTAATTGGTTTCTACACTCTTGTCCTTGGCATCAAACAAGTAATCGAG 3620

Qy   1100 sSerAla 1102
           |||||||

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnValLeuCysGlnArgArgThrSer 400
           |||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db   1461 GTTTTTGTAGAGGCCAAACATCCAGCAGGGCAACAGTCCTTTGCCAAAGGAGGAACCAGC 1520

Qy   401 ProLysProPheThrGluGluPheArgValLeuTrpAsnValTrpLeuGluPheSerIleLeuLysIle 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521 CCCAAACCCTTCACAGAGGAGTTCAGAGTGCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAAATC 1580

Qy   421 LysAspLeuProLysGlyAlaLeuLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581 AAAGACTTTCCCCAAAGGGGCTCTACTGAACCTCCAGATCTACGCGGTAAAGCTCCAGCA 1640

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
           ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db   1641 CTGTCCAGGAAGGCCTCTGCAGAGTGCCCAGTTCGAGTCCCAAAGGGCAAAGTTCGGCTT 1700

Qy   461 LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuArgHisGlyHisGlyTyr 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701 CTCTATTATGTGAACCTGCTGCTATAGACACCGTTTCCTCCGCCGCGTGAGAATAC 1760

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlyLysSerPheAsnAlaAsp 500
           |||||||||||||||||||::::|||||||||||||||||||||||||||||||||||||
Db   1761 GTCCTCCACAATGTGGCAGATATCTGGAGGGAGAAGACCAAGGGAAAGTCTTCAATGCTGAC 1820

Qy   501 LysLeuThrSerAlaThrAsnProAspLysSerGluAsnSerMetSerIleLeuLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821 AAACTCACGTCTGCAACTAACCCAGACAAGAGTGAGAATTCCATGTCCATTCTCCTG 1880

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
           ||||||||||||||||||||||||||||||||||||||::::||||||||||||||||||
Db   1881 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCACCCCCGACCCCGAAGGG 1940

Qy   541 AspArgValArgArgAlaGlyMetProAsnGlnLeuArgGlnLeuLysGlnLeuAlaIleIleAla 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 GACCGGGTGCGAGCGAGAAATGCCCAAACAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 2000

Qy   561 ThrAspProLeuAsnProLeuTrpThrAlaGluLysGlyAspLysLeuLeuTrpHisPheArgTyr 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001 ACTGATCCACTTAACCCTCTCACAGCAGAGAAAGGATTGTCTGGCATTTTAGATAC 2060

Qy   581 GluSerLeuLysAspProLysProLysAlaTyrProLysProLeuPheSerSerValLysTrpGlyGln 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061 GAAAGCCTTAAGACACCCAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG 2120

Qy   601 GlnGluIleValAlaLysThrTyrGlnLeuLeuLeuArgGlnLysValArgGluValTrpAspGlnSer 620
           ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db   2121 CAAGAAATTGTGGCCAAAACATACCAAATTGTTGGCCAGAAGGGAAGTCTGGGATCAAAGT 2180

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerGluAspAsnVal 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAAATGTA 2240

Qy   641 ArgAlaIleAlaValGlnLysLysValSerLeuGluGluAspAspAspValLeuHisTyrLeu 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241 AGAGCCATTGCAGTTCAGAAAAAGGTTTCAGAACTGGAGGAGACTTGAGGATGTTCTGCATTACCTT 2300

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuArgArgPhe 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGCGCCCTTGCCAGATTT 2360

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysTyrArgIleGlyHisPheLeuProTrpPheLeuArg 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||::::|||
Db   2361 CTGCTGAAGCGTGGTTTAAGAAACAAATACAGAATTGGTCACTTTTTGTTTTTGGTTCTTGAGA 2420

Qy   701 SerGluIleAlaGlnSerArgHisTyrArgGlnArgArgPheAlaValIleLeuAlaTyr 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 AGTGAGATAGCCCAGTCCAGACACTATCGCCAGAGGTTCGCTGTGATTCTGGCAAGCCTAT 2480

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnAsnValGlnIleIleAsp 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   2481 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAGTCCAAGTAATCGAG 2540

Qy   741 MetLeuGlnLysValThrIleAspIleLysProIleLysLysSerLeuSerAlaGluLysTyrAspValSer 760

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Db        3621 TTCAGCC 3627

RESULT 10
US-08-817-090B-1
; Sequence 1, Application US/08817090B
; Patent No. 5885777
; GENERAL INFORMATION:
;   APPLICANT: Stoyanov, Borislav
;   APPLICANT: Hanck, Theodor
;   APPLICANT: Wetzker, Reinhard
;   TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF
;   TITLE OF INVENTION: A NEW FORM OF PHOSPHATIDYLINOSITOL-3-KINASE
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
;     STREET: 655 Fifteenth Street N.W. Suite 330
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/817,090B
;     FILING DATE: 11-APR-1997
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 36 696.5
;     FILING DATE: 13-OCT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 45 562.3
;     FILING DATE: 20-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Berman, Richrd J.
;     REGISTRATION NUMBER: 39,107
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)638-5000
;     TELEFAX: (202)638-4810
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 4134 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: both
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     ORIGINAL SOURCE:
;       ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 423..3569
US-08-817-090B-1

Alignment Scores:
  Pred. No.:              0
  Score:             540.00
  Percent Similarity: 96.65%
  Best Local Similarity: 94.83%
  Query Match:        93.96%
  DB:                     2

Length:         4134
Matches:        1046
Conservative:     20
Mismatches:       35
Indels:            4
Gaps:              1
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US-09-974-573-1 (1-1102) x US-08-817-090B-1 (1-4134)

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Qy     1 MetGluLeuGlnAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg  20
           ||||||||||||||||||||||||:||:::|||||||||||||||||||||||||||
Db   324 ATGGAGCTGGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCGGAAGGGGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 CGGAGGATGAAGCCCGCAGT---GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 440

Qy   401 ProLysProPheThrGluGlyValLeuTrpAsnValTrpLeuGluPheSerLeuLysIle 420
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Db    3621 TTCAGCC 3627

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
           |||||||||||||||||||||||||||:||:::||||||||||||||||||||||||||
Db   441 GAGTTCGTGCTGCCCACCAGCCAAATGCAAGAGCCCGAAACGGCGCTGCTGCAC       500

Qy    61 ValAlaGlyHisGlyAsnValGlnMetLysAlaGlnLnValTrpLeuArgAlaLeuGlu  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTCCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ACCAGCT--GGCGGCGGACTTCTACCACCGGCTGGGACCGCATCACTTCCTCCTGCTCTAT 618

Qy   101 GlnLysLysGlyGlnTrpGluTyrAspIleTyrArgLeuHisTyrGlnValValGlnThrLeuAsp 120
           :::|||||||||||||||||:||||||||||||||||||:|::|||||||||||||||||
Db   619 CAGAAGAA-GGGCAGTGGTACGACGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 677

Qy   121 CysLeuArgTyrTlrProLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
           |||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db   678 TGCCTGCGCTACTGGAAGGCCACGCACCGGAGCCCGGGCCAGATCCACGTGGTGCAGCGG 737

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnAsnArgGlnLeuAsnAlaAlaLeuIleGlyTyr 160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738 CACCCGCCCTCCGAGGAGTCCCAAGCTTCCAGCGGCGCAGCTCACGCGCCTGATTGGCTAT 797

Qy   161 AspValThrAlaSerAsnValHisAspAspProGlyGluGluGlnProPheThrArgArgLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 GACGTCACTGCGTCCAAGCAACGTGCACGATGAGCTGGAGTTCACGCGCCGTGGCCTTG 857

Qy   181 ValThrProArgMetAlaGlyGluValAlaAlaGlyArgAspProLysGluTyrAlaMetHisPro 200
           |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db   858 GTGACCCCGCGCATGGCCGGAGGTGGCCAGCCGGGACCCCAAGCTCTACGCCATGCACCCG 917

Qy   201 TrpValThrSerLysProLeuProGluProGlyLeuTyrLeuLeuLysLysLysIleThrAsnAsnCysVal 220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||:::||
Db   918 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGAAGATTGCCAACAACTGCATC 977

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   978 TTCATCGTGACTCATTCACCCGCACGACACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1037

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db  1038 CCCGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1097

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
           |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db  1098 ATTCCAGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGTCTGTGGCCGGGATGAGTAC 1157

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1158 CTGGTGGGGGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA 1217

Qy   301 GluGluHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1218 GAAGAGCATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCCTAGACGAGGTGAGGAAG 1277

Qy   321 GluGluTrpProLeuValAspAspAspCysThrArgGlyValThrGlyTyrHisGlyGlnLeuThr 340
           ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db  1278 GAAGAGTGGCCGCTGGTGGACGACGACTGCACGGGAGTCACCGGCTACCATGGACAGCTTACC 1337

Qy   341 IleHisGlyLysLysAspHisGluSerValPheThrValSerLeuTrpAspCysGlyAspArgGlyLys 360
           ||||||||||||||||||||||||||||||||::|||||||||||||||||||||||||
Db  1338 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCGGCAAG 1397

Qy   361 PheArgValLysIleArgGlyIleAspIleProGluValLeuProArgThrAlaAspLeuThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db  1398 TTCAGGGTCAAGATCAGAGGCATTGACATCCCCGTCCTGGAACACCGACCTCCACA 1457

Qy   381 ValPheValGluAlaAsnIleGlnInTyrGlyValGlnInValLeuCysGlnInArgArgThrSer 400
           |||||||||||||||||||||:|:|||||||||||||||||||||||||||||||||||||
Db  1458 GTTTTTGTGGAGGCAAACATCCAGATGGGCAACAAGTCCTTTGCCAAAGGAGAACCAGC 1517
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Left column (positions, alternating Db / Qy lines): 1518, 421/440, 1577, 1578/1637, 441/460, 1638/1697, 461/480, 1698/1757, 481/500, 1758/1817, 501/520, 1818/1877, 521/540, 1878/1937, 541/560, 1938/1997, 561/580, 1998/2057, 581/600, 2058/2117, 601/620, 2118/2177, 621/640, 2178/2237, 641/660, 2238/2297, 661/680, 2298/2357, 681/700, 2358/2417, 701/720, 2418/2477, 721/740, 2478/2537, 741/760, 2538/2597, 761/780.

Right column (positions, alternating Db / Qy lines): 2598/2657, 781/800, 2658/2717, 801/820, 2718/2777, 821/840, 2778/2837, 841/860, 2838/2897, 861/880, 2898/2957, 881/900, 2958/3017, 901/920, 3018/3077, 921/940, 3078/3137, 941/960, 3138/3197, 961/980, 3198/3257, 981/1000, 3258/3317, 1001/1020, 3318/3377, 1021/1040, 3378/3437, 1041/1060, 3438/3497, 1061/1080, 3498/3557, 1080/1100, 3558/3617.

Terminal labels: Qy 1100 SerAla 1102 ; Db 3618 TTCAGCC 3624.

RESULT 11
US-08-162-081B-35
; Sequence 35, Application US/08162081B

```
;  Patent No. 5824492
;  GENERAL INFORMATION:
;  APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;  APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
;  APPLICANT: Joseph; Otsu, Maayuki; Panayotou, George; Volinia,
;  APPLICANT: Stefano; Gout, Ivan Tarasovitch
;  TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
;  TITLE OF INVENTION: THEIR PREPARATION AND USE
;  NUMBER OF SEQUENCES: 50
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Felfe & Lynch
;     STREET:  805 Third Avenue
;     CITY:  New York
;     STATE:  New York
;     COUNTRY: USA
;     ZIP:  10022
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: PC-DOS
;     SOFTWARE: Wordperfect
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/162,081B
;     FILING DATE:  February 7, 1994
;     CLASSIFICATION:  435
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/GB93/00761
;     FILING DATE: 13 April 1993
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Pasqualini, Patricia A.
;     REGISTRATION NUMBER: 34,894
;     REFERENCE/DOCKET NUMBER: LUD 5256
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 688-9200
;     TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO: 35:
;  SEQUENCE CHARACTERISTICS:
;     LENGTH:  3207 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;  US-08-162-081B-35
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Alignment Scores:
Pred. No.:            7.92e-160        Length:           3207
Score:                1465.50          Matches:          382
Percent Similarity:   51.40%           Conservative:     204
Best Local Similarity: 33.5%           Mismatches:       405
Query Match:          25.31%           Indels:           149
DB:                   1                Gaps:             39

US-09-974-573-1 (1-1102) x US-08-162-081B-35 (1-3207)
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Db  2248  GGCTTTCTGTCCTCTAAACCCTGCTCATCAGCTGGAAATCTCAGGCTTGAAGAGTGT  2307
Qy   802  LysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspProThr   821
           ::::::||||||:::||| |||||  ||||||||
Db  2308  CGAATTATGTCTTCTGCAAAAGGCCACTGGGTTGAATTGGGAG---AACCCAGAC      2361
Qy   822  AlaLeuSer----------------AsnGluThrIleGlyIleIlePheLysHisGly  835
           :: ||||
Db  2362  ATCATGTCAGAATTACTCTTTCAGAACAATGAG------ATCATCTTTAAAAATGGG   2412
Qy   836  AspAspLeuArgGlnAspMetLeuIleLeuArgGlnIleLeuArgIleMetGluSerIleTrp  855
           ||||||||||   :::
Db  2413  GATGATTTACGCAAGATATGCTAACCCTTCAGATTATTGCCATTATGGAAAATATCTGG  2472
Qy   856  GluThrGlySerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerGluThrGlyAspLys  875
           |||||| |||||
Db  2473  CAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGATCGTCTGTCAATCGGTGACTGT  2532
Qy   876  IleGlyMetIleGluIleValLysAspAlaThrIleAlaAlaLysIleGlnSerThr  895
           :::::||||||:::::::
Db  2533  GTGGGACTTATCGAGGTGGTGAGAAATTCCACACTATAATGCAGATT---CAGTGTAAA  2589
Qy   896  ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLeuLysGlu  913
           :::||||||
Db  2590  GGGAGGCCTGAAAGGTGCACTCGAGTTTAACAGCCACCACCTCCATCAGTGCTCAAAGAC  2649
Qy   914  LysCysProIleGluGluLysPheGlnIleAlaAlaValAlaGluArgPheValTyrSerCysAla  933
           ||:::
Db  2650  AAGAACAAG--GGGAAAATATGATGCGGCCATCGATTTGTTTACACGATCATGTGCT  2706
Qy   934  GlyTyrCysValAlaThrPheValLeuGlyIleIleGluGlyAspArgHisAsnAspAsnIleMet  953
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Db  2707  GGATATTGTGTTGCCACCTTCATTTTGGAATTGGAGAGATCGTCACAATAGTAATATCATG  2766
Qy   954  IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysLys  973
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Db  2767  GTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGACACTTTTTGGATCACAAGAAG  2826
Qy   974  SerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProAspPheLeuPhe  993
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Db  2827  AAAAAATTTGGTTATAAACGAGAGGCCGGTGCCATCGATTTGTTTGACACAAGATTTCTTAATA  2886
Qy   994  ValMetGlyThrSerGlyLys-------ThrSerLeuHisPheGlnLysPheGlnAsnAsp  1011
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Db  2887  GTGATTAGTAAAGAGCCCAAGAATGCAACAAGACAAGAGAATTTGAGAGGTTTCAGGAG  2946
Qy  1012  ValCysValAlaTyrLeuAlaThrPheValLeuGlyHisHisThrAsnLeuLeuIleLeuGluPhe  1031
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Db  2947  ATGTGTTACAAGGCTTATCTAGCTATTCCGGCAGACTGGCCAATCTCTTCATAAAATCTTTC  3006
Qy  1032  SerMetMetLeuMetThrGlyMetProGlnLeuThrSerGlyLysGluAspLysGlnGln  1051
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Db  3007  TCAATGATGCTTGGCCTGGAATGCCAAGAACTGCAATCTCTTTTGATGATATTGCATACATT  3066
Qy  1052  ArgAspAlaLeuThrGlyLysSerGluGluGluAspLysLysTyrPheLeuAspAspGln  1071
           ::||||
Db  3067  CGAAAGACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAA  3126
Qy  1072  IleGluValCysArgAspLysGlyLysGlyTrpThrValGlnProAsnTrpPheLeuHisLeuVal  1091
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Db  3127  ATGAATGATGCACACACCGTGGCTGCACAACAAAAATGATTGGATCTTCCACACAATT  3186
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RESULT 12
US-08-780-872-35
; Sequence 35, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE

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Db  1237  AAAGAGGAACACTGTCCATTGGCCTGGGGA                                1275
Qy   465  AsnLeuLeuIleLeuIle------AspHisAspLeuArgHisArgPheLeuGluValHisMet  484
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Db  1276  AATATAAAACTTGTTGATTACACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTT  1335
Qy   485  TrpGlnLeuSerGlyLysGlyLysAspGlnGlySerPheAsnAlaAspLysLeuThrSer  504
           |||
Db  1336  TGGCCAGTACCTCATGGACTAGAAGAT-------TTGCTGAACCCTATTGGTGTTACT--  1386
Qy   505  AlaThrAsnProAspLysGlyAsnSerMetSerIleSerIleLeuLeuAspAsnTyrCys  524
           ||| :::
Db  1387  GGATCAAAATCAAATAAAGAA-----ACTCCATGTTAGATTGGAGTTGACTGGTTCAGC  1443
Qy   525  HisProIleAlaLeuProLysHisArgProThrProAspProGluGlyArgVal---  543
           :::
Db  1444  AGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTATCC  1503
Qy   544  ------------------ArgAlaGluMetProAsn                          549
           |||
Db  1504  CGTGAAGCAGGATTAGTTATTCCCATGGACTGAGTAACAGACTAGCTAGACAGAGACAAT  1563
Qy   550  GlnLeuArg--------LysGlnLeuLeuGlnAlaIleAlaIleAlaThrAspProLeuAsn  565
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Db  1564  GAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAATTTGTACACGAATCCTCTATCT  1623
Qy   566  ProLeuThrAlaGluGlu---LeuGluLeuLeuTrpHisPheArgTyrGluSerLeuLysAsp  585
           ::::::
Db  1624  GAAATCACTGAGCAAGACAAGAGAGATTTTCGTGGAGCCACAGACACTATTGTGTAACTATC  1683
Qy   586  ProLysAlaValTyrProLysGlyLeuPheSerSerValLysTrpGlyGlnGlnIleLeuValAla  605
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Db  1684  CCCGAAATTCTACCCAAATTGCTTCTGTCTTGTTTAAATGAACTCTAGAGATGAAGTAGCT  1743
Qy   606  LysThrTyrGlnLeuLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspValGlyValGly  625
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Db  1744  CAGATGTACTGCTTG-----------GTAAAAGATTGGCCTCCAATCAAGCCTGAA  1788
Qy   626  LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluSerAspGluAsnValArgAlaIleAlaVal  645
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Db  1789  CAGGCTCCATGGAGCTTCTGGACTGCAATTACCCCAGATCCTATGGTTCAGGGTTTGCTGTT  1848
Qy   646  GlnLysLeuGluSer---LeuGluLeuAsp                                 664
           |||
Db  1849  CGGTGCTTAGAAAAATATTTAACAGAATGACAAACTTTCTCAGTACCTAACTACGCTAGTA  1908
Qy   665  GlnAlaValLysPheGluProTyrHisAspLeuArgAlaLeuAlaArgPheLeuLysGlyArg  684
           :::
Db  1909  CAGGTACTAAAATAATATGAAACAGGATCGGTCACTTTTTGGCATTTAAAATCTGAGATG--  1968
Qy   685  GlyLeuArgAsnLysArgIleGlyHisPheLeuValAlaValLeuIleLeuGlnValIleAlaAla  704
           ||||
Db  1969  GCGTTAACTAATCAAGGATCGGTCACTTTTTGGCATTTAAAATCTGAGATG--         2025
Qy   705  GlnSerArgHisTyrGlnArgPheThrGlnArgGlnAsn------LeuAsnLeuProGln  724
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Db  2026  CACAATAAAACAGTTAGTCAAGTTTGGCCTGAGTCCTATTCCGTGCATGT          2085
Qy   725  GlyThrAlaMetLeuHisAspPheThrGlnArgArgGluAspGluLysGlnLysLys  744
           ||| :::
Db  2086  GGGATGTATCTGAAGCAC---CTTAATAGGCAAGTTGAGGCTATGAGGGAAAAGCTCATTAAC  2142
Qy   745  ValThrIleAspIleLysSerLeuSerLeuAlaGluLysSerTyrAspValSerSerGlnValIle  764
           :::
Db  2143  TTGACT-----GACATT----CTCAAACAGAGAGGAAGGATGAAACACAAAAGGTA--    2190
Qy   765  SerGlnLeuLysGlnLysLeuAsnLeuGlnAsn--------LeuAsnLeuProGln  781
           :::::::
Db  2191  ---CAGATGAAGTTTTAGTTGAGCAAATGCGGCGACCAGATTTCATGGATGCTCTCCAG  2247
Qy   782  SerPheArgValProTyrAspProGlyLeuLysGlyAlaGlyValAlaLeuValIleGluLysCys  801
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NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Felfe & Lynch
   STREET: 805 Third Avenue
   CITY: New York
   STATE: New York
   COUNTRY: USA
   ZIP: 10022
COMPUTER READABLE FORM:
   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
   COMPUTER: IBM PS/2
   OPERATING SYSTEM: PC-DOS
   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/780,872
   FILING DATE: 09-JAN-1997
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: 08/162,081
   FILING DATE: February 7, 1994
   APPLICATION NUMBER: PCT/GB93/00761
   FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
   NAME: Pasqualini, Patricia A.
   REGISTRATION NUMBER: 34,894
   REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
   TELEPHONE: (212) 688-9200
   TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 3207 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
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Us-08-780-872-35

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Alignment Scores:
   Pred. No.:
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   Best Local Similarity:    33.51%             Conservative:  204
   Query Match:              25.31%             Mismatches:    405
   DB:                                          Indels:        149
                                                Gaps:          39
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US-09-974-573-1 (1-1102) x US-08-780-872-35 (1-3207)

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Qy   23  MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIlePro---------        39
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Db    1  ATGGCTCCAAGACCACCATCACAGGTGGGACTCGTGGGCATCCACTCACTGAGCCCCCAAGAATC  60

Qy   40  ---IleGluPheValLeuProThrSerGlnArgSerGlnAsnThrLysAsnThrLysProGluThrAlaLeu  58
            |||| :  ::|:
Db   61  CTAGTAGAAATGTTTACACCAAATGGATGAGATGACT------------------------       99

Qy   59  LeuHisValAlaGlyHisGlyAsnValGluGlnMetGlyAsnValGlnMetGlyAsnValMetGluValTrpLeuArgArgAla  78
             |||        :::|||    :::::::
Db  100  TTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGAAGCATTATTAAAGAAGCA         159

Qy   79  LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu        98
             :::                         |||
Db  160  AGAAAATACCCTCTC----------CATCAACTTCTTCAAGATGAATCTTCTTAC          204

Qy   99  LeuTyrGlnLysGlyGlnTrpTyrTrpTyrGluIleTyrAspLysTyrAspGlnValValGlnThr  118
             :::::                    ::::::
Db  205  ATTTTCGTAAGTGTTACCCAAGAAGCAGAAGGGAAGAATTTTTGATGAAACAAGACGA        264

Qy  119  LeuAspCysLeuArgTyrArgLysTrpLysValLeuValHisArgSerProGlyGlnIleHisValVal  138
             |||||                        :::
Db  265  CTTTGTGACCTTCGGCTTTTTCAACCCTTT-------------TTAAAAGTAATT           306

Qy  139  GlnArgHisAlaProSerGluGluThrLeuGluAsnLeuHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMet  158
             :::            |||   ||| :::::
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Qy  307                                                                        363
Db  307  GAACCAGTAGGCAACCGTGAGAGAAAAGATC---CTCAATCGAGAAATTGGTTTGCTATC       363

Qy  159  GlyTyrAspValThrAspValSerArgAsnValHisAspAspGluLeuGlyLysGluPheThrArgArg  178
             :::                            ||::::::
Db  364  GGCATGCCAGTGTGTGAATTGATATGGTTAAGATCCAGGAGTACAGGGACTTCCGAAGA        423

Qy  179  ArgLeuValThrProArgMetAlaGluValAlaAlaGlyArgAsp-------------         192
             ::::
Db  424  AATATTCCAATGTTGTAAAGAACGTGTGATCTTAGGGATCTTAATTCACCTCATAGT        483

Qy  193  ProLysLeuTyrAlaMetHisProValThrSerLysPro---LeuProGluTyrLeu       211
             :::                            :::
Db  484  AGAGCAATGTATGTTTATCCCAAATGTAGAAATCTTCACCAGAACTGCCAAAGCACATA      543

Qy  212  LeuLysLysIleThrAsnAsnCysValPheIleValIle--------His               225
             ||:::                      :::||||
Db  544  TATAATAAATTGGATAAAGGCAAATAAATAGTGGTAATAGTTTCTCCAAAT             603

Qy  226  ArgSerThrSerGlnThrIleLysValSerAlaAspAspProGlyThrIleLeu           245
             :::::                       |||
Db  604  AATGACAACAGAAGTATACTCTGAAAATCAACCATGAGTGTGTGCCAGAACAAGTAATT      663

Qy  246  GlnSerProPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGluSer---     264
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Db  664  GCTGAAGCAATCAGGAAA-------AAAACTGAAGGTATGTTGCTATCATCTGAACAACTA    717

Qy  265  -----------GlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGlu      279
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Db  718  AAACTCTGTGTTTTAGAATATCAGGGCAAGTATATTTTAAAGTGTGTGGATGTGATGAA     777

Qy  280  TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsn    299
             :::::                         |||
Db  778  TACTTCCTAGAAAAAATCCCTGAGTCAGTAGTATATAAGAAGCTGTATAATGCTT          837

Qy  300  GlyGluGlyIleLeuHisLeuLeuAspThrProProAspProAlaLeuAspGluValArg    319
             ::||::                        ::
Db  838  GGGAGGATGCCCAATTTGATGCTG-----------------ATGGCTAAAGAAAGCCTC      879

Qy  320  LysGluGluTrpProLeuValAspAspCysThrGlyValThrGlyIleTyrHisGluGlnAsnLeu  339
             :::::                       :::
Db  880  TATTCTCAACTGCCCAATG------GACTGTTTTACAATGCCATCATTCCAGACGGCATC     933

Qy  340  Thr-----------------IleHisGlyLysAspHisGluSerValPheThrValSerLeu  354
             :::                     ||||
Db  934  TCCCAGCTACGCCATATATGAATGAGAA-------------ACATCTACAAAATCCCTT    981

Qy  355  TrpAspCysAspSerArgLysPheArgValLys---------------               364
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Db  982  TGGGTTATAATAGTGCACTCAGAATAAAAATTCTTTGTCAACCTATGTGAATGAATAAAT    1041

Qy  365  IleArgGlyIleAspAspIleProArgValLeuProArgThrAlaAspLeuThrPheValGlu  384
             |||||                        ::||
Db  1042 ATTCGAGACATTGAC------------------------AAGATTTATGTTCGA         1071

Qy  385  AlaAsnIleGlnTyrGlyIleValLeuCysGlnArgArgThrArgSerProLysProPhe     404
             ||||                        :::
Db  1072 ACAGGTATCTACCATGGAGGAGAACCCTTATGTGATAATGTGAATATACCTTCAAAGAGTACCT 1131

Qy  405  ThrGlyGluLeuTrpAsnValTrpLeuTyrProValSerIleLeuLysLeuLysAspLeuPro  424
             :::::                       :::
Db  1132 TGTTCCAATCCAGGTGGAATGAATGGCTGAATTAAGTATATATTACGAATTACAATTCTGATCTTCCT 1191

Qy  425  LysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuArgSerGlyLys  444
             :::::                       ::::
Db  1192 CGTGCTGCTGACTTTGCCTTCCATT---TGT-------------TCTGTTAAAGGCCGA     1236

Qy  445  ThrSerAlaGluMetProSerProGluSerLysGlyLysGlyLysGlnLeuLeuTyrTyrVal  464
             |||||
Db  1237 AAGGGTGCT----------------------AAAGAGGAACACTGTCCATTGGCCTGGGGA    1275

Qy  465  AsnLeuLeuLeuIleAspHisArgPheLeuLeuGluArgHisGlyGluTyrValLeuHisMet  484
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Db  1276 AATATAAACTTGTTTGATTACACAGATACTCTAGTATCTGAAAAATGGCTTTGAATCTT    1335
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Qy    485  TrpGlnLeuSerGlyLysGlyAspGlySerPheAsnAlaAspLysLeuThrSer  504
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Db   1336  TGGCCGAGTACCTCATGGACTAGAAGAT-----TTGCTGACCCTATTGGTGTTACT---  1386

Qy    505  AlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeuAspAsnTyrCys  524
                   :::                              :::::
Db   1387  GGATCAAATCCAAATAAAGAA---ACTCCATGTTTAGAGTTGAGTTGACTGGTCAGC  1443

Qy    525  HisProIleAlaLeuProLysHisArgProThrProGluGlyAspArgVal---  543
                :::                              :::
Db   1444  AGTGTGTGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGTCTGTATCC  1503

Qy    544  ------------------------------------ArgAlaGluMetProAsn  549
                                                ||||
Db   1504  CGTGAAGCAGGATTAGTATTCCCATGCCAGCAGCACTGAGTAACGACTAGCTAGAGACAAT  1563

Qy    550  GlnLeuArg----------LysGlnLeuGluAlaIleAlaIleLeuAlaThrAspProLeuAsn  565
               :::             ||||||
Db   1564  GAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAATTTGTACACGAGATCCTCTATCT  1623

Qy    566  ProLeuThrArgAlaGluAspLysGluLeuLeuTrpHisPheArgTyrGluSerLeuLysAsp  585
                :::||    |||||   :::::
Db   1624  GAAATCACTGAGCAAGAGAAAGAATTTCTGTGGCACCACAGACACTATTGTGTAACTATC  1683

Qy    586  ProLysAlaTyrProLysPheSerGluSerValLysTrpGlyGlnGlnGluIleValAla  605
                |||||            :::
Db   1684  CCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAAATGGAACTCAGAGATGAAGTAGCT  1743

Qy    606  LysThrTyrGlnLeuLeuAlaLysAlaArgGluValTrpAspGlnSerAlaLeuAspValGly  625
               :::
Db   1744  CAGATGTACTGCTTG---------GTAAAAGATTGGCCTCCAATCAAGCCTGAA  1788

Qy    626  LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaVal  645
              |||||        :::::          ||||||
Db   1789  CAGGCTATGGAGCTTCGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTTGCTGTT  1848

Qy    646  GlnLysLeuGluSer---LeuGluAspGluAlaAspValLeuTyrLeuLeuGlnLeuVal  664
               :::
Db   1849  CGGTGCTTAGAAAAATATTTAACAGATGCAAACTTTCTCAGTACCTAATTCAGTAGTA  1908

Qy    665  GlnAlaValLysPheGluAspSerAlaHisAspAspTyrTyrHisProTyrHisIleAspSerSerAlaLeuAlaArgPheLeuLeuLysArg  684
              :::||                   :::::
Db   1909  CAGGTACTAAAAATATGACAGATTATACCGGTGTGATTTTACTCAAAAAA  1968

Qy    685  GlyLeuArgAsnAlaArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIleAla---  704
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Db   1969  GCGTTAACTAATCAAAAGGATCGGTCACTTTTCTTTCTTTGGCATTTAAAATCTGAGACTG---  2025

Qy    705  GlnSerArgHisTyrGlnArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCys  724
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Db   2026  CACAATAAAACAGTTAGTTCAGAAGGTTTGGCCTGCTTTTGGAGTCCTATTGCCGTGCATGT  2085

Qy    725  GlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnAsnValIleAspMetLeuGlnLys  744
              |||                      :::::
Db   2086  GGGATGTATCTGAAGCAC---CTTAAATAGGCCAAGTTGAGGCGTAGAGTTGAGAAAGCTCATTAAC  2142

Qy    745  ValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSerSerGlnValIle  764
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Db   2143  TTGACT---GACATT---------CTCAAACAAGAAGAAGGAGATGAAAACACAAAGTA---  2190

Qy    765  SerGlnLysLysGlnLysLeuGlnAsnLeuGlnAsn-------LeuAsnLeuProGln  781
              :::::
Db   2191  ---CAGATGAAGTTTTAGTTGGAGCAAAATGGCGGCGACCCAGATTGCATCTCCAG  2247

Qy    782  SerPheArgValProTyrAspProGlyLeuLysGlyAlaGlyLeuValAlaLeuValIleGluLysLysCys  801
              |||            :::::
Db   2248  GGCTTTCTGTCTCCTCAAACCCTCATCAGCTGCGAAATCTCAGGCTTGGAGAGTGT  2307

Qy    802  LysValMetAlaSerLysLysGluProLeuTrpLeuGluPheLysCysAlaAspProThr  821
              :::::                      :::
Db   2308  CGAATTATGTCTTCTGCAAAAGGCCACTGTGGTTGAATTGGGAG------AACCCAGAC  2361


Qy    822  AlaLeueuSer------------------------AsnGluThrIleGlyIleIlePheIleLysHisGly  835
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Db   2362  ATCATGTCAGAATTACTCTTCAGAACAATGAG---ATCATCTTTAAAAATGGG  2412

Qy    836  AspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrp  855
              |||||||||||||||||||||||    |||||||
Db   2413  GATGATTTACGGCAAGATATGCTAATCCTTCAGATTATTCGCATTATGGAAAAATATCTGG  2472

Qy    856  GluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLys  875
              :::                      ||||||
Db   2473  CAAAATCAAGGTCTTGATCTTCGAATGTCATTATGGATGTCTGTCAATCGGTGACTGT  2532

Qy    876  IleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleGlnGlnSerThr  895
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Db   2533  GTGGGACTTATCGAGGTGGTGAGAAATTCCACACTATAATGCAGATT---CAGTGTAAA  2589

Qy    896  ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLeuLysGlu  913
               :::                     :::::
Db   2590  GGAGGCCTGAAAAGGTGCACTGCAGTTTAACAGCACCACACTCCATCAGTGGCTCAAAGAC  2649

Qy    914  LysCysProIleGluGluLysProHisGlnAlaAlaAlaValGluArgPheValTyrSerCysAla  933
              |||||                    :::::
Db   2650  AAGAACAAG---GGGGAAATATATGATGCGGCATCAGATTGGTTTTACACGAGGCATGTGCT  2706

Qy    934  GlyTyrTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMet  953
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Db   2707  GGATTTGTGTTGTGCCACCTTCATTTGGAGATGGAGATCGTCACAATAGTAATATCATG  2766

Qy    954  IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys  973
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Db   2767  GTTAAAGATGATGGACAACGTTTCATATAGATTTTGGACACTTTTGGATCAAGAAG  2826

Qy    974  SerPheLeuGlyIleAsnLysGluArgValProPheValLeuProArgLysAspPheLeuPhe  993
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Db   2827  AAAAAATTGGTTATAAAGGAGCCCAAGATGCACAAAGAAGAATTTGAGGTTTCAGGAG  2886

Qy    994  ValMetGlyThrSerGlyLysLys-----ThrSerLeuHisPheGlnLysPheGlnAsp  1011
              :::                      :::
Db   2887  GTGATTAGTAAAGAGGCCCAAGATGCACAAAGAACAAGAGAATTTGAGGTTTCAGGAG  2946

Qy   1012  ValCysValLysValAlaTyrLeuAlaLeuArgHisHisThrAsnLeuIleLeuIleLeuPhe  1031
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Db   2947  ATGTGTTACAAGGCTTATCTGGCATGCCAGCATGCCAATCCTTCATAAATCTTTTC  3006

Qy   1032  SerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIle  1051
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Db   3007  TCAATGATGCTGGCTCTGGCAATGCCAGAATCTTTGATGATATTGCATACATT  3066

Qy   1052  ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaAlaLysTyrPheLeuAspGln  1071
              :::::                    |||||
Db   3067  CGAAAGACCCTAGCTTTAGATAAAACTGACCAAGAGGCTTTGAGTATTTCATGAAACAA  3126

Qy   1072  IleGluValCysArgAspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal  1091
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Db   3127  ATGAATGATGCACACACATGTGGCTGGACAACAAAAATGATTGGATCTTCCACACAATT  3186
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;       COUNTRY: USA
;       ZIP: 10022
;  COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;       COMPUTER: IBM PS/2
;       OPERATING SYSTEM: PC-DOS
;       SOFTWARE: Wordperfect
;  CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/085,957
;       FILING DATE:
;       CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/780,872
;       FILING DATE: 09-JAN-1997
;       APPLICATION NUMBER: 08/162,081
;       FILING DATE: February 7, 1994
;       APPLICATION NUMBER: PCT/GB93/00761
;       FILING DATE: 13 April 1993
;  ATTORNEY/AGENT INFORMATION:
;       NAME: Pasqualini, Patricia A.
;       REGISTRATION NUMBER: 34,894
;       REFERENCE/DOCKET NUMBER: LUD 5256
;  TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 688-9200
;       TELEFAX: (212) 838-3884
;  INFORMATION FOR SEQ ID NO: 35:
;  SEQUENCE CHARACTERISTICS:
;       LENGTH: 3207 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-09-085-957-35

Alignment Scores:
Pred. No.:                                    Length:          3207
Score:               7.92e-160                Matches:          382
Percent Similarity:  1465.50                  Conservative:     204
Best Local Similarity: 51.40%                 Mismatches:       405
Query Match:         33.51%                    Indels:          149
                     25.31%                    Gaps:              39
DB:                  3
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Qy 505 AlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuAspAsnTyrCys 524
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Qy 525 HisProIleAlaLeuProLysHisArgProThrProAspProGluGlyAspArgVal--- 543
         :: ::: |||||| :::
Db 1444 AGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAGAGAGCCAATGGTCTGTATCC 1503

Qy 544 ------------------------------ArgAlaGluMetProAsn 549
                                        ||||||
Db 1504 CGTGAAGCAGGATTAGTTATTCCCATGACGAGGACTGAGTAACAGCTAGGAGACAAT 1563

Qy 550 GlnLeuArg------------LysGlnLeuGluAlaIleAlaIleAlaThrAspProLeuAsn 565
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Db 1564 GAATTAAAGAGAAATGATAAAGACCTCCGAGCAATTTGTACACGAGATCCTCTATCT 1623

Qy 566 ProLeuThrAlaGluGluGluLeuLysGluLeuTrpHisPheArgTyrGluSerLeuLysAsp 585
         ||||||||
Db 1624 GAAATCACTGAGCAAGAGAAAGATTTTCGTGGAGCCAGACACTATTGTGTAACTATC 1683

Qy 586 ProLysAlaTyrProLysSerLeuPheSerArgValLysTrpLysGlnLeuIleLeuValAla 605
         |||||| :::::
Db 1684 CCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAAATGGAAGCTAGAGATGAAGTAGCT 1743

Qy 606 LysThrTyrGlnLeuLeuLysArgGluValTrpAspGlnSerAlaLeuAspValGly 625
         :::
Db 1744 CAGATGTACTGCTTG----------------GTAAAAGATTGGCCTCCAATCAAGCCTGAA 1788

Qy 626 LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaAlaVal 645
         ::::|||||||
Db 1789 CAGGTCATGGAGCTTCTGGACTGCAATTACCCAGATCCTATGTTTCGAGGTTTTGCTGTT 1848

Qy 646 GlnLysGluSer--LeuGluLeuAspGluHisLeuTyrLeuLeuGlnLeuVal 664
         :::
Db 1849 CGGTGTTAGAAAAATATTAACAGATGACAAACTTTCCAGTACCTAATTCAGCTAGTA 1908

Qy 665 GlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLysArg 684
         ::::|||||||
Db 1909 CAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTTACTCAAAAA 1968

Qy 685 GlyLeuArgAsnLysArgIleGlyHisPheLeuTrpProAsnArgGluLeuIleAla 704
         :::
Db 1969 GCGTTAACTAATCAAAGGATCGGTCACTTTTTGTTTTGGCCATTTTAAAATCTGAGAATG--- 2025

Qy 705 GlnSerArgHisTyrGlnArgGlnAlaValIleLeuGlnAlaTyrLeuArgGlyCys 724
         ::::|||||||
Db 2026 CACAATAAAAACAGTAGTCAGAGGTTTGGCCTGTTTGGAGTCCTATTGCCGGCATGT 2085

Qy 725 GlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleLeuAspMetLeuGlnLys 744
         |||||| ::::
Db 2086 GGGATGTATCTGAAGCAC--CTTAATAGGCAAGTTGAGGCTATGGAAAAGTCATTAAC 2142

Qy 745 ValThrIleAspIleLysSerLeuSerAlaGluLuLysTyrAspValSerSerGlnValIle 764
         :::||||||
Db 2143 TTGACT---GACATT------CTCAAACAGAGAGAGAGGATGAAACACAAAAGGTA--- 2190

Qy 765 SerGlnLeuLysGlnLeuLysGluLeuAsnLeuAsn------LeuAsnLeuProGln 781
         :::||||||
Db 2191 ---CAGATGAAGTTTTTAGTTGAGCAAATGCGGGCGACCCAGATTTCATGGATGCTCCAG 2247

Qy 782 SerPheArgValProTyrAspProGlyLeuLysAlaLeuValIleGluValLysLysCys 801
         ::::|||||||
Db 2248 GGCTTTCTGTCTCCTCTCAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAGTGT 2307

Qy 802 LysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspProThr 821
         ::: ||||||
Db 2308 CGAATTATGTCTTCTGCAAAAAGGCACTGTGGTTGAATTGGGAG------AACCCAGAC 2361

Qy 822 AlaLeuSer------------AsnGluThrIleGlyIleIlePheHisGly 835
         |||
Db 2362 ATCATGTTCAGAATTACTCTTTCAGAACAATGAG--------ATCATCTTTAAAAATGGG 2412

Qy 836 AspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrp 855
         ::: |||||| :::
Db 2413 GATGATTTACGGCAAGATATGCTAACCCTCCAGATTATTCGCATTATGGAAAATATCTGG 2472

Qy 856 GluThrGluSerLeuAspLeuCysLeuLysProTyrGlyCysIleSerThrGlyAspLys 875
         ::: :::   ::::|||||||
Db 2473 CAAAATCAAGGTCTTGATCTTCGAGTTACCTTATGGGATTGTCGTCAATGGTGACTGT 2532

Qy 876 IleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleLeuGlnGlnSerThr 895
         :::::|||||||
Db 2533 GTGGGACTTATCCAGGTGGTGAGAAAATCTCACACTATAATGCAGATT---CAGTGTAAA 2589

Qy 896 ValGlyAsnThrGlyAla----------PheLysAspGluValLeuSerHisTrpLeuLysGlu 913
         |||||| :::
Db 2590 GGAGGCGTGCACTGAGTTTAACAGCCACCAGTTTCATCAGTGGCTCAAAGAC 2649

Qy 914 LysCysProIleGluGluLysProGlnIleAlaAlaAlaValGlyPheValTyrSerCysAla 933
         :::|||||||
Db 2650 AAGAACAAG--GGGAAATATGATGCGGCCATCAGTTGTTTTACACGATCATGTGCT 2706

Qy 934 GlyTyrCysValAlaThrPheLeuGlyIleTyrLeuGlyAspArgHisAsnAspAsnIleMet 953
         :::|||||||
Db 2707 GGATATTGTTTGCCACCTTCATTTGGAATTGGAGATCGTCACCAATAGTAATATCATG 2766

Qy 954 IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys 973
         ::: ||||||
Db 2767 GTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGATCACTTTTGGATCACAAGAAG 2826

Qy 974 SerPheLeuGlyIleAsnLysGluGluValThrProValLeuThrProAspPheLeuPhe 993
         ::::|||||||
Db 2827 AAAAAATTGGTTATAAACGAGGAGCGGGTGCCGTTTGTTTGTTTGACACAAGATTTCTTAATA 2886

Qy 994 ValMetGlyThrSerGlyLysLys--------ThrSerLeuHisPheGlnLysPheGlnAsp 1011
         ||||||
Db 2887 GTGATTAGTAAAGAGCCCAAGAATGACAAAGAGAATTTGAGAGGTTTCAGGAG 2946

Qy 1012 ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleIleLeuPhe 1031
         ::::|||||||
Db 2947 ATGTGTTACAAGGCTTATCTAGCTCTTCGGCACCATACCAATCTCCTCATAAATCTTTTC 3006

Qy 1032 SerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluGlnValTyrIle 1051
         ::: ||||||
Db 3007 TCAATGATGCTTGGCTCTGGAATGCCACAACTTGCAATCTTTTGATGATATTGCATACATT 3066

Qy 1052 ArgAspAlaLeuThrValGlyLysSerGluGluAlaLysLysTyrPheLeuAspGln 1071
         ::: ||||||
Db 3067 CGAAAGACCCTAGCTTTAGATAAAAAGCTTTGAGGTATTTCATGAAACAA 3126

Qy 1072 IleGluValCysArgAspLysGlyTrpProThrValGlnProAsnTrpPheLeuHisLeuVal 1091
         :::|||||||
Db 3127 ATGAATGATGCACACCATGGTGGCTGACAACAAAAATGGATTGGATCTTCCACACATT 3186

RESULT 14
US-08-162-081B-34
; Sequence 34, Application US/08162081B
; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

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;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/162,081B
;   FILING DATE: February 7, 1994
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB93/00761
;   FILING DATE: 13 April 1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Pasqualini, Patricia A.
;   REGISTRATION NUMBER: 34,894
;   REFERENCE/DOCKET NUMBER: LUD 5256
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-162-081B-34

Alignment Scores:
Pred. No.:   3.09e-159   Length: 3240
Score: 1460.50   Matches: 385
Percent Similarity: 51.53%   Conservative: 206
Best Local Similarity: 33.57%   Mismatches: 394
Query Match: 25.22%   Indels: 163
DB: 1   Gaps: 40

US-09-974-573-1 (1-1102) x US-08-162-081B-34 (1-3240)

Qy   23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIlePro--------- 39
               ||| |||||| :::::: ||| ::: |||:::|||
Db   1 ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC 60

Qy   40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
                  :::||| :::|||||| |||
Db   61 CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACT--------------------- 99

Qy   59 LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla 78
               ||| :::   :::||| ::::::::: |||
Db   100 TTAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAAGCATGAACTATTTAAAGAAGCA 159

Qy   79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
                  :::   ::: |||:::||| |||
Db   160 AGAAAATACCCTCTC---------------CATCAACTTCTTCAAGATGAATCTTCTTAC 204

Qy   99 LeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThr 118
               :::::: ||| ||| :::   :::   :::
Db   205 ATTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAATTTTTTGATGAAACAAGACGA 264

Qy   119 LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal 138
               ||| |||||| ::::::   ::: |||:::
Db   265 CTTTGTGATCTTCGGCTTTTTCAACCATTT------------------TTAAAAGTAATT 306

Qy   139 GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIle 158
               ::: |||||| ::: |||:::::: |||
Db   307 GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATTGGTTTTGCTATC 363

Qy   159 GlyTyrAspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArg 178
               ||| ||| ::: ||| ||| |||:::::: ||||||
Db   364 GGCATGCCAGTGTGCGAATTTGATATGGTTAAAGATCCTGAAGTACAGGACTTCCGAAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGluValAlaGlyArgAsp------------------ 192
                  :::::: ||| ||||||
Db   424 AATATTCTTAATGTTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu 211
                     :::||| ||| ||| ||| ||| ||||||:::::::::
Db   484 AGAGCAATGTATGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCACATA 543

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIle------------------His 225
                     |||:::   :::   :::|||||| :::
Db   544 TATAATAAATTGGATAGAGGCCAAATAATAGTGGTGATTTGGGTAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeu 245
                                 |||:::|||:::::: ||| ||| ::::::
Db   604 AATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer--- 264
                              ||| ||| :::|||:::::: |||
Db   664 GCTGAAGCAATCAGGAAA------AAAACTAGAAGTATGTTGCTATCATCTGAACAATTA 717

Qy   265 ---------------GlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGlu 279
                              :::   :::   ::::::|||:::||||||||| ||||||
Db   718 AAACTCTGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAGTGTGTGGATGTGATGAA 777

Qy   280 TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsn 299
               ||| :::   ::: |||:::   ::::::::::::||| |||:::
Db   778 TACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATATAAGAAGCTGTATAATGCTT 837

Qy   300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg 319
               ||| ||| ||| :::
Db   838 GGGAGGATG------------------------------CCCAATTTGAAGATGATGGCT 867

Qy   320 LysGlu------------GluTrpProLeuValAspAspCysThrGlyValThrGlyTyr 335
               |||||| ::: |||::: |||||| ::: |||
Db   868 AAAGAAAGCCTTTATTCTCAACTGCCAATG------GACTGTTTTACAATGCCATCTTAT 921

Qy   336 HisGluGlnLeuThr---------------IleHisGlyLysAspHisGluSerValPhe 350
                     :::::::::   ::::::|||:::
Db   922 TCCAGACGCATTTCCACAGCTACACCATATATGAATGGAGAA------------ACATCT 969

Qy   351 ThrValSerLeuTrpAspCysAspArgLysPheArgValLys------------------ 364
               ||| ||||||||| :::||| |||:::|||
Db   970 ACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGTGCAACCTAT 1029

Qy   365 ------------IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
                           |||||| ||||||
Db   1030 GTGAATGTAAATATTCGAGACATTGAC-----------------------------AAG 1059

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnValLeuCysGlnArgArgThrSer 400
               ::::::||| ||| :::||| ::: |||||| :::
Db   1060 ATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACT 1119

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
                  ::: |||||| |||||| ::: ||| |||
Db   1120 CAAAGAGTACCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTATGATATATACATT 1179

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
                  |||||||||::: ||| ||| ||| ||| ||| :::
Db   1180 CCTGATCTTCCTCGTGCTGCTCGACTTTGCCTTTCCATT---TGC------------TCT 1224

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
               ::: |||::: ||| ||| :::
Db   1225 GTTAAAGGCCGAAAGGGTGCT---------------------AAAGAGGAACACTGTCCA 1263

Qy   461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
               ||| ::: |||::: ||| |||::: ||| |||:::
Db   1264 TTGGCATGGGGAAATATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAAATG 1323

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAsp 500
                  |||::::::||| ::: |||||| |||
Db   1324 GCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGAT------TTGCTGAACCCTATT 1377

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsn------------------------ 512
                  :::||| :::||||||:::||||||
Db   1378 GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGAC 1434

Qy   513 ------------------------------SerMetSerIleSerIleLeuLeuAspAsnTyr 523
                                             ||||||:::   ::::::
Db   1435 TGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTG---------ATTGAAGAGCA- 1484
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Qy    524 CysHisProIleAlaLeuProLysHisArgProThrProAspProGlu-GlyAspArgVa 543
          |||    :::  ||||||           :::    |||
Db   1485 TGCCAATTGGTCTGTATCCCGAGAAGCAGGGATTTAGCTATTCCCACGGACGAGACTAA 1544

Qy    543 lArgAlaGluMetProAsnGlnLeuArg--------------LysGlnLeuGluAlaIleIl 559
          ||||| :::   |||||||                         |||
Db   1545 CAGACTAGCTAGAGACAATGAATTAAGGAGAAAATGACAAGAACAGCTCAAAGCAATTTC 1604

Qy    559 eAlaThrArgProLeuAsnProLeuThrAlaGluAspLysGlyLeuLeuTrpHisPheAr 579
          ||||||| ::: |||          :::  ||||
Db   1605 TACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAG 1664

Qy    579 gTyrGluSerLeuLysAspTyrProLysAlaTyrProLeuPheSerSerValLysTrpG1 599
          :::    ||||||||| ::: |||||||||||||||||
Db   1665 ACACTATTCGTAACTATCCCGAAATTGCTTCGTCGTGTTAAATGAA 1724

Qy    599 yGlnGlyIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspG1 619
          :::|||      |||    ||||
Db   1725 TTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG------------GTAAAAGATTG 1769

Qy    619 nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerGluAs 639
          :::
Db   1770 GCCCCAATCAAACCTGACAGGCTATGGAACTTCTGAACCTGTAATTACCCCAGATCCTAT 1829

Qy    639 nValArgAlaIleAlaIleAlaValGlnGlyLeuGluser--LeuGluAspAspValLeuHi 658
          |||||        |||||
Db   1830 GGTTCGAGGTTTGCTGTGTTCGGTGCTTGGTGAAAAATATTTAACAGATGACAAACTTTCTCA 1889

Qy    658 sTyrLeuGluGlnLeuValGlnAlaValLysAspPheHisAspSerAlaLeuAl 678
          |||||||||   |:::
Db   1890 GTATTTAATTCAGCTAGCAGGTACAGGTCCTTATAAAATATCGATAAACTTGCTTGT 1949

Qy    678 aArgPheLeuLeuLysAspGlyLeuArgAsnLysArgIleGlyHisPheLeuTrpPh 698
          |||||    ::: ||||
Db   1950 GAGATTTTTACTGAAGAAGCATTGACTTATCAAGGATGGGCACTTTTTCTTTGGCA 2009

Qy    698 eLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGlnAsnArgPheAlaValIleLeuGl 718
          ||||   |:::||| ||||
Db   2010 TTTAAAATCTGAATG---CACAATAAAAACAGTAGCCAGAGGTTTGGCCTGCTTTTTGGA 2066

Qy    718 uAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValGlnAsp 738
          |||||| :::||| ::: |||
Db   2067 GTCCTATTGTCGTGCCAGGTGGGATGTATTGGACGCAC---CTGAATAGGCAAGTCGAGGGC 2123

Qy    738 lIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerArgAlaGluLysTyrAs 758
          ||| ::: |||||
Db   2124 AATGGAAAAGCTCATTAACTTAACT---GACATT-----CTCAAACAGGAGGAGAAGGA 2174

Qy    758 pValSerSerGlnValIleSerGlnLysGlnLeuLysGluAsnLeuGlnAsn------ 776
          ||| :::
Db   2175 TGAAACACAAAAGGTA------CAGATGAAGTTTTTAGTTGAGCAAATGAGGCGACCAGA 2228

Qy    777 ---LeuAsnLeuProGlnSerPheArgValProTyrAspTyrGlyProGlyLeuLysAlaGlyAl 795
          :::|||      |||:::|||
Db   2229 TTTCATGGATGCCCCTACAGGGCTTGCTGCTCGTCCCTCCATCAACTAGGAGAA 2288

Qy    795 aLeuValIleGluGlyLysGlyCysLysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPh 815
          ::: |||||||||     |||:::
Db   2289 CCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAAGGCCACTGTGGTTGAATTG 2348

Qy    815 eLysCysAlaAspProThrAlaLeuSer-------------------AsnGluThrIleGl 829
          :::||| ::::
Db   2349 GGAG------AACCCAGACATCATGTCAGAGTCAGAGTTACTGTTTCAGAACAATGAG---- 2394

Qy    829 yIleIlePheLysHisGlyAspLeuArgGlnIleLeuGluAr 849
          |||||       ::: |||
Db   2395 -ATCATCTTAAAAATGGGATGATTTACGGCAAGATATGTCTAACACTTCAAATTATTCG 2453

Qy    849 gIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy 869
          |||||        ||||:::
Db   2454 TATTATGGAAAATATCTGGCAAAATCAAGTCTTGATCTTCGAAATGTTACCTTATGGTTG 2513
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Qy    869 sIleSerThrGlyAspLysGlyMetIleGlyIleGluValLysAspAlaAlaThrThrIleAl 889
          ||| :::                |||||||
Db   2514 TCTGTCAATCGGTGACTGTGTGGGACTTATTGAGGTGGTCCGAAATTCTCACACTATTAT 2573

Qy    889 aLysIleGlnGlnSerThrValGlyAsnThrGlyAla------PheLysAspGluValLe 907
          ::: |||||||   |||
Db   2574 GCAAATT---CAGTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACT 2630

Qy    907 uSerHisTrpLeuLysGluLysCysProIleGluGlyLysPheGlnAlaAlaValGluAr 927
          ||| :::
Db   2631 ACATCAGTGGCTCAAAGACAAGAACAAA---GGAGAAATATGATGCAGCCATTGACCT 2687

Qy    927 gPheValTyrSerCysAlaGlyTyrProLysAlaThrPheValLeuGlyTyrIleGlyAspAr 947
          |||   :::|||
Db   2688 GTTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGGGATCG 2747

Qy    947 gHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHi 967
          :::
Db   2748 TCACAATAGTACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACA 2807

Qy    967 sIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluGluArgValProPheValLe 987
          ||| :::
Db   2808 CTTTTTGGATCACAGAGGATTTCTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAGACAAGAGA 2867

Qy    987 uThrProAspPheLeuPheMetValMetGly------ThrSerLeuHi 1005
          ||||||   :::
Db   2868 GACACAGGATTTCTCATAAATCTTTCTCAATGAAGCTTGGCTCTGGAATGCCAGAACAGAGA 2927

Qy   1005 sPheGlnLysPheGlnAspAspValCysValLysAlaTyrLeuAlaLeuArgHisThrAs 1025
          :::||| |||
Db   2928 ATTTGAGAGGTTTCAGGAGATGTGTTACAGCTATTCAGCTATTCGACAGCATGCCAA 2987

Qy   1025 nLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLy 1045
          ||||||   :::
Db   2988 TCTCTTCATAAATCTTTCTCAATGAAGCTTGGCTCTGGAATGCCAGAACTTACAATCTTT 3047

Qy   1045 sGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLy 1065
          ||| :::
Db   3048 TGATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAGGAGGCTTT 3107

Qy   1065 sLysTyrPheLeuAspGlnIleLeuGluValCysArgAspLysGlyGlyTrpThrValGlnPheAs 1085
          ::: |||
Db   3108 GGAGTATTTCATGAACAATGAACAAATGAGGCGACCCATGGTGGCTGGACACAAAAATGGA 3167

Qy   1085 nTrpPheLeuHisLeuVal 1091
          ||| :::
Db   3168 TTGGATCTTCCACACAATT 3186
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;    APPLICATION NUMBER:  US/08/780,872
;    FILING DATE:  09-JAN-1997
;    CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    APPLICATION NUMBER:  08/162,081
;    FILING DATE:  February 7, 1994
;    APPLICATION NUMBER:  PCT/GB93/00761
;    FILING DATE:  13 April 1993
;    ATTORNEY/AGENT INFORMATION:
;    NAME:  Pasqualini, Patricia A.
;    REGISTRATION NUMBER:  34,894
;    REFERENCE/DOCKET NUMBER:  LCD 5256
;    TELECOMMUNICATION INFORMATION:
;    TELEPHONE:  (212) 688-9200
;    TELEFAX:  (212) 838-3884
;    INFORMATION FOR SEQ ID NO: 34:
;    SEQUENCE CHARACTERISTICS:
;    LENGTH:  3240 base pairs
;    TYPE:  nucleic acid
;    STRANDEDNESS:  single
;    TOPOLOGY:  linear

US-08-780-872-34

Alignment Scores:
Pred. No.:            3.0e-159          Length:          3240
Score:               1460.50           Matches:          385
Percent Similarity:   51.53%           Conservative:     206
Best Local Similarity: 33.57%          Mismatches:       394
Query Match:          25.22%           Indels:           163
Db:                                    Gaps:              40

US-09-974-573-1 (1-1102) x US-08-780-872-34 (1-3240)
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Qy     23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluIlePro---------  39
            ||||||  |  :::::    :::::  :::    ||||||:::::
Db      1 ATGGCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAGAATC  60

Qy     40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu  58
                ||||  :  :::|||  :::
Db     61 CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACT---------------------  99

Qy     59 LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla  78
            |||          :::     :::|||     ::::::::
Db    100 TTAGAAATGCCCCGTGAGGCTACATTAGTAACTAGAAAGCATGAAACTATTTAAAGAAGCA 159

Qy     79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLys  98
            :::                               ||||  |  :::||||
Db    160 AGAAAATACCCTCTC----------------------CATCACTTCTTCAAGATGAATCTTCTAC 204

Qy     99 LeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrArgGluIleTyrAspLysTyrGlnValValGlnThr 118
            ||||  :::  :::  :::::::::  :::
Db    205 ATTTTCGTAAGTGTTACCCAAGAGAGCAGAAAGGAGAAGAAGAATTTTTGATGAAACAAGACGA 264

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Db    307 GAACCAGTAGGCAACCGTGAAGAAAGAATC---CTCAATCGAGAAATTGGTTTTGCTATC 363

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Qy    179 ArgLeuValThrProArgMetAlaGlyMetAlaGluValAlaGlyLysArgAsp---------  192
            ::::::
Db    424 AATATTCTTAATGTTTGTAAAGAAGCTGTGATCTTAGGGATCTTAATTCACCTCATAGT 483

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Qy    226 ArgSerThrSerGlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeu  245
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Db    604 AATACAAGCAGAAGTATCTCGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT  663

Qy    246 GlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGluSer----  264
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Db    664 GCTGAAGCAATCAGGAAA-----AAAACTAGAGTATGTTGTCTATCATCTGACAATTA  717

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Qy    320 LysGlu-----------GluTrpProLeuValAspAspPheCysThrGlyValThrGlyThrTyr  335
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Qy    336 HisGluGlnLeuThr-------------------------IleHisGlyLysAspHisGluSerValPhe  350
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Qy    351 ThrValSerLeuTrpAspCysAspAspArgLysPheArgValLys-----------  364
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Qy    365 ------------IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr  380
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Db   1180 CCTGATCTTCCTCGTGCTGCTGACTTTGCCTTCCATT---TGC---------TCT 1224

Qy    441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysLysAlaGlnLeuTyr  460
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Qy    461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuLeuArgHisGlyGluTyr  480
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Qy  907 uSerHisTrpLeuLysGluLysCysProIleGluGluLysPheGlnAlaAlaValGluAr 927
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Qy  927 gPheValTyrSerGlyAlaGlyTyrCysValAlaThrPheValLeuGlyLysGlyAspAr 947
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Search completed: February 15, 2004, 06:44:12
Job time : 486 secs

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Qy  559 eAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeueuThrHisPheAr 579
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Db 2175 TGAAACAAAAGGTA------CAGATGAAGTTTTTAGTTGAGCAAATGAGGGCGACCAGA 2228
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                    GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      February 15, 2004, 05:14:49 ; Search time 889 Seconds
                                            (without alignments)
                                            4566.213 Million cell updates/sec

Title:           US-09-974-573-1
Perfect score:   5790
Sequence:        1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:   BLOSUM62
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Searched:        2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters:   4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09974573/runat_11022004_180018_18255/app_query.fasta_1.1287
-DB=Published_Application_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	%	Length	DB	ID	Description
1	5538	95.6	5309	12	US-10-334-143-120	Sequence 120, App
2	5523.5	95.4	3342	13	US-10-101-235A-3	Sequence 3, Appli
3	5309	91.7	3237	13	US-10-101-235A-5	Sequence 5, Appli
4	1460.5	25.2	3213	13	US-10-101-235A-7	Sequence 7, Appli
5	1354.5	23.4	5220	12	US-10-440-464-145	Sequence 145, App
6	1352.5	23.4	5220	13	US-10-337-192-1	Sequence 1, Appli
7	1352.5	23.3	5287	14	US-10-027-591-1	Sequence 1, Appli
8	1349.5	23.1	3777	15	US-10-162-160-2	Sequence 2, Appli
9	1337.5	18.5	5061	13	US-09-814-353-19587	Sequence 19587, A
10	1074	17.9	3504	14	US-10-092-219-1	Sequence 1, Appli
11	1034	17.9	3504	9	US-09-205-658-47	Sequence 47, Appl
12	1034	17.9	3504	13	US-09-084-353A-47	Sequence 47, Appl
13	1034	16.3	627	13	US-09-963-693-47	Sequence 47, Appl
14	944	15.9	5990	13	US-10-101-235A-1	Sequence 1, Appli
15	922	15.9	5990	10	US-09-917-800A-477	Sequence 477, App
16	922	12.4	3473	12	US-10-388-934-72	Sequence 72, App
17	719.5	12.4	3063	13	US-10-252-157-370	Sequence 370, App
18	709.5	12.3	3063	13	US-10-117-722-474	Sequence 474, App
19	709.5	12.3	441	15	US-10-037-270-474	Sequence 474, App
20	699	12.1	3252	10	US-09-867-701-5505	Sequence 5505, Ap
21	690.5	11.9	3252	10	US-09-921-232-1	Sequence 1, Appli
22	690.5	11.9	3252	10	US-09-921-330-1	Sequence 1, Appli
23	690.5	11.9	2784	10	US-09-921-329-1	Sequence 1, Appli
24	678.5	11.7	2462	12	US-10-369-493-26898	Sequence 26898, A
25	638.5	11.0	2418	12	US-10-366-493-25482	Sequence 25482, A
26	561.5	9.7	473	9	US-09-771-161A-10	Sequence 10, Appl
27	384.5	6.6	5703	9	US-09-864-761-16057	Sequence 16057, A
28	380	6.6	2620	10	US-09-801-368-389	Sequence 389, App
29	356.5	6.2	3205	13	US-09-925-302-205	Sequence 205, App
30	345.5	6.0	7864	10	US-09-925-302-4	Sequence 4, Appli
31	330	5.7	7864	10	US-09-834-975-805	Sequence 805, App
32	322.5	5.6	2451	10	US-09-976-165-29	Sequence 29, Appl
33	322.5	5.6	2451	13	US-10-342-276-29	Sequence 29, Appl
34	322.5	5.6	2487	13	US-09-976-165-32	Sequence 32, Appl
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36	322.5	5.6	3324	13	US-10-342-276-33	Sequence 33, Appl
37	322.5	5.6	3324	13	US-10-342-276-33	Sequence 33, Appl
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40	294	5.1	339	12	US-09-796-692-7359	Sequence 7359, Ap
41	294	5.1	339	12	US-10-057-475B-7359	Sequence 7359, Ap
42	294	5.1	339	15	US-10-154-884B-7359	Sequence 7359, Ap
43	294	5.1	339	10	US-10-040-862-7359	Sequence 7359, Ap
44	281	4.9	1894	10	US-09-771-161A-11	Sequence 11, Appl
45	278	4.8	326	10	US-09-796-692-7451	Sequence 7451, Ap

ALIGNMENTS

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RESULT 1
US-10-334-143-120

; Sequence 120, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 5309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-334-143-120

Alignment Scores:
Pred. No.:        0              Length:        5309
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Percent Similarity:   97.10%         Conservative:     20
Best Local Similarity: 95.28%        Mismatches:       32
Query Match:          95.65%         Indels:            0
DB:                   12             Gaps:              0

US-09-974-573-1 (1-1102) x US-10-334-143-120 (1-5309)

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Db  671 TGCCTGCGCTACTGGAAGGTGCTACACCGGAGCCCAGGCCAGATCCACCTGGTGCAGCGG 730

Qy  141 HisAlaProSerGluGluThrGluLeuAlaPheGlnAsnArgGlnLeuAsnAlaAlaLeuIleGlyTyr 160
        |||:||::||||||||||||||||||||||||||||||||
Db  731 CACCCGCCCTCCGAGGAGACTGAACTCGCAGCTCCAGCGCCTGAATGCGGCTGATTGGTAT 790

Qy  161 AspValThrAspValSerAsnValHisAspAspLysPheThrLysLysThrArgArgLeu 180
        |||||||||||||||||||:::|||||||||||||||||||
Db  791 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGTTCACGCGCGCCGTGGCTTG 850

Qy  181 ValThrProArgMetAlaGluValAlaLysGlyTyrArgLeuTyrAlaMetHisPro 200
        ||||||||||||||||||||||||||||||||||||||||
Db  851 GTGACCCCCCGCATGGCCGAGGTGGCCAAGGGCCAGACCCGGCTCTACGCCATGCACCCG 910

Qy  201 TrpValThrSerLysProLeuProGluTrpTyrLeuLysLysLysIleThrArgAsnCysVal 220
        ||||||||||||||||||||||||||||||||||||||::
Db  911 TGGGTGACGTCCAAGCCCCTCCCCGAGTACTCTGGAAGAAGATTGCCAACACTGCATC 970

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
        ||||||||||||||||||||||||||||||||||||||||||||||
Db  971 TTCATCGTCATTCACCGCAGCACCACGAGCCAGACCATTAAGGTCTCACCCGACACACC 1030

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLeuLysLysSerLeuMetAsp 260
        |||||||||||||||||||||||||||||||||||||||||
Db 1031 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAGAAATCTCTGATGGAT 1090

Qy  261 IleProLeuGlnAsnGluArgIleLeuSerPhePheThrValArgGlnCysLeuLysAsnGly 280
        |||||||||||||||::||||||||||||||||||||||||
Db 1091 ATCCCGAAAGCCAAAGCCAAACGGAACATTTGTGCTCAGCACCCATCAGAGCTTTGTACTTCAT 1150

Qy  281 LeuValGlyGluThrProIleLeuProValArgGlnPheAsnPheSerLeuLysAsnGly 300
        ||||||||::::|||||||||||||||||||||||||||||
Db 1151 CTGGTGGGCGAAACGCCAATCTCCAGTGGGGTGAGCCAGTTCAACTTCTCATTACCTT 1210

Qy  301 GluIleHisLeuValLeuAspGlnThrProProAspProAlaLeuHisAspAlaPheLysLys 320
        ||||||||||||||||||||||||||||||||||||||||||||
Db 1211 GAAGAGATTCACGTGGTACTGGACACGCCCCGACACCGCCCTAGACGAGGTGGAGAAAG 1270

Qy  321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyValThrGlyTyrHisGluTyrHisGluGlnLeuThr 340
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 1271 GAAGAGGTGGCCGCTGGTGGACGACTGCACGGAGGTCACCGGCTACCATGAGCAGCTTACC 1330

Qy  341 IleHisGlyLysLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
        ||||||||||||||||||||||||||||||||||||||||||||
Db 1331 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGGAAG 1390

Qy  361 PheArgValLysIleArgGlyIleLeuAspIleProValLeuProArgThrAlaAspLeuThr 380
        ||||||||||||||||||||||||||||::||||||||||||||
Db 1391 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTCGGACAGCAGACCTGACTCACA 1450

Qy  381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnInValLeuCysGlnValArgThrSer 400
        :::||||||||||||||||||||||||||||||||||||||
Db 1451 GTTTTTGTAGAGGCAAACATCCAGTACGGCGTGCAGAACGTGCTCTGTCAAAGGAGAACCAGC 1510

Qy  401 ProLysProPheThrGluValLeuTrpLeuGluThrAsnValTrpLeuGluSerIleLysIle 420
        ||||||||||||||||||||||||||||||||||||||||||
Db 1511 CCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTGTGGCTTGAGAGTATCAAAATC 1570

Qy  421 LysAspLeuProLysGlyLysAlaLeuLeuAsnLeuIleTyrCysGlyLysAlaProAla 440
        |||||||||||||||||||||||||||||||||||||||||
Db 1571 AAAGACCTGCCCAAGGGGCTTACTGAACCTCCAGATCACTGCGGTAAAGCTCCAGCA 1630

Qy  441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnInLeu 460
        |||||||||||||||||||||||||||||||||||||||||||
Db 1631 CTGTCCAGCAAGGGCCTTCTGCAGAGTCCCCAGTTCTGAGTCCAAGGGCAAAGTTCAGCTT 1690

Qy  461 LeuTyrTyrValAsnLeuLeuLeuIleAspAspHisArgPheLeuLeuArgLysHisGlyGluTyr 480
        |||||||||||||||||||||||||||||||||||||||||||
Db 1691 CTCTATTATGTGAACCTGCTGCTGATAGACCACCGGTTCCTTCTGCGCCGTGGAGAATAC 1750

Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysValGluAspGlnIleGlySerPheAsnAlaAsp 500
        ||||||||||||||||||||||||||||||||::|||||||||||||
Db 1751 GTCCTCCACATGTGGCAGATATCTGGAAGAGGGAGACCAAGGAAGCTTCAATGCTGAC 1810

Qy  501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuLeu 520
        |||||||:||||||||||||||||||||||||||||||||||
Db 1811 AAACCACGTCTGCAACTACCCACCACAAGGAGACTCAATGTCCATCTCCATTCTCCTG 1870

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
        ||||||||||||||||::::||||||||||||||||||||||
Db 1871 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCACCCCAGACCCGGAAGGG 1930

Qy  541 AspArgValArgValAlaGluMetProAsnGlnInLeuArgLysGlnInLeuArgLysGlnInLeuIleIleAla 560
        ||||||||||||||||||||||||||||||||||||||||
Db 1931 GACCGGGTTCGAGCAGAAATGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 1990

Qy  561 ThrAspProLeuAsnProGluThrAlaGluLysLysGluLeuTrpHisPheArgTyr 580
        ||||||||||||||||||||||||||||||||||||||||
Db 1991 ACTGATCCACTTAACCCTCTCCACAGCAGAGGAGAAGAAATTGCTCTGGCATTTTAGGATAC 2050

Qy  581 GluSerLeuLysAspProLysLeuPheSerSerValLysTrpTyrGlyGln 600
        |||||||||||||||||||||||||||||||||||||||||
Db 2051 GAAAGCCTTAAGCACCCAAAAGCATATCCTAAGCATTTTAGTTGTGAAATGGGGACAG 2110

Qy  601 GlnGluIleLeuValAlaAlaLysGlyLeuThrMetGlnInLeuLeuLeuLeuArgLysArgGluValTrpAspGlnSer 620
        |||||||||||||||||||||||||||||||:::|||||||||||||||||
Db 2111 CAAGAAATTGTGGCAGCAAAAACATACCAATTGTTGGCCAGAGGGAAGTCTGGGATCAAAGT 2170

Qy  621 AlaLeuAspAspThrLysGlyLeuPheMetGlnLeuLeuLeuAspCysAsnPheSerAspGluAsnVal 640
        ||||||||||||||||||||||||||||||||||||||||||
Db 2171 GCTTTGGATGGTGGGTTAACATGCAGCTCCTGCTGGACTGCCAACTTCTCAGATGAAAATGTA 2230

Qy  641 ArgAlaIleAlaValGlnLysLeuLeuSerLeuGluLeuGluAspAlaAspValLeuHisTyrLeu 660
        ||||||||||||||||||||||||||||||||||||||||||
Db 2231 AGAGCCATTGCAGTTCAGAAACTGCTGAGTCTTGAGGAGACTTGAGGATGATGTTCTGCATTACCTT 2290

Qy  661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
        ||||||||::||||||||||||||||||||||||||||||||
Db 2291 CTACAATGGTCCAGGCTGTGAAATTTGAACCTATCACGATAGTGCCCTTGCCAGGATTT 2350

Qy  681 LeuLeuLysArgGlyValLeuArgAsnGlyAsnGlyIleGlyHisPheLeuPheTrpPheLeuArg 700
        ||||||||||||||||||||||||||||||||||||||||
Db      LeuLeuLysArg...
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Db   2351 CTGCTGAAGCGTGGTTTAAGAAACAAAAGAATTGGTCACTTTTTTGTTTTGGTTCTTGAGA 2410
```

```
Qy   1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluGluValCysArgArgAspGlyTrp 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3491 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTGCAGAGAGAAAGGGATGG 3550
```

```
Qy    701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaTyr 720
Db   2411 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGTTCGCTGATCCTGGAAGCCTAT 2470
```

```
Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyLleLysGlyGluLysHis 1100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3551 ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAAGGAGAAACAT 3610
```

```
Qy    721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheGlnIleValGlnValIleAsp 740
          |||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db   2471 CTGAGGGGGCTGTGGCACAGCCATGCTGCACGACTTACCCAACAAGTCCAAGTAATCGAG 2530
```

```
Qy   1101 SerAla 1102
          ||||||
Db   3611 TCAGCC 3616
```

```
Qy    741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
          |||||||||||||||||||::::|||||||||||||||||||||||||||||||||||||
Db   2531 ATGTTACAAAAGTCACCCTGATATTAAATCGCTCTCTGCTGAAAAGATGACGTCAGT 2590
```

```

```
Qy   761 SerGlnValIleSerGlnLeuLysGlnLysGlnGluAsnLeuGlnAsnLeuAsnLeuPro 780
Db   2591 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAACCTGCAGAATTCTCAACTCCCC 2650
```

Alignment Scores:
```
Pred. No.:   0
Score: 5523.50   Length: 3342
Percent Similarity: 97.10%   Matches: 1049
Best Local Similarity: 95.19%   Conservative: 21
Query Match: 95.40%   Mismatches: 31
DB: 13   Indels: 1
                                                      Gaps: 1
```

```
Qy    781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyValAlaLeuValIleGluLys 800
          :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCGCTGCAATTGAAAAA 2710
```

US-09-974-573-1 (1-1102) x US-10-101-235A-3 (1-3342)

```
Qy    801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 2770
```

```
Qy      1 MetGluLeuGluAsnGlyAsnProValValArgGluAlaArgGluArgArg 20
          ||||||||||||||||||||:::||||||||||||||||||||||||||||
Db      1 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 60
```

```
Qy    821 ThrAlaLeuSerAsnGluThrGlyIleIlePheLysHisHisGlyAspAspLeuArgGln 840
          ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db   2771 ACAGCCCTATCAAATGAACAATTGAATTATCTTAAACATGGTGATGATCTGCGCCAA 2830
```

```
Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
          ||||||||||||||||||||||||||||::--||||||||||||||||||||||||||
Db     61 CGGAGGATGAAGCCGCGCAGT--GTGCCAGCCTGTCCATGGAGCTCATCCCCATC 117
```

```
Qy    841 AspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
          ||||||||||||::::||||||||||||||||||||||||||||||||||||||||||
Db   2831 GACATGCTATTTTTTACAGATTCTACGAATCATGAGTCTCATTTGGGAGACTGAATCTTTG 2890
```

```
Qy     41 GluPheValLeuProThrSerGlnAsnArgAsnThrLysProGluThrArgAlaLeuLeuHis 60
          ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db    118 GAGTTCGTGCTGCCCACCAGCCAGAACCGCAAAATGCAGGACCCGAAACGGGCGCTGCTGCAC 177
```

```
Qy    861 AspLeuCysLeuLeuProTyrGlyCysValSerSerThrGlyAspLysIleGlyMetIleGlu 880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2950
```

```
Qy     61 ValAlaGlyHisGlyAsnValGluArgGlnIleMetLysGlyAlaGlnIleTrpLeuArgAlaLeuGlu 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGTGGTGCTGGCGAGCGCTGGAG 237
```

```
Qy    881 IleValAspAlaThrArgIleLeuAlaLysIleGlnGlnSerThrValGlyAsnThrGly 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 ATTGTGGATGCAACGCGCCACGACCAATTGCAAAATTCAGCAAAGCACAGTGGGCAACACCGGA 3010
```

```
Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
          ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db    238 ACCAGCGTGTCGGCGGGACTTCACCACGGCTGGGACCCATCACTTCCTCCTGCTCTAT 297
```

```
Qy    901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
          |||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db   3011 GCATTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATCCCCTACTGAAGAAAAG 3070
```

```
Qy    101 GlnLysLysGlyGlnIleTrpTyrGluLysTyrAspLysTyrGlnValValGlnInThrLeuAsp 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 CAGAAGAAGGGGCAGTGTACCAAGATCTACGACAAGTACCAGGTGGTGCAGACTCTCGAC 357
```

```
Qy    921 PheGlnAlaAlaValAlaValGluArgPheValTyrSerCysSerAlaGlyTyrCysValAlaThrPhe 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3071 TTTCAGGCAGCAGTGGCAGAGATTTGTTTATTCCTGCGAGGCTACTGTGTGCAACCTTT 3130
```

```
Qy    121 CysLeuArgTyrTrpLysValLeuHisIleArgSerProGlyGlnIleIleHisValValGlnArg 140
          |||||||||||||||||||||||||||||||||||||||||||||::::|||||||||||
Db    358 TGCCTGCGCTACTGGAAGGTCCTGCACATCCGGAGCCCCGGCCAGATCCACCTGGTGCAGCGG 417
```

```
Qy    941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3131 GTTCTTGGAATAGGGGACAGACGCAATGACAATATCATGATCTCGGAGACAGGAAACCTA 3190
```

```
Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3191 TTTCATATTGACTTCGGCCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3250
```

```
Qy    981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3251 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3310
```

```
Qy   1001 LysThrLeuHisGlyLeuPheGlnLysAspValCysValLysAlaTyrLeuAlaLeu 1020
          |||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db   3311 AAGACAAGCCCACACTTCCAGAAATTTCAGGACACATCTGTTTAAGGCTTATCTAGCCCTT 3370
```

```
Qy   1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3371 CGTCATCACCAAACCTACTGACCTCCTGTTCTCCATGATGCTGATGACAGGAATGCCC 3430
```

```
Qy   1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
          |||||||||||||||||||||||||||||||||||||::::|||||||:::|||||||||
Db   3431 CAGTTAACAAGCAAAGAAGACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT 3490
```

```
Qy  141  HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
         |||  ||| | ||| |  |||||||| | ||| ||||||||  |||| || |
Db  418  CACCCGCCCTCCGAGGAGTCCCAAGCTTCCAGCGGCAGCTCACGGCGCTGATTGGCTAT  477

Qy  161  AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu  180
         |  || ||| || | ||  | |||  ||  | || ||| ||  ||| |  || || | ||
Db  478  GACGTCACTGACGTGCACGAACGTGAGCGTGGAGTTCACGCGGCGCGTGGCTTG  537

Qy  181  ValThrProArgMetAlaGluValAlaAlaGlyTyrArgAspProLysLeuTyrAlaMetHisPro  200
         || || ||| |||  | ||||| || || |  ||| | || |||||  ||  || | |  |||||
Db  538  GTGACCCCGCGATGGGGAGGTGGCCAGCCGGCGACCCCAAGCTCTACGCCATGCACCCCG  597

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
         ||| || |  |||||| ||  | ||| || |  |  |   |||  || ||  || |
Db  598  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC  657

Qy  221  PheLeuValIleHisArgSerThrSerGlnThrIleLysValSerValAlaAspAspThr  240
         || ||| || |  ||| |  |  || |   ||   || || |   |  || ||  || |
Db  658  TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC  717

Qy  241  ProGlyThrIleLeuGlnSerArgPhePheThrLysMetAlaLysLysSerLeuMetAsp  260
         || || || || |   |  ||| || || ||  ||  | || ||  |  |    |||||
Db  718  CCCGGCGCCATCCTGCAGAGTCTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  777

Qy  261  IleProGluSerGlnAsnGluArgAspPheAsnPheValCysGlyArgValCysGlyGluTyr  280
         || ||| || ||  |  || |   || ||  | ||| || ||  ||  ||  || ||| || |
Db  778  ATTCCCGAAAGCCAAAACGAACAGGATTTGTCTGCCGTCTGTGGCCGGAAATGTA  837

Qy  281  LeuValGlyGluThrIleLysLysGlnArgGlnCysLeuLysAsnGly  300
         || ||  ||  ||   |  |   ||  ||  ||  ||  |   ||  ||
Db  838  CTGGTGGGCGAAACGGCCATCAAAAGAACCAGCAGTGCCTCCTTCAAGAACGGA  897

Qy  301  GluLeuIleHisLeuValLeuAspProThrProAlaLeuAspGluValArgArg  320
         || || | |  || || |   |   | ||| |   || ||  | |   ||  ||
Db  898  GAAGAGATTCACGTGGTACTGGACCCCACGCCCGCCCTAGACGAGGTGAGGAAG  957

Qy  321  GluGluTrpProLeuValAspAspCysThrGlyValThrGlyValThrHisGluLeuThr  340
         || || ||| |  || ||  ||  || |   || || |   | ||  |||  || |   |
Db  958  GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCGGCGTACCCATGAGCAGCTTACC  1017

Qy  341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgArgLys  360
         | |  || | || |  || |   |   | || |   |  ||| ||  ||  || || || |
Db  1018  ATCCACGGCAAGGACACCAGAGAGTGTGTTCACCGTGTCCCTGTCCGGGACTGCGACCGGCAAG  1077

Qy  361  PheArgValLysIleArgGlyTyrIleAspIleProValLeuProValLeuProValLeuAsp  380
         || | || |   ||| || |  |  ||  | ||  ||  |   |  | ||  || || |||
Db  1078  TTCAGGGTCAAGATCAGAGGCTACATTGATATCCCCGTCTTCCTGGAACACCGACCCTCACA  1137

Qy  381  ValPheValGluValGlnValAlaAsnIleGlnTyrGlyValGlnLeuCysGlnArgThrSer  400
         || || || || |  |  | ||  ||   | |  || |  ||  |   ||  || |  ||
Db  1138  GTTTTTGTAGAGGTGCAGGTGGCCAACATCCAGTACGGTGTGCAGCTGTGCCAAAGGACGAGC  1197

Qy  401  ValPheThrLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyGlyLysLysProAla  420
         || || | || |  || |  || ||  ||  ||  | |  |  || |  || |  | |||
Db  1198  GTGTTCACCCTGCCCAAGGGGCCCTCCCTGCTGAATCTTCAGTTCTACTGTGGTGGCCTAAAAATC  1257

Qy  421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuLysAspGlyAlaLeuProAla  440
         || ||  |  || |  || ||  ||  || |   |  ||  |||   ||
Db  1258  AAAGACTTGCCCAAAGGGGGCTCCACTGGCAGATCCAGATCCTAGCCTCCAGCA  1317

Qy  441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysValAlaGlnLeuLeu  460
         || || || |  |  | ||  |||||| || || |   |  || |  | ||   | | |
Db  1318  CTGTCAGGGAAGACAAGGGCCTCTGCAGATCCCCAGTCTGAGTCCCAAAGTTCGGCTT  1377

Qy  461  LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuArgHisGlyGluTyr  480
         || |  | || ||  ||  |  |  ||  ||  |  ||  || |  | |  || |  ||
Db  1378  CTCTATTATGTGAACCTGCTGCTATAGACCACCGGTTTCCTCGGCCGTGGAGAATAC  1437

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlyValSerPheAsnAlaAsp  500
         || || || |   ||  |  || || |  ||  | ||  |  || |  |  || ||  | ||
Db  1438  GTCCTGCACATGTGGCAGATATCCGGAAGGGGAGGACCAAGGAAGACTTCAATGCTGAC  1497

Qy  501  LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu  520
         |
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Qy  521  HisAlaProSerGluThrLeuAlaPhe
         |
Db  1498  AAACTCACGTCGCACTAACCCAGACAAGAGACTCAATGTCCATCTCATTCTCTG  1557

Qy  540  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  540
         ||  |  || | || |   |   || ||  | |   || | ||  |  ||  || ||
Db  521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  1617
Db  1558  GACAATTACTGCCACCCGATAGCCCCTGCCTAAGCATCAGCCCACCCTGACCCCGAAGGG  617

Qy  560  AspArgArgValArgAlaGlyMetProAsnGlnLeuArgLysGlnLeuUalAlaIleIleAla  560
         || |  | |  |  |  |||  |  ||  |  ||  |   |  |  | |  || || |
Db  541  AspArgArgValArgAlaGlyMetProAsnGlnLeuArgLysGlnLeuValAlaIleIleAla  1677
Db  1618  GACCGGGTTCGAGCAGAAAATGCCCAACCAGCTTCGCAAGCAGCTTGGAGGCGATCATAGCC  560

Qy  580  ThrAspProLeuAsnProLeuThrAlaGluAsnProLysGlyLeuLeuTrpHisProArgTyr  580
         |  ||  |  ||  | || |  ||  |  || |   | |  ||  || ||  |    | |
Db  561  ThrAspProLeuAsnProLeuThrAlaGluAsnProLysGlyLeuLeuTrpHisProArgTyr  1737
Db  1678  ACTGATCCACTTAACCCTCTCACAGCAGGACAAAGAATTGCTCTGGCATTTTAGATAC  580

Qy  600  GluSerLeuLysAspProLysAlaTyrProLysSerSerValLysTrpGlyGln  600
         || || || || ||  | || || |  || |  | |  ||  | |  |||   |
Db  581  GluSerLeuLysAspProLysAlaTyrProLysSerSerValLysTrpGlyGln  1797
Db  1738  GAAAGCCTTAAGACACCCAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAAATGTA  600

Qy  620  GlnGlyIleValAlaAlaLysThrTyrGlnLeuLeuAlaAlaLysArgGluValTrpAspGlnSer  620
         ||  | || |  |  ||  | |  |  ||  |  |  || |  | | |  |  |||  |||  |
Db  601  GlnGlyIleValAlaAlaLysThrTyrGlnLeuLeuAlaAlaLysArgGluValTrpAspGlnSer  1857
Db  1798  CAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAGAAGGGAAGTCTCGGATCAAAGT  620

Qy  640  AlaLeuAspValGlyValThrMetGlnLeuLeuAspCysAsnPheSerArgGluAsnVal  640
         || ||  ||  | || |   ||| |   |   || | || ||  || |   | || |
Db  621  AlaLeuAspValGlyValThrMetGlnLeuLeuAspCysAsnPheSerArgGluAsnVal  1917
Db  1858  GCTTTGGATGTTGGGTTAACATGCAGCTCCTGGACTGCAACTTCTCGAGTGAAAAATGTA  640

Qy  660  ArgAlaIleAlaValGlnLeuLysGluSerLeuGlnAsnAspAlaAspValHisTyrLeu  660
         ||  | | ||  | |  || |  || |  || |   ||  | || |  |  |   || |
Db  641  ArgAlaIleAlaValGlnLeuLysGluSerLeuGlnAsnAspAlaAspValHisTyrLeu  1977
Db  1918  AGAGCCATTGCAGTTCAGAAACTTGGAGAGCTTGGAGGACCATGATGTTCTCATTACCTT  660

Qy  680  LeuGlnLeuValGlnAlaValLysAspArgAsnLysArgIleGlyTyrHisAspAlaAlaArgPhe  680
         || |  |  | |  || |   || ||  ||  |  ||  | ||  |  ||  || || | |  ||
Db  661  LeuGlnLeuValGlnAlaValLysAspArgAsnLysArgIleGlyTyrHisAspAlaAlaArgPhe  2037
Db  1978  CTACAATTGGTCCAGGCTGTGAAATTGACAATAAAAGAATTGGTCACTTTTTGTTTGGTTCTTGGA  680

Qy  700  LeuLeuLysArgGlyLeuGluArgAsnLysArgIleGluGlyValHisPheLeuPheTrpProLeuArg  700
         || || || || |  || |   ||  | ||  | || || |  |  || || || ||| | ||
Db  681  LeuLeuLysArgGlyLeuGluArgAsnLysArgIleGluGlyValHisPheLeuPheTrpProLeuArg  2097
Db  2038  CTGCTGAAGCGTGGTTAAGAACAAAAGAATTGGTCACTTTTTGTTTGGTTCTTGAGA  700

Qy  720  SerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGluLeuGlyValAlaTyr  720
         || ||  | ||  |  || |  |  | |  ||  |  | | | |  || |  || |  || |
Db  701  SerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGluLeuGlyValAlaTyr  2157
Db  2098  AGTGAGATAGCCCAGTCCAGACACTATCAGCAGACACTTCGCTGTGATTCTGGAAGCCTAT  720

Qy  740  LeuArgGlyCysGlyThrAlaMetLeuHisSerAlaPheThrGlnValGlnIleValIleAsp  740
         || || || || ||  | |  |  |  | || || || |  |  |  |  || |  | ||
Db  721  LeuArgGlyCysGlyThrAlaMetLeuHisSerAlaPheThrGlnValGlnIleValIleAsp  2217
Db  2158  CTGAGGGGCTGTGGCACAGCCATGTGCACACTTCACCCAACAAGTCCAAGTAATCGAG  740

Qy  760  MetLeuGlnLysValThrThrIleAspIleLysSerLeuSerAlaLysAlaLysTyrAspValSer  760
         |   || |  || | | |   ||  | |  |  ||  || |  ||  | |  |  || ||  |
Db  741  MetLeuGlnLysValThrThrIleAspIleLysSerLeuSerAlaLysAlaLysTyrAspValSer  2277
Db  2218  ATGTTACAAAAAGTCACCACTATTAAATCGCTTCTGTCTGCAAAAGTATGACGGTCAGT  760

Qy  780  SerGlnValIleSerGlnAsnLeuLysLysLeuGlnAsnLeuAsnLeuAsnLeuAsnLeuPro  780
         || |  | || |  || || |  || |  || |  || |  ||  |  ||
Db  761  SerGlnValIleSerGlnAsnLeuLysLysLeuGlnAsnLeuAsnLeuAsnLeuPro  2337
Db  2278  TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC  780

Qy  800  GlnSerPheArgValProTyrProGlyAspValLysAspGlyLysValAlaLeuValIleGluLysLys  800
         ||  | ||  | ||| |  | ||  ||  ||  | ||  || | || |  || | |   |   ||
Db  781  GlnSerPheArgValProTyrProGlyAspValLysAspGlyLysValAlaLeuValIleGluLysLys  2397
Db  2338  GAAAGCTTTAGAGTTCCATATGCCTGGACTGGAGTGAAAGACAGGAGCGGCCTGGCAATTGAAAAA  800

Qy  820  CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysGluArgGlyCysAlaAspPro  820
         ||  | ||  | || |  || |  || ||  ||  | || |  |  | | | || |   |||
Db  801  CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysGluArgGlyCysAlaAspPro  2457
Db  2398  TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAAGTGCCGATCCT  820

Qy  840  ThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheLysHisGlyLysAspLeuArgGln  840
         | |  || |   || |  | |  || | | |  || |  | |  ||  | ||  |   ||
Db  821  ThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheLysHisGlyLysAspLeuArgGln  2517
Db  2458  ACAGCCCTATCAAATGAAACAATTGAATATCTTTAAACATGGTAAAGATCTGCGCCAA  840

Qy  860  AspMetLeuIleLeuGlnIleLeuArgIleMetGluGlnArgIleGluThrGluIleGluLeu  860
         || |  || | |  || |  |  ||  |   || || |   | ||  || || | | || |
Db  841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluGlnArgIleGluThrGluIleGluLeu  2577
Db  2518  GACATGCTTATTTTACAGATTCTACGAATCATGGAGCAGAGGATCGAAACTGAAATCTTTG  860

Qy  880  AspLeuCysLeuLeuProTyrGlyCysIleSerSerThrGlnLysGlyMetIleGlyGlu  880
         |
```

```
Pred. No.:                        0          Length:           3237
Score:                            5309.00    Matches:          1015
Percent Similarity:               93.92%     Conservative:     20
Best Local Similarity:            92.11%     Mismatches:       31
Query Match:                      91.69%     Indels:           36
DB:                               13         Gaps:             2

US-09-974-573-1 (1-1102) x US-10-101-235A-5 (1-3237)
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```
Qy    1  MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg    20
         ||||||||||||||||||||||||||||||||||   ::|||::|||||||||||
Db    1  ATGGAGCTGGAAAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC   60

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerMetGluSerMetGluLeuIleProIle   40
         :::|||||::||||:|||:||||||:||::||:    |||::|||:|||||::|||||
Db   61  CGGAGGATGAAGCCGCGGAGT---GCTGCCAGCCTGTTCCTCGCTTCATCCCCATC   117

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
         ||:|||:|||||||||||:|||:|||||||:||||||||||||||||||:||:|||||
Db  118  GAGTTCGTGCTGCCAACCAGCCAGCGCAAATGCAAGAGACCCGAAACGGGCTGCTGCAC   177

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnIleValTrpLeuArgAlaLeuGlu   80
         |||:|||||::||||:|||:|||:|||||||:|::||||||:|||||||||:||:|||||
Db  178  GTGGCCGGCCACGTGGGCAGTGAGCAGATGAAGGCCCAGGTGGTGGTGCTGCGAGCGCTGGAG   237

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
         |||:|||||::||||||:||:||:||||||:||||||:|||||::|||:|||||||:||
Db  238  ACCAGCGTGGGCGGGACTTCTACCACCGGCTGGGACCGCATCACTTCCTCTGCTCTAT   297

Qy  101  GlnLysGlyGlnTrpTyrGluIleTyrGluIleTyrAspLysTyrGlnValValGlnThrThrLeuAsp   120
         |||::||||||||||:||::|||||:|||||||||::|||||||||:||::|||:||:|||
Db  298  CAGAAGAAGGGCAGTGCAGTCTACGAGATCTACCAGAGTGGTGCGACTCTTGGAC   357

Qy  121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg   140
         |||||:||:||:|||::||||:||||||:||:||||||:|||||||:||:||||||
Db  358  TGCCTGCGCTACTGGAAGGTGGCCGGGATCCACAGTGGTGGCGCGG   417

Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuLeuAsnAlaLeuIleGlyTyr   160
         |||:||||||:|||||||:|||||::||:||:||::||||:|||||:|||||::||:||
Db  418  CACCCGCCCTCCGAGGAGTCCCAAGCCTTCAGCCGCCAGCTGCTGAATGCGCTGATTGGCTAT   477

Qy  161  AspValThrAspValSerAsnValHisAspAspArgProGlyThrArgArgArgLeu   180
         :||||::||::||||:||:||||||:||||:||:||:||||||:||:||::||
Db  478  GACGTCACTGACGTCAGCAACGTGCACGACGATGCGGAGTTCACGCGCCGTGGCTTG   537

Qy  181  ValThrProArgMetAlaGluValAlaGlyArgAspProLeuTyrArgAlaMetHisPro   200
         |||||:||:||||||:|||:||:||:||::|||:|||||:|||:|||||:|||:||||:|
Db  538  GTGACCCCGCGCATGGCGGAGGTGGCAGGCCGCGACCCGAGCTCTACGCCATGCACCCG   597

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal   220
         |||:|||||:||||||:||||:||||||:|||::|||:|||||::||||||||:|||:
Db  598  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC   657

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrThrIleLysValSerAlaAlaAspAspThr   240
         |||||:||::|||:||||||:||||||:||:||::||:||||||||:||:||:|||:||:|||
Db  658  TTCATCGTCATTCATCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCAGCCGACGACACC   717

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrLeuAlaLysAlaLysSerLeuMetAsp   260
         |||||:||:||||::||:||::||||:||:||||||:||:||||::||:||:||:|||
Db  718  CCCGGCGGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAATCTCTGATGGAT   777

Qy  261  IleProGluSerGlnAsnGluArgAspPheValLeuArgGlyValCysGlyArgAspGluTyr   280
         ||:|||::||||||::||:||:||:|||:||:||||::||::|||:|||::||:||::|||
Db  778  ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTCCTGCGCGGTGGCTGTGGCCGGGATGAGTAC   837

Qy  281  LeuValGlyLysThrProIleLeuValAsnPheGluGlnProValArgGlnTrpValArgGlyAsnGly   300
         ||::||||::||:|||||:||::||||:|||::|||::||:||:||||::|::||::||||:||||
Db  838  CTGGTGGGCGAAACGCCCATCAAAAACTTCAGTGGTGAGGACACTGCCTCAAGAACGGGA   897

Qy  301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspThrProProAlaLeuAspThrValArgLysArgLys   320
         ||::|||||:|||:||||||:||||::||:|||:|||:||:||::||::||:||||::|||:||
Db  898  GAAGAGATTCACGTGGTACTGGACACGCCCTCCAGACACCGGCCCCAGACGAGGTGAGGAAG   957
```

```
Db  2578  GATCCATGCCTCCTGCCCATAGTTGCATTCAACTGGTGACAAAATAGGAATGATCGAG   2637
Qy   881  IleValLysAspAlaThrArgIleAlaLysIleGlnGlnSerThrValGlyAsnThrGly   900
          |||||:||||:||::|:|||||||::|||:|||||||:||:||:|||||:|||||:|||
Db  2638  ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAGACACAGTGGGCAACACGGGA   2697
Qy   901  AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys   920
          |||||:|||||:|||:|||::::||:|||||||::|||||::|||||:||:|||||||
Db  2698  GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG   2757
Qy   921  PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe   940
          |||||:||:||:|||||||||:|||::||::||:||||||||:|||::||:|||:|||
Db  2758  TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT   2817
Qy   941  ValLeuGlyValIleGluGlyAspArgArgHisAsnAspAsnMetIleSerGluThrGlyAsnLeu   960
          |||::||||::|||||::||:||::|:||::||:||:||:|||||:||:||::||:|||
Db  2818  GTTCTTGGAATAGGCGACAGGAGACAATGACAATTATGATCACCGGAGACAGGAAACCTA   2877
Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys   980
          |||||:||:||:||||||||:|||||:||::||::||:||||||::||::||||:||
Db  2878  TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA   2937
Qy   981  GluArgValProPheValProTrpAspPheLeuProPheValMetGlyThrSerGlyLysLys   1000
          |||:||||||||:|||||:||:|||||:|||||:||||:|||||||:||:||::|||
Db  2938  GAGAGAGTGCCATTTGTGCCAACCCCTGACTTCCTTCCTTTGTGATGGGAACTTCTGGAAAG   2997
Qy  1001  LysThrSerLeuHisProGlnLysAspPheGlnAsnLeuLysAlaTyrLeuAlaLeu   1020
          |||||::||::|||||:||:||:||||||||:||:||||:|||||::||::|||||
Db  2998  AAGACAAGCCCACACTTCCAGAAATTTCAGGACATCGTGTTAAGGCTTATCTAGCCCTT   3057
Qy  1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro   1040
          ||:||:||::||:||||||:||:|||||::||:||::||:|||::||:|||::|||:||
Db  3058  CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC   3117
Qy  1041  GlnLeuThrSerLysGluAspProIleGluTyrIleArgAspAlaLeuThrValGlyLysLysSer   1060
          |||||:||::||||:||:||||::||||||::||||:||:||:|||::||:||:|::
Db  3118  CAGTTAACAAGCAAGAAGACAATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAT   3177
Qy  1061  GluGluAspAlaLeuLysLysLeuTyrPheLysLysTyrPheLeuAspAspGlnIleLeuGluValCysArgAspLysSerGlyArgSerTrp   1080
          ||:||::||||:||:||||::||||:|||||:|||:|||:||::|||::||||:||:||
Db  3178  GAGGAGGATGCTAAAAAGTATTTTCTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG   3237
Qy  1081  ThrValGlnAsnTrpPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGlnGluLysLysHis   1100
          |||:|||||:||:||:||:||||:|||::||:||::|||||:||::||::|||::|||
Db  3238  ACTGTGCAGTTTAATTGGTTTCTTCTACATCTGTTCTTGGCCATCAAACAGGAGAGAAACAT   3297
Qy  1101  SerAla   1102
          ||:|||
Db  3298  TCAGCC   3303
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RESULT 3
US-10-101-235A-5
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; Sequence 5, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.
;   APPLICANT: Caron, Marc G.
;   TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
;   FILE REFERENCE: 033072-064
;   CURRENT APPLICATION NUMBER: US/10/101,235A
;   CURRENT FILING DATE: 2002-03-19
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 3237
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-235A-5
```

Alignment Scores:

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Qy   321  GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr  340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   958  GAAGAGTGGCCGCTGGATGACTGCACACTGGGAGTCACCGGGCTACCATGAGCAGTTACC  1017

Qy   341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysArgLys  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018  ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCCGCAAG  1077

Qy   361  PheArgValLysIleArgGlyIleAspIleProValLeuProValArgThrAlaAspLeuThr  380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1078  TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTCCGGAACACCGACCTCACA  1137

Qy   381  ValPheValGluAlaAsnIleGlnTyrGlyValGlnLeuCysGlnArgArgThrSer  400
          ||||||||||||||||||||||||::::|||||||||||||||||||||||||
Db  1138  GTTTTTGTAGAGGCAAACATCCAGTATGGCGTCCAAAGGAACCAGC  1197

Qy   401  ProLysProPheThrGluLeuTrpAsnValTrpLeuGlyPheLeuSerIleLysIle  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1198  CCCAAACCCTTCACAGAGCTGTGGAATGTGTGGCTTGGCTTCAGTATCAAAATC  1257

Qy   421  LysAspLeuProLysSerGlyAlaLeuLeuAsnLeuTyrCysGlyLysLysAlaProAla  440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1258  AAAGACTTGCCCAAGAGGGGCTCTACTGACCTCTACTGCGGTAAAGCTCCAGCA  1317

Qy   441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerGlyLysLysAlaGlnLeu  460
          ||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db  1318  CTGTCCAGCAAGACCTCTGCAGAGTCCCCCAGTTCTGAGTCTGGCAAAGTCGGCTT  1377

Qy   461  LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyTyr  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378  CTCTATTATGTGAACCTGCTGCTATAGACCACCGTTTCCTCCTGCGTCGTGAGAATAC  1437

Qy   481  ValLeuHisMetTrpGlnLeuSerGlyLysLysGlyValGluAspPheAsnAlaAsp  500
          :::|||||||||||||||||||||||||||||||||::::||||||||||||||
Db  1438  GTCCTCCCACATGTGGCAGATATCTGGGAAGGAGAAGTCAAGCTTCAATGCTGAC  1497

Qy   501  LysLeuThrSerAlaThrAsnProAspLysLeuProLysLeuAlaLeuProLeuLeuLeu  520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1498  AAACTCACGTCTGCAACTAACCCAGACAAGCTCCCTAAGCTGGCACTCCCATTCCTG  1557

Qy   521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1558  GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCACCCCCGACCCGGAGGGG  1617

Qy   541  AspArgValArgAlaAlaGlnMetProAsnGlnLeuGlnLeuGluLysArgGlyIleIleAla  560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1618  GACCGGGTTCGAGCAGCAAATGCCCAACCAGTCCTTCGGCTCAGCAATTGCAGCGGCGATCAGCC  1677

Qy   561  ThrAspProLeuAsnProLeuTrpAlaGluLysLysProHisProHisArgTyr  580
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1678  ACTGATCCACTTAACCCTCTCACAGGAGGCTTCGGAGAGATTGCTCTGGCATTTAGATAC  1737

Qy   581  GluSerLeuLysAspProLysAlaThrTyrProLysLeuPheSerSerValLysTrpProGln  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1738  GAAAGCCTTAAGGACCCTAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG  1797

Qy   601  GlnGluIleValAlaLysLysThrTyrArgGlnLeuLeuLysArgGluValTrpAspGlnSer  620
          ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db  1798  CAAGAAATTGTGGCCAAAAACATACCGGCAGAAGAGGAAGTCTGGGATCAAAGT  1857

Qy   621  AlaLeuAspValGlyLeuThrMetGlyLysAspCysAsnPheSerGluAspGluAsnVal  640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1858  GCTTTGGATGTTGGGTTAACAATGCAGCTCTGCAACTTCTCAGATGACGAAAATGTA  1917

Qy   641  ArgGlyIleAlaValGlnIleLysLysSerLeuGlnLysAspAspArgValHisTyrLeu  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1918  AGAGGCCATTGCAGTTCAGAACAGCTTCAGGAAGACGATGATGATGTTCTGCATTACCTT  1977

Qy   661  LeuGlnLeuValGlnAlaValGlnPheGluProTyrHisAspSerArgAlaLeuAlaArgPhe  680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1978  CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCAGGGCCCTTGCCCAGATTT  2037

Qy   681  LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyIleGlyHisLeuPheLeuTrpPheArg  700
          |||||||||||||||||||||||||||||||::::
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```
Db  2038  CTGCTGAAGCGGTGGTTAAGAACAAAAGAATTGGTCACTTTGTTTGGTTCTGAGA  2097

Qy   701  SerGluIleAlaGlnSerArgHisTyrGlnGlnIleArgPheAlaValIleLeuGluLeuAlaTyr  720
          |||||||||||||||||||||:::|||||||||||||||||||||||||||
Db  2098  AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGAGTTCGCTGTGATTCTGGAAGCCTAT  2157

Qy   721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp  740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  2158  CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAG  2217

Qy   741  MetLeuGlnLysValThrLeuLysSerLeuSerAlaGluLysLysTyrAspValSer  760
          ||||||||||||||||||||||||::::|||||||||||||||||||||||
Db  2218  ATGTTACAAAAAGTCACCCTGATATTAAATCGGCTCTCTGCTGAAAAGAAGTACGTCAGT  2277

Qy   761  SerGlnValIleSerGlnLeuLysLysGluGlnAsnLeuGlnLysLeuAsnLeuAsnLeuPro  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2278  TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAAGCTGCAGAATTCCAACTCCCC  2337

Qy   781  GlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuValIleGluGluLys  800
          :::|||||||||||||||||||||||||||||||||||||||||||||||||
Db  2338  GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCCGTGGCAATTGAAAAA  2397

Qy   801  CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro  820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2398  TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT  2457

Qy   821  ThrAlaLeuSerAsnGluThrIleGlyIleIleGlyPheLeuHisGlyAspArgLeuArgGln  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2458  ACAGCCCTATCAAATGAAACAATTGGAATTATCTTAAACATGGTGATGATCTGCGGCCAA  2517

Qy   841  AspMetLeuLeuLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2518  GACATGCTTAATTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG  2577

Qy   861  AspLeuCysLeuLeuProTyrTyrGlyCysIleSerThrGlyLysSerProLysMetIleGlu  880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2578  GATCTATGCCTCCTGCCATATTATGGTTGCATTTCAACTGGTCAAAAATAGGAAGATGATGGAG  2637

Qy   881  IleValLysAspAlaThrThrIleAlaLysIleGlnSerThrValGlyAsnThrGly  900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2638  ATTGTGAAAGACGCCACGACCATTGCCAAATTCAGCAAGACACAGTGGGCAACACGGGA  2697

Qy   901  AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys  920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2698  GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAATCCCTACTGAAGAAAAG  2757

Qy   921  PheGlnAlaAlaValGluArgPheValTyrSerCysValAlaGlyTyrCysValAlaThrPhe  940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2758  TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGTGGCTGGCTACTGTGTGGCAACCTTT  2817

Qy   941  ValLeuGlyIleLeuGlyAspAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
          ||||||||||||||||||||||||||||||
Db  2818  GTTCTTGGAATAGGCGAC                                              2835

Qy   961  PheHisIleAspPheHisGlyHisIleLeuGlyLeuAsnTyrLysLysSerPheLeuGlyIleIleAsnLys  980
          ------------------------------------------------------------
Db  2836  ------------------------------------------------------------  2835

Qy   981  GluArgValProPheValLeuThrProAspPheLeuGlyThrSerGlyLysLys  1000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2836  ---AGAGTGCCATTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG  2892

Qy  1001  LysThrSerLeuHisPheGlnLeuTyrLeuAlaLeuCysGlyValAlaTyrLeuAlaLeu  1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2893  AAGACAAGCCCACACTTCCAGAAATTTCAGGACATCTGTGTTAAGGCTTATCCAGCCCTT  2952

Qy  1021  ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetGlyMetPro  1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2953  CGTCATCACACAAACCTACTGATCACTCTGTTCTCCATGATGGGGATGCCC  3012

Qy  1041  GlnLeuThrSerLysGluAspProIleGluTyrIleLeuArgGlyAspAlaLeuThrLeuValGlyLysSer  1060
          |||||||||||:::
```

```
Db   3013 CAGTAACAAGCAAGAAGACATTGAATATATCCGGGATGCCCTTCACAGTGGGGAAAAAT 3072

Qy   1061 GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
          | | |      |||||      ||  :||      || |||   | | :  ||
Db   3073 GAGGAGGATGCGATGGTCTAAAAGTATTTCTTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG 3132

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuGlnGlyGluLysHis 1100
          ||||      |||      || | |   ||||      |||
Db   3133 ACTGTGCAGTTTAATTGGTTTCACATCTTGTTCCTGGGCATCAAACAAGGAGAGAAACAT 3192

Qy   1101 SerAla 1102
          ||||||
Db   3193 TCAGCC 3198


RESULT 4
US-10-101-235A-7
; Sequence 7, Application US/10101235A
; Publication No. US20030182669A1
GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE:  2002-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3207
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-235A-7

Alignment Scores:
Pred. No.:
Score:              5.34e-160       Length:         3207
                    1460.50         Matches:        385
Percent Similarity: 51.53%          Conservative:   206
Best Local Similarity: 33.57%       Mismatches:     394
Query Match:        25.22%          Indels:         163
                    13              Gaps:           40

US-09-974-573-1 (1-1102) x US-10-101-235A-7 (1-3207)
```

```
Qy    481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlyAspGlnGlySerPheAsnAlaAsp  500
                ||||||||||     :::|||
Db   1324  GCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGAT-----TTGCTGAACCCTATT  1377

Qy    501  LysLeuThrSerAlaThrAsnProAspLysGluAsn-----------  512
                :::|||        :::||||||||
Db   1378  GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTGAC  1434

Qy    513  -----------------SerMetSerIleSerIleLeuLeuAspAsnTyr  523
                                :::       ::: :::
Db   1435  TGGTTCAGCAGTGTGGTAAAGTTCCCAGATATCTCAGTG------ATTGAAGAGCA-  1484

Qy    524  CysHisProIleLeuPheLysProThrProAspProGlu-GlyAspArgVa  543
                ||||| :::||||||       ::: ||||||| :::
Db   1485  TGCCAATTGGTCTGTATCCCGAGAAGCAGGATTAGCTATTCCCACCAGGACTGAGTAA  1544

Qy    543  lArgAlaGluMetProAsnGlnLeuArg----------LysGlnLeuGluAlaIleIl  559
                ||||||      :::||||:::||||
Db   1545  CAGACTAGCTAGAGACAATGAATTAAGGAGAAAATGACAAAGACAGCTCAAAGCAATTTC  1604

Qy    559  eAlaThrAspProLeuAsnProLeuThrAlaGlyAspLysGluGluLysTrpHisPheAr  579
                |||||||||||      :::     :::|||||
Db   1605  TACACGAGATCCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAG  1664

Qy    579  gTyrGluSerLeuLysAspProLysAlaTyrProLysSerSerValLysTrpGl  599
                :::       ||||||||| :::||||
Db   1665  ACACTATTGTAACTATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAA  1724

Qy    599  yGlnGlnGluIleValAlaLysThrTyrGlnLeuLeuAlaTyrArgGluValTrpAspGl  619
                ||||||||        :::
Db   1725  TTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG-----------GTAAAAGATTG  1769

Qy    619  nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAs  639
                |||||:::||||||||||||:::|||||
Db   1770  GCCTCCAATCAAACCTGAACAGGCTATGGAACTTCTGGACTGTAATTACCCAGATCCTAT  1829

Qy    639  nValArgAlaIleAlaValGlnLeuValGluSer---LeuGluAspAspAspValLeuHi  658
                |||||| :::        ||||||
Db   1830  GGTTCGAGCTATTGCTGTTCGGTTGCTTGGAAAATATTACAAGATGACAAACTTTCTCA  1889

Qy    658  sPheGlnLysPheGlnAspSerAlaLeuAl  678
                :::::||||||||||
Db   1890  GTATTTAATTCAGCTAGTACAGTCCAAAAATATTGGATAACTTGCTTGT  1949

Qy    678  aArgPheLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisProLeuPheTrpPh  698
                ||||||||||:::       ||||||
Db   1950  GAGATTTTTACTGAAGAAAGCATTCGACTAATCAAAGGATTGGGCACTTTTCTTTTTGGCA  2009

Qy    698  eLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGl  718
                :::       ||||||||
Db   2010  TTTTAAATCTGAGATG---CACAATAAAACAGTTAGCCAGAGTTTGGCCTGCTTTTGGA  2066

Qy    718  uAlaTyrLeuArgGlyGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGln  738
                ::: ||||||||| :::
Db   2067  GTCCTATTGTCGTGCATGTGGAATGTATTGGAAGCAC---CTGAATAGGCAAGTCGAGGC  2123

Qy    738  lIleAspPheMetLeuGlnLysValThrLeuAspIleLeuSerLeuSerAlaGluLysTyrAs  758
                ::: ||||||        :::||||
Db   2124  AATGAAAAGCTCATTATTAACTTAACT---GACATT------CTCAAACAGGAGGAGGA  2174

Qy    758  pValSerSerGlnValIleSerGlnPheLysSerGlnLeuGlnLysLeuGlnAsn-----  776
                ||||||     :::|||
Db   2175  TGAAACACAAAAGTA------CAGATGAAGTTTTTAGTTGAGCAAATGAGGCGACCAGA  2228

Qy    777  ---LeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAl  795
                   |||||| :::       :::
Db   2229  TTTCATGGATGCCCTACAGGGCTTCCGTGTCCCTTAAACCCTGCTCATCATCATAGGAAA  2288

Qy    795  aLeuValIleGluLysCysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPh  815
                ::: ||||||||:::
Db   2289  CCTCAGGCTTAAAGAGTGTCGAATTAATGTCTTCTGCAAAAAGGCCACTGTGGTGAATTG  2348

Qy    815  eLysCysAlaAspProThrAlaLeuSer--------------AsnGluThrIleGl  829
                :::     :::
Db   2349  GGAG------AACCCAGACATCATGTCAGAGTTACTGTTCAGAACAATGAG-------  2394

Qy    829  yIleIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuLeuAr  849
                ||||||||       :::
Db   2395  -ATCATCTTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCG  2453

Qy    849  gIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy  869
                |||||||||       :::
Db   2454  TATTATGGAAAATATCTGGCAAAAATCAAGGTCTTGATCTTCGAATGTACCTTATGGTTG  2513

Qy    869  sIleSerThrGlyAspLysIleGlyMetIleGluValLysAlaThrThrIleAl  889
                ||||||       :::|||
Db   2514  TCTGTCAATCCGTGACTGTGTGGACTTATTGAGGTGCGAAATTCCACACTATTAT  2573

Qy    889  aLysIleGlnSerThrValGlyAsnThrGlyAla------PheLysAspGluValLe  907
                :::|||       :::||
Db   2574  GCAAATT--CAGTGACAAAGGCGGCTTGAAAGGTGCACTGCAGTCAACAGCCACACACT  2630

Qy    907  uSerHisTrpLeuLysGlyCysProIleGluGluLysPheGlnAlaAlaValGluAr  927
                |||       :::
Db   2631  ACATCAGTGGCTCAAAGACAACACAAA--GGAGAAATATGATGCAGCCATTGACCT  2687

Qy    927  gPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIleGlyAspAr  947
                ::: |||       :::
Db   2688  GTTTACACGTTCATGTGCTGGATACGTGTAGCTACCTTCATTTTGGAATTGGAGATCG  2747

Qy    947  gHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHi  967
                ||||||||||       :::
Db   2748  TCACAATAGTAACATCATGATGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACA  2807

Qy    967  sIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluValProPheValLe  987
                |||||||       :::
Db   2808  CTTTTTGGATCACAAGAGAAAAAATTGGTTATAAACGGACCGTGTGCCATTTGTTT  2867

Qy    987  uThrProAspPheValPheValMetGlyThrSerGlyLysLys-----ThrSerLeuHi  1005
                |||||||       :::
Db   2868  GACACAGGATTTCTTAATAGTGATTAGTAGAAGAGCCCAAGAATGCACAAAGACAAGAGA  2927

Qy   1005  sPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAs  1025
                ::: ||||||||
Db   2928  ATTTGAGAGGTTTCAGGAGATGTGTACAAGGCTTATCTAGCTATTCGACAGCATGCCAA  2987

Qy   1025  nLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLy  1045
                ||||||||       :::||
Db   2988  TCTCTTCCATAAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTT  3047

Qy   1045  sGluAspIleLeuTyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLy  1065
                ||||||||       :::
Db   3048  TGATGACAATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTT  3107

Qy   1065  sLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpThrValGlnPheAs  1085
                ::: |||||||
Db   3108  GGAGTATTTCATGAAACAAATCAAATGAATGCAGTGGCTCGGACAACAAAAAATGGA  3167

Qy   1085  nTrpPheLeuHisLeuVal  1091
                :::||
Db   3168  TTGGATCTTCCACACAATT  3186
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```
;   TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
;   FILE REFERENCE: 038602/1592
;   CURRENT APPLICATION NUMBER: US/10/440,464
;   CURRENT FILING DATE: 2003-05-19
;   PRIOR APPLICATION NUMBER: 60/380,872
;   PRIOR FILING DATE: 2002-05-17
;   PRIOR APPLICATION NUMBER: 60/448,922
;   PRIOR FILING DATE: 2003-02-24
;   PRIOR APPLICATION NUMBER: 60/448,874
;   PRIOR FILING DATE: 2003-02-24
;   NUMBER OF SEQ ID NOS: 185
;   SEQ ID NO 145
;     LENGTH: 3213
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-10-440-464-145

Alignment Scores:
Pred. No.:              1.52e-147    Length:         3213
Score:                  1354.50      Matches:        361
Percent Similarity:     49.60%       Conservative:   202
Best Local Similarity:  31.81%       Mismatches:     407
Query Match:            23.39%       Indels:         165
DB:                     12           Gaps:           37

US-09-974-573-1 (1-1102) x US-10-440-464-145 (1-3213)
```

Sequence alignment data (nucleotide and protein alignments between Qy and Db sequences, positions 30–569 / 625–1596).

```
Qy      917 IleGluGluLysPheGlnAlaAlaValAlaValArgPheValTyrSerCysAlaGlyTyrCys 936
              :::::|:|             ||:::||
Db     2671 GGGGATGAC---CTGGACCGAGCCATTGAGGAATTACACGTCCGTCCGTGGCCACTGT 2727

Qy      937 ValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGlu 956
              |||:||||          |:|:|         ::::
Db     2728 GTAGCTCTTATGTCCTTGGGATTGGTGACAAGACATAGTGACAATCATGGTCAAAAAA 2787

Qy      957 ThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeu 976
              ||||||||||||||||||||||||||:||
Db     2788 ACTGGACCAGCTCTTCCACATTGGACTTTGGACATATTCTTGGAAATTCAAATCTAAGTTT 2847

Qy      977 GlyIleAsnLysGluArgValProPheValThrProAspPheLeuProValMetGly 996
                  ::|:||
Db     2848 GGCATTAAAAGGGAGGAGTGGCCTTTATTCTTACCTATGATTTCATCCATGTCATTCAA 2907

Qy      997 ThrSerGlyLysLysThrSerLeuHisPheGlnLysPheGlnGlnLeuCysValValLysAla 1016
              ::::
Db     2908 CAAGGAAAACAGGAAATACAGAAAAGTTTGGCCGGTTCCGCCAGTGTGTTGGAGGATGCA 2967

Qy     1017 TyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMet 1036
              ::::||::::|
Db     2968 TATCTGATTTTACGACCGCATGGGAATCTCTTCATCACTCCTTTGCCGCTGATGTTGACT 3027

Qy     1037 ThrGlyMetProGlnLeuThrSerLysGlnAspLeuTyrIleArgGluValAlaLeuThr 1056
              |||:|||:
Db     3028 GCAGGGCTTCCTGAACTCACATCAGTCAAAGATATACAGTATCTTAAGGACTCTCTTGCA 3087

Qy     1057 ValGlyLysLysSerGluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArg 1076
              :::|||||||
Db     3088 TTAGGGAAGAGTGAAGAAGAAGCAACTCAAACAGTTTAAGCAAAAATTTGATGAGGCGCTC 3147

Qy     1077 AspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal 1091
              |||||
Db     3148 AGGGAAAGCTGGACTACTAAAGTGACCTGGATGGCCCACCAGTT 3192
```

```
Alignment Scores:
Pred. No.:                           6.05e-147      Length:           5220
Score:                 1352.50                      Matches:          365
Percent Similarity:    49.87%                        Conservative:     200
Best Local Similarity: 32.22%                        Mismatches:       415
Query Match:           23.36%                        Indels:           153
DB:                    13         (3327)             Gaps:             40

US-09-974-573-1 (1-1102) x US-10-337-192-1 (1-5220)

Qy       20 ArgArgMetLysProArgSerThrAlaAla--------SerLeuSerSerMet 35
```

```
Db     1597 AAGTTTCCTGTATTGAAAGAAATCTTGGACAGGGATCCCTTGTCTCAACTGTGTCGAA 1656

Qy      570 GlnAspLysGluLeuLeuTrpHisPheArgTyrGluSerLeuLys---AspProLysAla 588
              ||:|                             ::::::||       |||
Db     1657 AATGAAAATGGATCTTATTTGACTTTGGACAACAGACGTGCCGAGAGATTTTCCCACAATCA 1716

Qy      589 TyrProLysPheSerSerValLysTrpGlyValGlnGluLeuValAlaLysThrTyr 608
              |||||                 ||:|:||||
Db     1717 CTGCCAAAATTACTGCTGTCAATCAAGTGGAATAAACTTGAGGATGTTGCT------ 1767

Qy      609 GlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMet 628
              |||||                 :::||
Db     1768 CAGCTTCAGGCGCGTCCTTCAGATTTGGCCTAAA-----CTGCCCCCGGGAGGCCCTA 1821

Qy      629 GlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaAlaValAlaValGlnLysLeu 648
              ::||||||||:|:                    :::||
Db     1822 GAGCTTCTGGATTTCAACATCCAGACCAGTACGTTCGAGAAATGCTGTAGGCTGCCTG 1881

Qy      649 GluSerLeuGluAspAspAspValHisLeuValLeuGlnLeuValGlnAlaAlaValLys 668
              :::|||:|||
Db     1882 CGACAGATGAGTGATGAAGAACTTTCTCAATATCTTTACAACTGGTCAAGTGTTAAAA 1941

Qy      669 PheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLysArgGlyLeuArgAsn 688
              :::||||||||
Db     1942 TATGAGCCTTTTCCTGATTGCGCCCTCTCTAGATTCCTATTAGAAAGAGCACTTGGTAAT 2001

Qy      689 LysArgIleGlyHisPheLeuLeuProThrPheProLeuArgSerGluIleAlaGlnSerArgHis 708
              :::|||||||
Db     2002 CGGAGGATAGGGCAGTTTCTATTTTGGCATCTTAGGTCAGAAGTG----------CAC 2049

Qy      709 ------TyrGlnIleArgPheAlaValIleLeuGlnAlaTyrLeuArgGlyCysGly 725
                        :::||
Db     2050 ATTCCTCGTGTCTCAGTACAATTTGGTGTCATCCTGAGCATACTGCCGGGGA---AGT 2106

Qy      726 ThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleAspMetLeuGlnLysVal 745
              :::                 |||
Db     2107 GTGGGGCACATGAAAAGTGCTTTCTAAGCAGGTTGAAGCACTCAATAAGTTAAAAACTTTA 2166

Qy      746 Thr-------IleAspIleLysSerLeuSerAlaGluLysTyrAspValSerSerGlnVal 763
              :::                 :::
Db     2167 AATAGTTAATCAAACTGAATGCCTGAAGTCAAAGGAACCAAAGGGAAGGAAGACGGCCATG 2226

Qy      764 IleSerGlnLeuLysGlnLys------------LeuGluAsnLeuGlnAsnLeuAsn 778
              ||||
Db     2227 CATACCTGTTTAAAACAGAGTGCTTACCGGGAAGCCCTTCTGACCTGCAGTCA------ 2280

Qy      779 LeuProGlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIle 798
                                      :::
Db     2281 -----------------CCCTGAACCCATGTGTATCCTCTCCAGAACTCTATGTT 2319

Qy      799 GluLysCysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAla 818
              |||||||                 |||
Db     2320 GAAAAGTGCAAATACACATGGATTCCAAAATGAAGCCTTTGTGGCTGGTATAC------ 2370

Qy      819 AspProThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheGlyLysHisGlyAspAspLeu 838
              ||||||
Db     2371 AATAACAAGGTATTGGTGAGGATTCAGTGGAGTGATTTTTAAAAATGGTGATGATTTA 2430

Qy      839 ArgGlnAspMetLeuThrLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlu 858
              ::||:|||                 :::|||
Db     2431 CGACAGGATATGTTGACACTCCAAATGTTGCGCTGGATTTACTCTGGAAAGAAGCT 2490

Qy      859 SerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMet 878
              :::|||||                 |||||
Db     2491 GGTTTGGATCTTCGGATCTGCCTTATGGCTGTTTAGCACAGGATGCTCGCTGGCCTC 2550

Qy      879 IleGluIleValLysAspAlaThrThrIleAlaLysIleGln------GlnSerThrVal 896
              |||||:                 |||||
Db     2551 ATTGAAGTGTGAGCACCTCTGAAACAATTGCTGACATTCAGCTGAACAGTAGCAAATGTG 2610

Qy      897 GlyAsnThrGlyAlaPheLysAspAspGluValLeuSerHisTrpLeuLysGluCysCysPro 916
              |||||                 :::|||
Db     2611 GCTGCTCGCAGCAGCCTTCAACAAAGATGCCCTTCTGAACTGGCTTAAAGAAATACAACTCT 2670
```

```
Db 1123 :::||||||||||                                                      |||
        AAGCTTCCTCT--------GTGTCCCTGTGTCCCTGGAGCAGCCGTTCCGCATGAG 1173

Qy  365 ---IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThrValPheVal 383
           :::| |:       ::                    ||||  :||
Db 1174 CTCATCCAGGGCAGCAAAGTGAACGCCAGACAGCGG--------ATGAAGTGGGTGGTG 1224

Qy  384 GluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSerProLys--- 402
          ::|:|| :    |||||     :::||||| |||
Db 1225 CAGGCCGGGCTTTTCCACGGCAACGAGATGCTGTCCAAGACGGTGTCCAGCTCGGAGGTG 1284

Qy  403 ProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysGluLysAsp 422
          ||||                    |||
Db 1285 AGGGTGGTCGGAGCCCGTGTGGAAGCAGCGGCTGGAGTTCGACATCAACATCTGCCGAC 1344

Qy  423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSer 442
            :::
Db 1345 CCGGAGGGCCCTATGTGTTCCACCTGACCTTCTGTTTGCCGTGTACGCC--------GTGATCGAG 1392

Qy  443 GlyLysThrSerAlaGluMetProSerProGluSerPheGlyLysAlaGlnLeuLeuTyr 462
           :::|
Db 1393 AAAGCCAAGAAGGCTCGCTGCACACGGGACTCCACCAAGAGAAGGCGGACCTGCCCCATTGCC 1452

Qy  463 TyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGlyGluTyrValLeu 482
          ::|                    :::||||
Db 1453 TGGGCCCACCTCATGCTGTTTGACTACAAGGACCAGTTAAGACCCGGGGAACCGCTGCCTC 1512

Qy  483 HisMetTrpGlnLeuSerGlyLeuGluAspGlnGlySerPheAsnAlaAspLysLeu 502
           ::|||||||
Db 1513 TACATGTGTG--------CCCTCCGTGCCAGATGAGAAGGGCGAGCGCTGCTGAACCCCACGGGC 1566

Qy  503 ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuAspAsn 522
          |||||||
Db 1567 ACTGTGGCAGTAACCCCAACACGGATAGCGCCGCTGCCCCGCTCGCTGCTGCTCCGGAG 1626

Qy  523 ---------------------LysHis 532
                               ||:|||
Db 1627 GTGGCCCCGTGTACTACCCGTGCCCCTGGAGAGATCTTGGGGGCGACAC 1686

Qy  533 ArgProThrProAspProGluGlyAspArgValArgAlaGluMetProAsnGlnLeuArg 552
                               |
Db 1687 --------AGCGAGTGTGTGCATCGTCACCGAGGAGGAGCAGCTG--- 1722

Qy  553 LysGlnLeuGluAlaIleAlaIleAlaThrAspProLeuAsnProLeuThrAlaGluAspLys 572
          :::::|                    |||::|
Db 1723 ---CAGTTGCGGGGAAATCCTGGACGCGGCGGGGGTCTGTATGAGCACGAGAAG 1779

Qy  573 GluLeuGlnLeuTrpPheHisArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLys 591
          ::::||||                    |||
Db 1780 GACCTGGTGTGGAGAGCTGCGGGGATGAAGTCCAGGAGCACTTCCCGAGGCCCTAGCCCGG 1839

Qy  592 LeuPheSerSerValLysTrpValTrpAsnTrpLysAspAsnGlnSerAlaLeuAsnGlyLysGlyLeuGlnLeuThrGlyLeuThrMetGlnLeuLeu 611
           ||||                    :::|
Db 1840 CTGCTGCTGGTCACCAGTGGAACAAGCATGAGGATGTGGCCCAGATGCTCTACCTGCTG 1899

Qy  612 AlaLysArgGluValTrpAspAspAspGlnSerAlaLeuAspLeuAlaAlaLysGlyLeuThrMetGlnLeuLeu 631
           :::
Db 1900 TGGTCC--------TGGCCGGAG--------CTGCCCGTTCCTGAGCCGGCCCCTGAGCGAGCTGCTA 1944

Qy  632 AspCysAsnPheSerAspGluAsnValArgAlaIleAlaValGlnLysLysLeuGluSerLeu 651
          ::|                    :::|
Db 1945 GACTTCAGCTTCCCGATTGCCACGTAGCCTCCTTCGCGCTCCATCAAGTCGCTCGGGAAACTG 2004

Qy  652 GluAspAspAspValLeuHisTyrLeuLeuGlnLeuAlaValLysPheGluPro 671
          ::::|                    |||::|
Db 2005 ACGGACCATGAGCTGTTCCAGTACCTGCTGCTGGTGCAGCTGGTCTCAGGTGCACGACGTCC 2064

Qy  672 TyrHisAspSerAlaLeuAlaArgPheLeuLysArgArgPheLeuArgArgGlyLeuArgAsnLysArgArgIle 691
          |||                    ||::|
Db 2065 TACCTGGACTCGGCAGCTGACCAAATTCCTGCTGGACGGGCCCTGCCAACCGCAAGATC 2124

Qy  692 GlyHisPheLeuPheTrpPheLeuArgArgSerGluIleAlaGlnSerArgHisTyrGlnGln 711
          |||                    |||:|
Db 2125 GGCCCACTTCCTTTTCTGCGACACCTCCGCTCCCAGATG--------CACGTGCCGTCG 2172
```

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Db  187 :::|||||||||                                                      |||
        CAACCCAGGATGCCCCTGGGGTGGGACTGACTGCCCATGGAATTCTGACCAAGAGGAGAGAT 246

Qy   36 GluLeuIleProIleGluThrPheLeuProArgThrSerGlnArgAsnThrLysThrProGlu 55
          ::|                    |||
Db  247 CAGAGCGGTTGGGTTGACTTCCTGCTGCCCACAGGG--------282

Qy   56 ThrAlaLeuLeuHis--------ValAlaLeuGlyHisGlyAsnValGlnMetLysAlaGln 73
          :::|                    |||
Db  283 --GTCTACCTGAACTTCCCTGTCCCCAATGCCAACCTCAGCACCATCAAGCAGCTG 339

Qy   74 ValTrpLeuArgAlaLeuGluThrSerValSerAlaAlaAspPheTyrHisArgLeu--Gly 92
          :::|||                    |||
Db  340 CTGTGGCACCGGCCGCCAGTATGAGCCGGCTC--------TTCCACATGCTCAGTTGC 387

Qy   93 ProAspHisPheLeuLeu--LeuTyrGlnLysLysGlyGlnTrpTyrGlnIleTyrAsp 111
          :::                    |||
Db  388 CCCGAGGGCCTATGTGTTCCACCTGACCAAGCAGCAGCAAGAGCTGGAGGAC 447

Qy  112 LysTyrGlnValValGlnIleThrLeuAspCysLeuArgTyrTrpLysTrpLysHisArgSer 131
          :::                    ||||||
Db  448 GAGCAACGG--------CGTCTGTGTGACGTGCAGCCCTTCCTGCCCGTCCTG--- 492

Qy  132 ProGlyGlnIleHisValValGlnArgHisAlaProSerGluGluThrLeuAlaProAlaGln 151
          :::                    ::|
Db  493 ---CGCCTGGTGGCCCGTGAGGGGCGACCGCGTGAAGAAGTC---ATCAAC 537

Qy  152 ArgGlnLeuAsnAlaLeuIleGlyTyrArgAspValThrArgAspValSerAsnValHisAspAsp 171
          :::|                    |||
Db  538 TCACAGATCAGCCTCTCATCGGCAAAGGCCTCCACGAGTTTGACTCCTTGTGCGACCCA 597

Qy  172 GluLeuGluPheThrArgArgArgLeuValThrProAlaMetAlaGluValAlaAlaGlyArg 191
          |||||                    :::|
Db  598 GAAGTGAACGACTTTCGCGCCAAGATGTGC--------CAATTCTGCAGGAGGGGCGCGCC 651

Qy  192 AspProLysLeuTyrAlaMetHisProValThr---SerLysProLeu--------- 207
           ||||||                    |
Db  652 CGCCGGCAGCTGGGCTGGGAGGCCTGGCTGCAGTACCTGTTTCCCCCTGCGAGCTGGAG 711

Qy  208 --------ProGluTyrLeuLeuLysLysLysIleThrAsnAsnCysSerVal 220
          :::|
Db  712 CCCTCGCTCAAACCTGGGGCGTCTGGTACCCTG--------CGGCTCCCGAACCGGGCCCTT 765

Qy  221 PheIleValIle--------HisArgSerThrSerGlnThrArgIleLysValSerValSerAlaAsp 238
          :::|                    ||||
Db  766 CTGGTCAACCGTTAAGTTTGAGGGCAGCGAGAGCTTCACCTTGTCCTGTGTCCACCAAG 825

Qy  239 AspThrProGlyThrIleLeuGlnIleLeuGlnSerPheThrGlyThrMetAlaLys--------LysLys 256
          :::|                    :::|
Db  826 GACGTGGTGTGGAGAGCTGCGGGCGGATGAAGTCCAGGAGCCACAGTGTTCCGGCAG 885

Qy  257 SerLeuMetAspIleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGly 276
          :::|||                    |||::|
Db  886 CCGGGTGGTGCAGCAGCCGGAA--------GACTACACGGTGCAGGTGAACCGG 930

Qy  277 ArgAspGluTyrLeuvalGlyGluThrProIleLysProIleLysAspAspGlnSerAlaLeuAspLeuAlaAspGlnCys 296
          :::                    |||
Db  931 AGGGCATGAGTACCTGTATGGCAACTACCCGCTCTGCCAGCTCTGCAGCTGC 990

Qy  297 LeuLysAsnGlyGluGluValHisLeuValLeu-------- 307
          :::|                    ::|
Db  991 CTGCACAGTGGGTTGACCCCCTCACCTGACCATGGTCCATTCCTTCCTCCATCCTCGCCATG 1050

Qy  308 --------AspThrProProAspProAlaLeuAspGluValArgLysValGluTrpProPro 324
          :::|                    |||::|
Db 1051 CGGGATGAGCAGAGCAACCCTGCCCCCCAGGTCCGTCCAGAAACCGCTGCCAAACCACCTCC 1110

Qy  325 LeuValAspAspCysThrGlyValThrGlyValThrHisGluGlnLeuThrIleHisGlyLys 344
          :::                    :::
Db 1111 --------ATTCCTGCGACAAG 1122

Qy  345 AspHisGluSerValPheThrValSerLeuTrpAspCysCysAspArgLysPheAspArgValLys 364
          ::::::                    |||::|
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Qy 1059 LysSerGluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLys 1078
             :::||||||||::|||||:|::|||
Db 3211 AAAACAGAGGAGGAGGCACTGAAGCACTTCGAGTGAAGTTTAACGAAGCCCTCCGTGAG 3270

Qy 1079 GlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal 1091
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Db 3271 AGCTGGAAAACCAAACTGAACTGGCCTGGCCCACACGTG 3309
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RESULT 7
US-10-027-591-1
; Sequence 1, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
US-10-027-591-1

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Alignment Scores:
Pred. No.:
Score:                  6.05e-147      Length:       5220
Percent Similarity:     1352.50        Matches:      365
Best Local Similarity:  49.87%         Conservative: 200
Query Match:            32.22%         Mismatches:   415
DB:                     23.36%         Indels:       153
                        14             Gaps:         40
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US-09-974-573-1 (1-1102) x US-10-027-591-1 (1-5220)

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Qy   20 ArgArgMetLysProArgSerThrAlaAla--------SerLeuSerSerMet 35
           :::|||||||||:::|||||:::
Db  187 CAACGGCAGGATGCCCCTGGGGTGGACTGCCCCATGGAATTCTGGACCAAGGAGGAGGAAT 246

Qy   36 GluLeuIleProIleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGlu 55
           ||||:::||||||||:::|||||:::|||||
Db  247 CAGAGCGGTTGTGGTTGACTTCCTGCCTGCCCACAGGG------------------ 282

Qy   56 ThrAlaLeuLeuHis-------ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGln 73
                        :::|||||||:::|||||
Db  283 --GTCTACCTGAACTTCCCTGTGTCCCAACCTCAGCACCATCCAGCAGCAGCTG 339

Qy   74 ValTrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeu----Gly 92
           :::|||||||:::
Db  340 CTGTGGCACCGGGCCCCAGTATGAGGCCGTC----------TTCCAATGCTCAGTGGC 387

Qy   93 ProAspHisPheLeuLeu--LeuTyrGlnLysLysGlyGlnTrpTyrGlnIleTyrArgAsp 111
           ||||:::||||||:::
Db  388 CCCGAGGCCTATGTGTTCAACCGGCAGCAGCAGCTGAAGACGCTGGAGGAC 447

Qy  112 LysTyrGlnValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSer 131
           ::: :::|||||||
Db  448 GAGCAACGG------CGTCGTGTTGACGTGCAGCCCTTCCCGCGTCCTG--------- 492

Qy  132 ProGlyGlnIleHisValValGlnArgHisAlaProSerGluThrLeuAlaPheGln 151
                       :::|||||||:::
Db  493 ---------CGCTCGGTGGCCGGCGTGAGGGGCGCACCGCGTGAAGAGAGCTC---ATCAAC 537
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Qy  712 --------ArgPheAlaValIleLeuGluAlaTyrLeuArgGlyGlyThrGlyThrAlaMet 728
            :::|||||||:::|||:::|||
Db 2173 GTGGCCCTGCGCTTCGGCCTCATCCTGGAGGCCTACTGCAGGGGC---AGCACCACCAC 2229

Qy  729 LeuHisAspPheThrGlnGlnValGlnValGlnLysMetLeuGlnLysValThrIleAsp 748
            ::: :::
Db 2230 ATGAAGGTGCTGATGAGCAGGGGAAGCACTGAGCAAACTG--AAGGCCCTGAATGAC 2286

Qy  749 IleLysSerLeuSerAlaGluLysGluTyrAspValSerSerGlnValIleSerGlnLeuLys 768
            |||:::|||:::
Db 2287 TTCGTCAAGCTGAGCTCCAGAGACCCCC----------AAG 2319

Qy  769 GlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSer----------- 782
            :::
Db 2320 CCCCAGACCAAGGAGCTGATGCACTTGTGCGCGGAGGAGGCCTACCTAGAGGCCCTC 2379

Qy  783 ------PheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
            :::  ::: :::|||||||
Db 2380 TCCCACCTGCAGTCCGACAGCACCCCAGCACCCTGGCCTGAAGTCTGCCTGGAGCAG 2439

Qy  801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
            |||||||
Db 2440 TGCACCTTCATGGACTCCAAGATGAAGCCCTGTGGGATCATGTAC-------AGCAACGAG 2493

Qy  821 ThrAlaLeuSerAsnGluThrGlyIleIleGluPheLysHisGlyAspAspLeuArgGln 840
            :::|||:::|||||||:::|||:::|||
Db 2494 GAGGCAGGCAGCGGCCAGCCGTGGCATCATCTTAAGAACGGGGATGACCTTCGGCAG 2553

Qy  841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
            |||||||||||:::|||||||:::
Db 2554 GACATGCTACCCTGCAGATGATCCAGCTCAGGTCCTGTGAAGCAGCAGGAGGGGCTG 2613

Qy  861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
            |||||||
Db 2614 GACCTGAGGATGATGCACCCCTATGGCTGCCTCTCCACCGGGGACCCCAGGGCCTCATTGAG 2673

Qy  881 IleValLysAspAlaThrLysIleLysGln------GlnSerThrValGlyAsn 898
            :::||||||:::  :::|||
Db 2674 GTGGTACTCCGTTCAGACACCATCTCCAACTCAACAAGAGCAACATGGCAGCC 2733

Qy  899 ThrGlyAlaPheLysAspAspGluValLeuSerHisTyrLeuLysGluLysLysCysProIleGlu 918
            :::|||:::|||||||:::
Db 2734 ACAGCCCGCCTTCAACAAGGATGCCGCTCAAGGCTCAAGTCCAAGAACCCG---GGG 2790

Qy  919 GluLysPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAla 938
            |||:::|||||||
Db 2791 GAGGGCAGGATGATCGGCCATTGAGGAGTTCACCCTCTCTGTCTGGCTATTGTGTGGCC 2850

Qy  939 ThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGly 958
            |||||||||||||||:::
Db 2851 ACATATGTGTGGGCATTGGCGATGGCACAGACAACATCATGATCCGAGAGAGTGGG 2910

Qy  959 AsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle 978
            ||||||:::|||
Db 2911 CAGTTGTTCCACATTGATTTTGGCCACTTTCTGGGGAATTACAAGACCAAGTTTGGAATC 2970

Qy  979 AsnLysGluArgValProPheValProPheProAspPheLeuGlnValMetGlyThrSer 998
            |||:::|||||||
Db 2971 AACCGCGAGCGTGTCCCATTCATCCTCACCTATGACTTTGTCCATGTGATTCAGCAGGGG 3030

Qy  999 GlyLysLysThrSerLeuHisPheGlnLysAspValPheValCysValLysAlaTyrLeu 1018
            ||:|||||||
Db 3031 AAGACTAATAATAGTGAGAAATTTGAACGGTTCCGGGGCTACCTGTGAAAGGGCCTACACC 3090

Qy 1019 AlaLeuArgHisHisThrAsnLeuIleLeuIleLeuPheSerMetMetLeuMetThrGly 1038
            ||||||
Db 3091 ATCCTGCGGCACCACGGCTTCTCTCTTCCCTCACCTCTTGCCCTGACCGGGGCCGGCAGGC 3150

Qy 1039 MetProGlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGly 1058
            |||||||
Db 3151 CTGCCCTGAGCTCAGCTGCTCCAAAGACATCCAGTATCTCCAAGGACTCCCTGGCACTGGGG 3210
```

```
Qy   152 ArgGlnLeuAsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAspAsp 171        Qy       :::||||                                                               
         |||| |||| ::: :::                    ||                                          :::||||------CCCTCCTGTCCCAGATGAGAAGGCCGAGCTGCTGAACCCCACGGGC 1566
Db   538 TCACAGATCAGCCTCCTCATCGGACAAAGGCCTACCGAGTTTGACTCCTTGTGCGACCCA 597        Db  1513 TACATGTGG

Qy   172 GluLeuGluPheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyValArg 191        Qy   503 ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuAspAsn 522
         |||| ||| :::                 :::                                                 ||||||||| :::::::::                       :::::::::
Db   598 GAAGTGAACGACTTTCGGCCGCCAAGATGTC------CAATTCTGCAGGAGGCGGGCGCC 651        Db  1567 ACTGTGCGCAGTAACCCAACCAAACGGATAGCGGCCGTGCCCTGCCATCCTGCCTGCCCGAG 1626

Qy   192 AspProLysLeuTyrAlaMetHisProTrpValThr---SerLysProLeu 207              Qy   523 TyrCys---HisProIleAlaLeuPro------------LysHis 532
         ||| :::                                                                           ||| :::::
Db   652 CGCCGGCAGCAGCTGGGCTGGGAGGCCTGGCTGCAGTACAGTTTCCCCCTCGAGCTGGAG 711        Db  1627 GTGGCCCCGCCCCGTGTACTACCCCGGACAAGATCTTGGAGCTGGCGGCACAC 1686

Qy   208 ------------ProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220              Qy   533 ArgProThrProAspProGluGluGlyGlyValAspArgArgValAlaAlaGlyMetProAsnGlnLeuArg 552
         |||                                           ||                                           |||
Db   712 CCCTCGCCTCAAACCTGGGGCCTGGTACCCTG------CGGCTCCCGAACCGGCGGCCTT 765        Db  1687 ----------------AGCGAGTGTGTGCATGTCACCGAGGAGGAGCAGCTG--- 1722

Qy   221 PheIleVallle------HisArgThrSerGlnThrIleLysValSerAlaAsp 238              Qy   553 LysGlnLeuGluAlaIleIleIleIleAlaThrAspProLeuAsnProLeuThrGluAlaGluAspLys 572
         |||:::                  ||                                                              :::
Db   766 CTGGTCAACGTTAAGTTTGAGGGGCAGCGAGGAGAGCTTCACCTTCCAGGTGTCCACCAAG 825        Db  1723 ---CAGCTGCGGGAAATCCTGGAGCGGCGGGGAGTCTGGGGAGCTGTATGAGCACCAGAGAAG 1779

Qy   239 AspThrProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLys------LysLys 256              Qy   573 GluLeuLeuTrpHisPheArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLys 591
         |||:::                                                                             |||
Db   826 GACCTGGTGTGGAAGCCTGTGCTCGTGACCAGTACCAGTGTTCCGGCAG 885        Db  1780 GACCTGGTGTGGAAGCCTGTGCTCGTGACCAGTGAAGTCCCGGAGGGCCCTAGCCCCGG 1839

Qy   257 SerLeuMetAspIleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGly 276              Qy   592 LeuPheSerSerValLysTrpGlyGlyIleGlnIleLeuValAlaLysThrTyrGlnLeuLeu 611
         |||:::                                                                             ||||
Db   886 CCGGTGGTGAGCAGCCGGAA------------GACTACACGTTCAGGTGAACGGC 930        Db  1840 CTGCTGTCGGTCACCAGGTGGAACAAGCACATGAGGATGTGGCCAGATGCTCTACCTGCTG 1899

Qy   277 ArgAspGluTyrLeuValGlyGluThrProIleLysAsnPheGlnIleTrpValArgGlnCys 296              Qy   612 AlaLysArgGluValTrpAspGlnSerAlaLeuAspAlaValGlyLeuThrMetGlnLeuLeu 631
         |||:::                                                                             ||||
Db   931 AGGGATGAGTACCTGTATGGCAACTACCCGCTCTGCAGTACATCTGCAGCTGC 990        Db  1900 TGGTCC------------CTGCCCGTCCTGAGCGCCCTGCAGGAAACTG 1944

Qy   297 LeuLysAsnGlyGluGluIleHisLeuValLeu--- 307              Qy   632 AspCysAsnPheSerAspGluAsnValArgAlaIleAlaValGlnLysLeuSerLeuSerLeu 651
         ||| :::                                                                            |||||||
Db   991 CTGCACAGTGGGTGACCCCTCACCTGACCATGGTCCATTCCTCCTCCATCCTCGCCATG 1050        Db  1945 GACTTCAGCTTCCCCGGATTGCCACGTAGGCTCCTTCGCCATCAAGTCGCTGCGGAAAACTG 2004

Qy   308 -------AspThrProAspProAlaLeuAspLeuValArgGlyLysGluGluTrpPro 324              Qy   652 GluAspAspAspArgValLeuHisTyrLeuLeuGlnLeuValAlaValLysPheGluPro 671
         |||                                                                                |||:::
Db  1051 CGGGATGAGCAGAGCAACCCTGCCCCCAGGTCCAGAAACCGGTGCCAAACCACCTCCC 1110        Db  2005 ACGGACGATGAGCTGTGTTCCAGTACCTACCTGGCGGTCGTGGTCAGGAGTGCTCAAGTACGAGTCC 2064

Qy   325 LeuValAspAspCysThrGlyValThrGlyTyrTyrHisGluTrpIleHisGlyLys 344              Qy   672 TyrHisAspSerAlaLeuLeuGluAlaPheLeuLeuLysArgPheLeuLeuArgArgIle 691
         ||| :::                                                                            |||:::
Db  1111 ------------------ATTCCTGCGAAG 1122        Db  2065 TACCTGGACTGCGAGCTGATGAAGCAGGGGAAGCACTGAGCAAACTG---AAGGGCCCTGAATGAC 2124

Qy   345 AspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLysPheArgValLys 364              Qy   692 GlyHisPheLeuPheTrpPheSerLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGln 711
         |||:::                                                                             :::::
Db  1123 AAGCTTCCT--------GTGTCCCGTGTGGTCCCCAGGAGCAGCCGTTCCGCATCGAG 1173        Db  2125 GGCCACTTCCTTTTCTGGCACCTCCGCTCCGAGATG------------CACGTGCCGTCG 2172

Qy   365 ---IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThrValPheVal 383              Qy   712 ------ArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMet 728
         ||| :::                                                                            |||
Db  1174 CTCATCCAGGGGCAGCAAAGTGACGCCGACGAGCGG------ATGAAGCTGGTGGTG 1224        Db  2173 GTGGCCCCTGCGGTTCGGCCTTCGGCCTTCATCCTCGGAGCGGGGC--AGACCACCACAC 2229

Qy   384 GluLeuAsnIleGlnTyrGlyGlnValCysGlnArgArgThrSerProLys--- 402              Qy   729 LeuHisAspPheThrArgGlnIleValGlnIleValIleIleSerValThrArgIleAsp 748
         :::|||                                                                             :::
Db  1225 CAGGCCGGCTTTTCCACGGCACGAGATGTGTGTCAAGACCGGTCCGGAGGTG 1284        Db  2230 ATGAAGGTGCTGATGAAGCAGGGGGAAGCACTGAGCAAACTG---AAGGGCCCTGAATGAC 2286

Qy   403 ProPheThrGlyGluGluLeuArgTrpAsnValTrpLeuGluPheSerIleLeuLysAsp 422              Qy   749 IleLeuLysSerLeuAlaGluLysTyrAspAspCysIleValIleLeuSerSerGlnLeuLys 768
         |||:::                                                                             ||||||
Db  1285 AGGCTGTGCTCGGAGCCCGTGTGGAAGCAGCCGCTGGAGTTCCACATCTGCGAC 1344        Db  2287 TTCGTCAAGCTGAGCCTCCAAGAGACCCCC--------------------AAG 2319

Qy   423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSer 442              Qy   769 GlnLeuLysGluAsnLeuAsnLeuGlnAsnLeuProGlnSer------------------ 782
         |||:::                                                                             |||
Db  1345 CTGCCCCCAATGGCCATGGCTCGCTCTGCTTTGCGCTGTACGCC----GTGATCGAG 1392        Db  2320 CCCCAGACCAAGGAGCTGATGCACTTGTGCATGCGGCAGGAGGGCCTACCTAGAGGCCCTC 2379

Qy   443 GlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyr 462              Qy   783 ------PheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuValIleGluLysLys 800
         |||:::                                                                             :::
Db  1393 AAAGCCAAGAAGCTGCGTCCACCAAGAGAGTCCAAGAAGCGGACTGCCCCATTGCC 1452        Db  2380 TCCCAGTCCAGTGCCCACTGTGAAGGGGAGCACCCTGAGCTGTGAGTCTGGAGGGACCAG 2439

Qy   463 TyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeu 482              Qy   801 CysLysLysValMetAlaSerArgLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
         ||| :::                                                                            :::
Db  1453 TGGGCCAACCTTCATGGCGTTTGACTACAAGGACACCGGGGAACGCTGCCTC 1512        Db  2440 TGCACCTTCATGACCTCCAAGATGAAGAATGGATCATGTAC----AGCACAGAG 2493

Qy   483 HisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlnLysGlySerPheAsnAlaAspLysLysLeu 502              Qy   821 ThrAlaLeuSerAsnGluThrGlyIleGlyIleProPheLysHisGlyAspAspLeuAspLeuArgGln 840
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```

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Db   2494  GAGGCAGGCAGCCGCGGCCGCGGCGCTGGGCATCATCTTTAAGACGGGATGACCTCCGGCAG  2553
Qy    841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu    860
                |||:::   :::  ||:::::  :::   ::::  :::  ||||||||||
Db   2554  GACATGCTGACCCCTGCAGATGATCAGCTCATGGAACGTCCTGGAAGCAGCAGAGGGGCTG  2613

Qy    861  AspLeuCysLeuLysProTyrGlyCysIleSerThrGlyLysIleGlyMetIleGlu       880
                |||   :::    ||||||||||
Db   2614  GACCTGAGCATGACAGATGACCCCCTATGGCTGCTCCCACCGGGACACCAGGCCTCATTGAG  2673

Qy    881  IleValLysAspAlaThrThrIleAlaLysIleGln-----GlnSerThrValGlyLysAsn  898
                :::   :::     |||           :::   :::
Db   2674  GTGGTACTCCGTTCAGACACCATGCAACATCCAACTCAACAGAGCAACATGGCAGCC      2733

Qy    899  ThrGlyTyrAlaPheLysAspGluValLeuSerHisTrpLeuCysProIleGlu          918
                ||||||       :::::    ||||||
Db   2734  ACAGGCCGCTTCAACAAGGATGCCCTGCTCAACCTGGCTCAAGAACCCG--GGG    2790

Qy    919  GluLysPheGlnAlaAlaValAlaGluArgPheValTyrSerCysValAlaGlyTyrCysValAla  938
                ||| :::::           :::::      :::
Db   2791  GAGGGCCTGGATCGGACCATTGAGGAGTTCACCCTCCTGTCCTGCTATTGTGTGGCC  2850

Qy    939  ThrPheValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGly    958
                |||
Db   2851  ACATATGTCCTGGGCATTGGCGATCGGCACAGCGACAACATCATGATCCGAGAGAGTGGG  2910

Qy    959  AsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle    978
                |||  :::     :::
Db   2911  CAGCTGTTCCACATTGATTTTGGCCACTTTCTGGGGAATTTCAAGACCAAGTTTGGAATC  2970

Qy    979  AsnLysGluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSer    998
                |||::::     :::
Db   2971  AACGGCGAGCGTGTCCCATTCATCCTCACCTATGACTTTGTCCATGTGATTCAGCAGGGG  3030

Qy    999  GlyLysLysThrSerLeuHisPheGlnIleAspPheGlnAsnHisAlaProSerGluGluThrLeuAlaTyrLeu  1018
                ||||||      :::
Db   3031  AAGACTAATAATAGTGAGAAATTTGAACGGTTCCGGGGACTGTTCGAAAAGGGCCTACACC  3090

Qy   1019  AlaLeuArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetGluThrGly       1038
                ||| :::::     :::
Db   3091  ATCCTGGCGGCGCACGAGGGCTTCTCTTGCCCTGATGCGGGCCAGGC    3150

Qy   1039  MetProGlnLeuThrSerLysGluAspLeuGluTyrIleLeuArgAspAlaLeuThrValGly  1058
                ||||||
Db   3151  CTGCCTGAGCTCAGCTGCTCCAAAGACATCCAGTATCTCAAGGACTCCCTGGCACTGGGG  3210

Qy   1059  LysSerGluGluAspAlaLysLysTyrPheLeuAspGlnIleIleGluValCysArgAspLys  1078
                ||||||
Db   3211  AAAACAGAGGAGGAGGCACTCCGAGTGAAGTTAACGAGCCCCTCCGTGAG    3270

Qy   1079  GlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal  1091
                ||||||
Db   3271  AGCTGGAAAACCAAAGTGAACTGGCTGGCCCACAACGTG  3309
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                  ;       TYPE: DNA
                  ;   ORGANISM: Homo sapiens
                  US-10-162-160-2

                  Alignment Scores:
                  Pred. No.:              6.45e-147          Length:              3387
                  Score:                  1349.50            Matches:             361
                  Percent Similarity:     50.23%             Conservative:        197
                  Best Local Similarity:  32.49%             Mismatches:          404
                  Query Match:            23.31%             Indels:              149
                  DB:                     15                 Gaps:                39

                  US-09-974-573-1 (1-1102) x US-10-162-160-2 (1-3387)
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Qy     38  IleProIleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAla   57
                :::                :::::  |||||||:::|||||||||
Db     58  GTTGTGGTTGACTTCCTGCTGCCACCAGGG--------------------------GTC  90

Qy     58  LeuLeuHis------ValAlaGlyHisGlyAsnValGluMetLysAlaGlnValTrp  75
                |||::::   ||| :::     :::||||
Db     91  TACCTGAACTTCCCTGTGCCCGCAATGCCAACCTCAGCACCATCAAGCAGCTGCTGTGG  150

Qy     76  LeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeu---GlyProAsp  94
                |||                  :::  :::::||||||||
Db    151  CACCGCGCCCCAGTATGAGCCCCTC-----------------TTCCACATGCTCAGTGCCCCGAG  198

Qy     95  HisPheLeuLeu--LeuTyrGlnLysLysGlyIleTrpTyrIleTyrIleTyrAspLysLysTyr  113
                :::                :::
Db    199  GCCTATGTGTTCACCTGCATCAACCAGACAGCAGCAAGAGCTGGAGGACGAGCAA  258

Qy    114  GlnValValGlnThrLeuAspCysLeuArgTyrTrpLysTrpLeuHisArgSerProGly  133
                :::          :::::     :::
Db    259  CGG------CGTCTGTGTGACGTGCAGCCCCTTCCTGCCCGGCCTG---------  297

Qy    134  GlnIleIleHisValValGlnArgGlnHisAlaProSerGluGluThrLeuAlaPheGlnArgGln  153
                :::                :::
Db    298  -----CGCTCGTGGCCCGTGAGGGCGACCGGCGTGAAGAAGCTC---ATCAACTCACAG  348

Qy    154  LeuAsnAlaLeuIleGlyTyrValAspValThrAspValSerAsnValHisAspGluLeu  173
                :::::   :::     :::::
Db    349  ATCAGCCTCCCTATCGGCAAAGGCCTGCCAGTTGACTCTTGTGCCCAGAAGTG  408

Qy    174  GluPheThrArgArgLeuValThrProArgMetAlaGlyValAlaGlyAlaAspPro     193
                :::   :::
Db    409  AACGACTTTCGGCCCAAGATGTGC-----------CAATTCTGCGAGGAGCGGCGCCCCGG  462

Qy    194  LysLeuTyrAlaMetHisProTrpValThr-----SerLysProLeu              207
                 |||     :::
Db    463  CAGCAGCTGGCTGGCCGAGGGCTGGCTGCAGTACAGTTCCCCCTGCAGTCGACAGTTGGAGCCCTCG  522

Qy    208  ------------ProGluTyrLeuLeuLysLysIleThrAsnAsnCysValPheIle      222
                ||||      :::
Db    523  GCTCAAACCTGGGGGGCCTGGTACCCTG-----CGCTCCCGAACCGGGGCCCTTCTGGGTC  576

Qy    223  ValIle------HisArgSerThrThrSerGlnThrIleLeuValSerAlaSerAspThr  240
                |||
Db    577  AACGTTAAGTTGAGGGGCAGCGAGAGAGAGTTCACCTTCCCAGGTGTTCCACCAAGGACGTG  636

Qy    241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLys-----LysLysSerLeu  258
                :::::
Db    637  CCGGTGCCGCTGTGATGGCTGTGCCCTGGCGAAGAGAGGCCAACAGTGTTCCGGCAGCCGCTG  696

Qy    259  MetAspIleProGluSerGlnAsnGluArgGlyAspPheValCysGlyValArgArgAsp  278
                |||
Db    697  GTGGAGCAGCCCGGAA-----------GACTACACGCTGCAGTGAACGTGCAGCAGCAT  741

Qy    279  GluTyrLeuValGlyGluThrProIleLysAsnPheGlnTrpProValArgGlnCysLysLys  298
                |||||
Db    742  GAGTACCTGTATGGCAGCTACCCGTCTCGCCAGTACATCTGCAGTGCTCACTGCCTCAC  801

Qy    299  AsnGlyGluGluHisHisLeuValLeu---------------                   307
                |||:::
Db    802  AGTGGGTTGACCCCCTCACCTGACCATGGTCCATTCCTCCTCCATCCTCCTCCGCCATGCGGGAT  861
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RESULT 8
US-10-162-160-2
; Sequence 2, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
;   APPLICANT: Van Haesebroeck, Bart
;   APPLICANT: Waterfield, Michael D.
;   TITLE OF INVENTION: No. US2003003099627A1e1 Lipid Kinase
;   FILE REFERENCE: 2332-1-002
;   CURRENT APPLICATION NUMBER: US/10/162,160
;   CURRENT FILING DATE:  2002-06-03
;   PRIOR APPLICATION NUMBER: US/09/194,640
;   PRIOR FILING DATE: 1998-12-01
;   PRIOR APPLICATION NUMBER: 9611460.8
;   PRIOR FILING DATE: 1996-06-01
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 2
; LENGTH: 3387
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Qy   654  AspAspValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHis   673
          ||||:::     |       :::||||||
Db  1816  GATGAGCTGTTCCAGTACCTGCTGCAGCTGGTGCAGGTGCTCAAGTACGAGTCCTACCTG  1875

Qy   674  AspSerAlaLeuAlaArgPheLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHis   693
          ||:|||    |||||||        :::||:
Db  1876  GACTGCGGAGCTGACCAAATTCCTGCTGAAGCGGGGCCTGCGCAACAAGCGCATCGGCCAC  1935

Qy   694  PheLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGln------   711
          ||||||   |||||        :::
Db  1936  TTCCTTTTCTGGCCACCTCCGCTCCGCCATCGGAGCTGCAGAGTGCC--------------  1983

Qy   712  ---ArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHis   730
              ::: |||       ||||||||||       :::
Db  1984  CTGCGCCTTCGGCTGCATCCTGGAGGCCTACTGCAGGGGC---AGGACCCACCACATGAAG  2040

Qy   731  AspPheThrGlnIleValGlnValIleAspMetLeuGlnLysValThrIleAspIleLys   750
          |||||   ::: ||||||    |||:::
Db  2041  GTGCTGATGAAGCAGCGGGGGAAGCACACTGAGCAAACTG--AAGCCCTGAATGACTTCGTC  2097

Qy   751  SerLeuSerAlaGluLysTyrAspValSerSerGlnValIleSerGlnLeuLysGlnLys   770
          |||      :::::::
Db  2098  AAGCCCAGAGTCTTCAGAGACCCC---------------------AAGCCCCAG        2130

Qy   771  LeuGluAsnLeuGlnAsnLeuAsnLeuGlnSer---------------------------   782
          |||           |||
Db  2131  ACCAAGGACGTGATGCACTTGTGCATGGCAGGAGGAGCCCTACCTAGAGCCCTTCTCCCAC  2190

Qy   783  PheArgValProTyrAspPheProGlyLeuLysAlaAlaGlyAlaLeuValIleGluLysCys   802
          ::: ||||||||||          |||
Db  2191  CTGCAGTCCCCACTGCATCCCGCACCCTGCTGGCTGGAAGTCTGCGGTGGGACAGTGCACC  2250

Qy   803  ValMetAlaSerIleLysLysLysProLeuTrpPheLeuGluPheLeuLysCysAlaAspProThrAla   822
          ::: ||||||||          :::
Db  2251  TTCATGGACTCCAAGATGAAGCCCGTGGATCATGTAC-----AGCAACGAGGAGGCA       2304

Qy   823  LeuSerAsnGluThrIleGlyIleIlePheLysHisGlyHisGlyAspAspLeuArgGlnAsnAspMet   842
          ||||||             |||
Db  2305  GGCAGCGGCGGCAGCGTGGGCATCATCTTTAAGAACGGGGATGACCTTCCGGCAGGACATG  2364

Qy   843  LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuLeuAspLeu   862
          |||     :::                ::: |||
Db  2365  CTGACCCTGCAGATGATCCAGTTCATGGACGTTCCTGTGGAAGCAGCAGAGGGGCTGGACCTG  2424

Qy   863  CysLeuLeuProTyrGlyTyrGlyCysIleSerSerThrGlyIleAspLysIleGlyMetIleGluIleGluVal   882
          :::                 |||||||||
Db  2425  AGGATGACCCCCATGGGCTGCCTCCCCACCGGGCACCGCCACGGCCCCATTGAGGTCGGTA  2484

Qy   883  LysAspAlaAlaValAlaThrThrIleAlaLysLysGlnIle------GlnSerThrValGlyAsnThrGly   900
          |||
Db  2485  GCCTTCACCAAGGATGCCGTGCTCAACATCCAACTCAACAAGAGCCAGACCATGAGTCCACAGTAT  2544

Qy   901  AlaPheIleAspAspPheGlyHisHisLeuSerHisSerHisTrpLeuLysGluSerProIleGluGluLys   920
          :::                       ::: |||||||
Db  2545  GCCTTCACCAAGGATGCCGTGCTCAACATCCAACTCAACAAGAACCCG--GGGGAGGCC  2601

Qy   921  PheGlnAlaAlaValAlaGluArgPheTyrSerCysValAlaGlyThrPhe   940
          |||||        :::
Db  2602  CTGGATGCAGCCATTGAGGAGTTCACCCTCTCGTGTGTGGCTGGCACCTTTGTGTGCCACATAT  2661

Qy   941  ValLeuGlyIleGlyAspHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
          |||||       :::
Db  2662  GTGCTGGGCATTGGCGATCACAACGACAACATCATGATCTCCGAGACGGGCAACCTG  2721

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyAsnLys   980
          |||||       :::
Db  2722  TTCCACATTGATTTTGGCCACTTTCTGGGAAATTACAAGAGTTTCTTGGGAAATAAG  2781

Qy   981  GluArgValProPheLeuThrProMetValMetGlyTyrSerGlyLys   1000
          |||||||       :::
Db  2782  GAGCGTGTCCCATTCCTCACCCCAATGGTTGTCATGTGATTCAGCAGGGGAAGACT  2841

Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnLysAspValCysValCysValAlaTyrLeuAlaLeu   1020
```

```
Qy   308  ---AspThrProProAspProAlaLeuAlaAspGluValArgLysGluGluTrpProLeuVal   326
             :::        |||
Db   862  GAGCAGAGCAACCCTGCCCCCAGGTCCAGAAACCGGTCCAAAACCACCTCCC------   915

Qy   327  AspAspCysThrGlyValThrGlyValThrGlyHisTyrHissGluGlnLeuThrIleHisGlyLysAspHis   346
          :::                |||
Db   916  ------------------------------ATTCCTGCGAGAAGCCT  933

Qy   347  GluSerValPheThrValSerLeuTrpAspCysAspArgLysPheArgValLys---Ile   365
          |||                      :::::::
Db   934  TCCTCCT------GTGTCCCTGGTCCCTCCGGTGCCCATCGAGCTCATC  984

Qy   366  ArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThrValPheValGluAla   385
          |||                      :::
Db   985  CAGGGCAGCAAAGTGAACGCCACGACGAGCGG--------ATGAAGCTGGTGGTGCAGGCC  1035

Qy   386  AsnIleGlnTyrGlyValGlnGlnValLeuCysGlnValLeuCysGlnLeuArgArgThrSerProLys---ProPhe   404
          :::                |||
Db  1036  GGGCTTTTCCACGGCAACGAGATGCTGTCAAGACGGTGTCCAGCTCGGAGGTGAGCGTG  1095

Qy   405  ThrGluGlyValLeuValLeuTrpAsnValTrpLeuGluPheSerIleLeuLysIleLysAspLeuPro   424
          :::                |||
Db  1096  TGCTCGGAGCCCGTGTGGAAGCAGCGGCTGGAGTTTGACACATCAACATCTGCGACCTGCCC  1155

Qy   425  LysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLeuTyrCysGlyLysLeuAlaProAlaLeuSerGlyLysLys   444
          :::                |||
Db  1156  CGCATGCCCGTGTCTGCTTGCGCTGTACGCC---------GTGATCGAGAAAGCC  1203

Qy   445  ThrSerAlaGluMetProSerProGluSerLysGlyLysLysLeuLysLeuAlaGlnIleLeuLeuTyrTyrVal   464
          :::                |||
Db  1204  AAGAGAGGCTGCTCCACCAAGAGAAGTCCAAGAAGGCCGACTGCCCCATTGCCTGGGCC  1263

Qy   465  AsnLeuLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyLeuTyrValLeuHisMet   484
          :::                |||
Db  1264  AACCTCATGCTGTTGACTACAAGGACCCAGCTTAAGACAACGGGGAACGCTGCCCTCTACATG  1323

Qy   485  TrpGlnLeuSerGlyLysGlyLysGlyLysGlyAspProAsnAlaAspLysLeuThrSer   504
          |||
Db  1324  TGG------CCCTCCGTCCCAGATGAGAGGGCCAGCTGCTGAACCCCACGGGCACTGTG  1377

Qy   505  AlaThrArgAsnProAspLysLysGluAsnSerMetSerIleLeuSerLeuLeuAspAsnTyrCys   524
          :::                |||
Db  1378  CGCAGTAACCCACACGGATAGGCGCCGGTCCGCCTGCCCTGCCTGCCTGCCTGCCTGCCTGCCGGAGGTGGCC  1437

Qy   525  ---HisProIleAlaLeuPro---------------------LysHisArgPro   534
             :::                      |||
Db  1438  CCGCACCCCGTGTACTACCCCCGGAGAAGATCTTGGGAGTCTGGGGCGGACAC--  1491

Qy   535  ThrProAspProGlyGluArgValArgArgValAlaGluMetProAsnGlnLeuArgLysGln   554
          :::                |||
Db  1492  --------------------AGCGAGTGTGTGCATGTCACCGAGGAGGAGCAGGTG------CAG  1530

Qy   555  LeuGluAlaIleIleAspAspPheGlyHisHisLeuThrLeuAlaGluAspLysGluLeu   574
          |||
Db  1531  CTGCGCGGGAAATCCTGGAGCGCGGGGGTCTGGAGCGGTGTATGAGCAGGAGAGGACCCTG  1590

Qy   575  LeuTrpHisPheArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLysLeuPhe   593
          :::                :::||||||
Db  1591  GTGTGGAAGCTGGCGGCCATTGAGGAGTTCACCCTCTCGAGCTAGCCCCGGCTGCTG  1650

Qy   594  SerSerValLysTrpProGluGlyValTrpProAspValArgValAlaLysLysThrTyrGlnLeuLeuAlaAlaLys   613
          :::                |||
Db  1651  CTGGTCACCAAGTGACAACATGAGAAGATGTGGCAGCATGATCCCAGTGCTCTACCTGCTGTGCTCC  1710

Qy   614  ArgGluValTrpAspAspGlnSerAlaLeuAspValGlyLeuThrMetGlnSerAlaLeuAlaLys   633
          :::
Db  1711  ------------TGGCCGGAG------CTGCCCGTCCTGAGCCGTGCTGCTAGACTTC  1755

Qy   634  AsnPheSerAspGluAsnValArgArgIleAlaValAlaValGlnLysLeuGluSerLeuGluAsp   653
          :::                :::
Db  1756  AGCTTCCCCAATTGCCACGTAGGCTCCTTCCGCCATCAAGTCGCTGCGGAAACTGACGGAC  1815

Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnLysAspValCysValCysValAlaTyrLeuAlaLeu   1020
```

```
Db  2842  AATAATAGTGAGAAATTGAACGGTTCCCGGGCTACTGTGAAAGGGCCTACACCATCCTG  2901
               |||||||||:::::::||||:::                    |||  :::||||||
Qy          --------------------------------ATTTATATCCAGTTGGAGGTACCTCGGAAGCTACCATTTCTTAT  500

Db   70   MetLysAlaGlnValTrpLeuArgAlaLeuGlnThrSerValSerAlaAspPheTyrHis  89
               :::|||                  |||:::||
Qy  1021  ArgHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro  1040

Db  501  ATTAAGCAGATGTTATGGAAGCAAGTTCACATTACCCAATG---  542
             ||||||                      ||||||
Qy  2902  CGGGCCACAGGGCTTCTCTTCCTCACCCTTTGCCCTGATGCGGCGGGCCAGGCCTGCCT  2961

Db   90   ArgLeuGlyProAspHisPheLeuLeuTyrGlnLysLysGlyValGlnTrpTyrGluIle  109
               ||||||                         :::
Qy  1041  GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer  1060

Db  543  ----------------------------TTCAACCTCCTTATGGATATTGACTCCTATATGTTTGCATGT  584
                                           :::||||||:::||||||:::||||||
Qy  2962  GAGCTCAGCTGCTCCAAAGACATCCAGTATCTCAAGGACTCCCGGCACTGGGGAAAACA  3021

Db  110  TyrAspLysTyrGlnValGlnThrLeuAsp  121
              :::|||                      ---------Cys--------
Qy  1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp  1080

Db  585  GTGAATCAGACTGCTGTATATGAGGAGCTTGAAGATGAAACAGAAGACTCTGTGATGTC  644
             ||||||                                 :::
Qy  3022  GAGGAGGAGGCACTGAAGCACTTCCGAGTGAAGTTAACGAAGCCCTCCGTGAGAGCTGG  3081

Db  122  ----------LeuArgTyrTrpLysValLeuHisArgSer-------ProGlyGlnIleHis  136
                    ||||||:::                  ||||||:::
Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuVal  1091

Db  645  AGACCTTTTCTTCCAGTTCTCAAATTAGTGACAAGAAGTTGTGACCCAGGGGAA------  698
            |||||                      ||||||
Qy  3082  AAAACCAAAGTGAACTGGCTGGCTGGCCCACACGTG  3114

Db  137  ValValGlnLysArgHisAlaProSerGluGluThrLeuAlaPheGlnLysArgGlnLeuAsnAla  156
                                             :::|||:::||
Qy        --------------------AAATTAGACTCAAAAATTGGAGTC  722

Db  699  ------------------------------------------------------------  699
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Alignment Scores:
Pred. No.:
Score:                2e-145
Percent Similarity:   1337.50
Best Local Similarity: 49.65%
Query Match:          31.99%
DB:                   23.10%
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Length:       3777
Matches:      364
Conservative: 201
Mismatches:   407
Indels:       167
Gaps:         38
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US-09-974-573-1 (1-1102) x US-09-814-353-19587 (1-3777)
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Db  157  LeuIleGlyTyrAspValThrAspValSerAsnValHisAspAspGluLeu---GluPhe  175
                 ||||||:::                        :::
Qy  723  CTTATAGGAGAAAAGGTCGCATGAAATTGATCCTTGAGGATCCTGAAGTAAATGAATTT  782

Db  176  ThrArg------ArgArgLeuValThrProArgMetAlaGluValAlaAlaGlyArgAsp-  192
             :::|||                                   :::|||
Qy  783  CGAAGAAAAATGCGCAAATTCAGGCAGGAAAAATCCTGTCACTTGTGGGATTGTCTTGG  842

Db  193  ---ProLysLeuTyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeu  211
                  |||                  :::||||||
Qy  843  ATGGACTGGCTAAAACAACATATCCACCAGAGCATGAACCATCCCGAAAACTTA  902

Db  212  LeuLysLysIleThrAsnAsnCysValPheIleValIleHisArgSerThrSerGln  231
              ||||||                               :::|||
Qy  903  GAAGAGATAAACTTATGGGGAAAGCTCATCGTAGCTGTTCATTTGAAAACTGCCAGGAC  962

Db  232  -----ThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerProPhe  249
                  :::|||||                       :::|||
Qy  963  GTGTTTAGCTTTCAAGTGTCTCCTAATATGAATCCTATCAAAGTAAATGAA---  1013

Db  250  ThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp  269
              |||||                                  :::
Qy  1014  TTGGCAATCCAAAAACGTTTGACTATTCATGGGAACGAAGATGAAGTTAGCCCCTATGAT  1073

Db  270  PheValLeuArgValCysGlyArgAspGluThrTyrLeuValGlyGluThrProIleLysAsn  289
              :::||||||:::                      |||||||
Qy  1074  TATGTTTTGCAGTCAGCGGGAGAGTAGAATATGTTTTGGTGATCATCCACTAATTCAG  1133

Db  290  PheGlnTrpProValArgGlnCysGlyLeuLysAsnGlyValGluGlnIleHisLeuValLeuAspThr  309
              :::||||||                  |||
Qy  1134  TTCCAGTATATCCGGAACTGTGTGAACAGAGACGAGCCCGCCCCCATTTTATACTT---  1187

Db  310  ProProAspProAlaLeuAspGluValArgLysGluGluTrpProLeuValAspAspCys  329
              ---------------------------------------------GTGGAATGC  1196
Qy  1188  ----------------------------------------------------------  1188

Db  330  ThrGlyValThrGlyTyrHisGluGln------------LeuThrIleHisGlyLysAspHisGlu  347
              :::|||||:::                        :::||||||
Qy  1197  TGCAAGATCAAGAAAATGTATGAACAGAAGATGATTGCCATAGAGGCTGCCATAAATCGA  1256

Db  348  SerValPheThrValSerLeu-------  354
              ||||||                  |||
Qy  1257  AATTCATCTAATCTTCTTCCATTACCACCAAAGAAAACACGAATTATTTCTCATGTT  1316

Db  355  TrpAspCysAspArgLysPheArg---ValValSerArgGlyIleAspIleAspProValLeu  373
              :::|||||                  :::||||||
Qy  1317  TGGGAAAATAACAACCCTTTCCAAATTGTCTTGGTTAAGGGA---AATAAACTT  1367

Db  374  ProArgThrAlaAspLeuThrValPheValGlnAlaAsnIleGlnIleTyrGlyGlnValGlu  393
              :::||||||                      |||
Qy  1368  AACACAGGAGGAAACTGTAAAAGTTCATGTCAGGGCTGGTCTTTTTTCATGTACTGAGCTC  1427
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```
Qy   30   AlaSerLeuSerSerMetGluLeuIleProIleGluProValLeuProThrSerGlnArg  49
              ||| :::|||                      ||||||
Db  402  TCACCAGATAGCATCTGATGGCTCCATAACCTGTGGATTTCCTTTTGCCCACTGGG-----  455

Qy   50   AsnThrLysThrProGluThrAlaLeuHisValAlaLeuGlyHisAlaGlyHisGlyAsnValGluGln  69
              |||                               :::
```

```
Qy  726 ThrAlaMetLeuHisAspPheThrGlnValGlnValIleAspMetLeuGlnLysVal  745
Db 2445 GTGGGGCACATGAAAGTGCTTTCTAAGCAGGTTGAAGCACTCAATAAGTTAAAAACTTTA 2504

Qy  746 Thr-----IleAspIleLysSerLeuSerAlaGluLysTyrAspValSerSerGlnVal  763
Db 2505 AATAGTTTAATCAAACTGAATGCCGTGAGTGAAGCAAAACAGAGCCAAAGGAGGAGGCCATG 2564

Qy  764 IleSerGlnLeuGlyLys------------------LeuGluAsnLeuGlnAsnLeuAsn  778
Db 2565 CATACCTGTTTAAAACAGAGTGCTTACCGGAGAAGCCCTTCTGACCTGCAGTCA------ 2618

Qy  779 LeuProGlnSerPheArgValProTyrArgGlyLeuLysLysGlyAlaLeuValIle  798
Db 2619 ------CCCCTGAACCCATGTGTATCCTCCAGAACTCTATGTT 2657

Qy  799 GluLysCysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysLysCysAla  818
Db 2658 GAAAAGTGCAAATACATGATGCTTCAAAATGAAGCCTTTGGCGTGGTATAC-------- 2708

Qy  819 AspProThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeu  838
Db 2709 AATAACAAGGTATTTGGTGGAGATTCAGTTGGAGTGATTTTTAAAAATGGTGATGATTTA 2768

Qy  839 ArgGlnAspMetLeuIleLeuGlnIleIleLeuArgIleMetGluSerIleTrpGluThrGlu  858
Db 2769 CGACAGGATATGTTGACACTCCAAATGTGCCTTAGTCCTTGATGATTACCTGGAAAGAGCT 2828

Qy  859 SerLeuAspLeuCysSerLeuLeuProTyrGlyTyrGlyAspLysIleGlyIleGlyMet  878
Db 2829 GGTTTGGATCTTCGGATGTTGCCTTATGGCGTGTTTAGCAACAGGAGACTCGGCTCTGGCCTC 2888

Qy  879 IleGluIleValLysAspAlaThrThrIleAlaLysIleGln------GlnSerThrVal  896
Db 2889 ATTGAAGTTGTGAAGCACCCTCGAAACAATTGCTGACATTCAGCTGACAATGTG 2948

Qy  897 GlyAsnThrGlyAlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysPro  916
Db 2949 GCTGCTGCAGCGCCTTCAACAAGATGCCCCTCTGAACTGCTTAAAGAATAACAACTCT 3008

Qy  917 IleGluGluLysPheGlnAlaLeuAlaValGluArgPheValTyrSerCysAlaGlyTyrCys  936
Db 3009 GGGGATGAC---CTGGACACCGAGCCATTGAGGAATTTACACTGTCCTGTGCCTACTGT 3065

Qy  937 ValAlaThrPheValLeuGlyIleGlyHisAspAsnAlaAsnIleMetIleSerGlu  956
Db 3066 GTAGCTTCTTTATGTCCTTGGGATTGGTGACAACATCATGATCCTCAAAAAA 3125

Qy  957 ThrGlyAsnLeuPheHisIleLeuAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeu  976
Db 3126 ACTGGCCAGGTCTGCTTCCACATTTGGACATATTCTTGGAAATTTCAAATCTAAGTTT 3185

Qy  977 GlyIleAsnLysGluArgValProPheLeuThrProAspPheLeuPheValMetGly  996
Db 3186 GGCATAAAAGGAGGAGCCAGTGCCTTTTATTCTTACCTATGATTTCATCCATGTCATTCAA 3245

Qy  997 ThrSerGlyLysThrSerLeuHisPheGlnLeuLysPheGlnLeuAspValCysValLysAla 1016
Db 3246 CAAGGAAAAACAGAAATACAGAAAAGTTTGGCCGGTTCCGCCAGTGTTGTGAGGATGCA 3305

Qy 1017 TyrLeuLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetGly 1036
Db 3306 TATCTGATTTTACGACGGGATGGGAATCCTTCATCACTCCTTCGCGTGATGTTGACT 3365

Qy 1037 ThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIleLeuArgAspAlaLeuThr 1056
Db 3366 GCCAGGGCCTTCCTGAACTCACATCAGTCAAAGATAATACAGTATCTTAAGGACTCTCTTGCA 3425

Qy 1057 ValGlyLysSerGluGluLysAspAlaLysLysTyrPheLeuAspGlnIle---GluValCys 1075
Db 3426 TTAGGGAAGAGTGAAGAGAAGGCACTCAAACAGTTTAAGCAAAAATTTGATGAGGGCGCTC 3485

Qy 1076 ArgAspLysLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyLeuGly 1093
```

```
Qy  394 LeuCysGlnArgArgThrSerProLys---ProPheThrGluGluValLeuTrpAsnVal  412
Db 1428 CTGTGTAAAAACCATCGTAAGCTCAGAGGTATCAGGGAAAAATGATCATATTTGGAATGAA 1487

Qy  413 TrpLeuGluPheSerIleLysIleLysAspLeuProLysGlyGlyAlaLeuAsnLeuGln  432
Db 1488 CCACTGGAATTTGATATTAATATTTGTGACTTACCAAGAAATGGCTCGAATTATGTTTTGCT 1547

Qy  433 IleTyrCysGlyLysAlaProAlaLeuSerGlyLysLysThrSerAlaGluMetProSerPro  452
Db 1548 GTTTAT--GCAGTTTTGGATAAAGTAAAAACGAAGAAATCAACGAAAACTATTAATCCC 1604

Qy  453 -------GluSerLysLysGlyLysLysAlaGlnLeuLeuTyrTyr------ValAsn  465
Db 1605 TCTAAATATCAGACCATCAGGAAAAGCTGGAAAAGTGCATTATCCTGTAGCGTGGGTAAAT 1664

Qy  466 LeuLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMetTrp  485
Db 1665 ACGATGGGTTTTTGACTTTAAAGGACAATTGAGAACTGGAGACAATATTACACAGCTGG 1724

Qy  486 GlnLeuSerGlyLysGlyGluGlnGlnGlySerPheAsnAlaAspLysLeu--------  502
Db 1725 -----------------TCTTCATTT---CCTGATGAACTCGAAGAAATG 1754

Qy  503 ---------ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSer  517
Db 1755 TTGAATCCAATGGGAACTGTTCAAACAAATCCATATACTGAAAATGCAACAGCTTTGCAT 1814

Qy  518 IleLeuLeu--AspAsnTyrCysHisProIleAlaLeuPro--------------  530
Db 1815 GTTAAAATTTCCAGAGAATAAAAAAACAACCTTATTATTACCCTCCCTTCGATAAGATTATT 1874

Qy  531 --LysHisArgProThrProAspProGluGlyValAspAlaArgValAlaArgAlaGluMetProAsn  549
Db 1875 GAAAAAGGCAGCTGAGATTGCAAGCAGTGATAGTGTCAAGTCGAGGTGGAAAA 1934

Qy  550 GlnLeuArgLysGlnLeuGluAlaIleIleIleAlaThrArgProLeuAsnProLeuThrAla  569
Db 1935 AAGTTTCTTCCTGTATTGGAAAGAAATCTTGGACAGGGATCCCTTGTCTCAACTGTGTGAA 1994

Qy  570 GluAspLysGluLeuTrpHisPheArgTyrGluSerLeuLys---AspProLysAla  588
Db 1995 AATGAAAATGGATCTTATTTGGACTTTGCCAACAAGACTGCCGAGAGATTTCCCACAATCA 2054

Qy  589 TyrProLeuPheSerSerValLysTrpGlyGlnGluIleValLeuValAlaLysThrTyr  608
Db 2055 CTGCCAAAATTACTGCTGTCAATCAAGTGGAATAAACTTGAGGATGTTGCT------ 2105

Qy  609 GlnLeuLeuAlaLysGlyArgGluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMet  628
Db 2106 CAGCTTCAGGCGCGTGCTTCAGATTTGGCCTAA--------CTGCCCCCCGGGAGGCCCTA 2159

Qy  629 GlnLeuLeuAspCysAsnPheSerAspArgGluAlaAsnValArgAlaIleAlaValGlnLeuLysLeu  648
Db 2160 GAGCTTCTGGATTTCCAACTATCCCAGACCACCAGTACGTTCGGAGAATATGTGTAGGCTGCCTG 2219

Qy  649 GluSerLeuGluAspAspAspAspValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLys  668
Db 2220 CGACAGAGTGATGAGGACGCGTTCTCAATATCTTTTACAACTGGTGCAGTGTTAAAA 2279

Qy  669 PheGluProTyrHisAspSerArgAlaLeuAlaArgPheLeuLeuLysArgGlyLeuArgAsn  688
Db 2280 TATGAGCCCTTTCCTGATTGTGCCCTCCAGATTCCTATTAGAAAAGAGCACTTGGTAAT 2339

Qy  689 LysArgIleGlyHisPheLeuTrpHisGluSerGluIleAlaGlnSerArgHis  708
Db 2340 CGGAGGATAGGGCCAGTTCTTTCTATTTTGGCATCTTAGGTCAGAAGTG------CAC 2387

Qy  709 ------TyrGlnArgPheAlaValIleLeuGluLysAlaTyrLeuArgGlyCysGly  725
Db 2388 ATTCCTGCTTGTCTCAGTACAAATTTGGTCATCCTTGAGCATACTGCCGGGGGA---AGT 2444
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```
Db   3486  AGGGACAAGCT-GGACTACTAAAGTTGAACTGGATGGCCACACAGTTCCGGGA  3538
           ||||||||||              :::::::   ||||||   |||

RESULT 10
US-10-092-219-1
; Sequence 1, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114Alel Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

Alignment Scores:
Pred. No.:              3.01e-114          Length:         5061
Score:                  1074.00            Matches:         309
Percent Similarity:     45.60%             Conservative:    178
Best Local Similarity:  28.93%             Mismatches:      343
Query Match:            18.55%             Indels:          238
DB:                     14                 Gaps:             32

US-09-974-573-1 (1-1102) x US-10-092-219-1 (1-5061)

Qy   194  LysLeuTyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeuLeuLys  213
          ||||  :::                                       ||||||||
Db  1168  AAATTGAAGACCAAATTTCCATATACCAATCACCGCCACAAACCCAGGCTATTTGTTAAGT 1227

Qy   214  LysIleThr-------AsnAsnCysValPheIleValIleHisArgSerThrSer  230
          ||||||||:::::::                         ::: :::::
Db  1228  CCAGTCACACAGCGCAAAGAAACATATGC--------------------GGAGAAAAT  1263

Qy   231  GlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerPhePheThr  250
          :::||||||||||||||||||                |||||||||||||||||||||
Db  1264  GCTAGTGTGGAGGTCTCCATT--GACATTGAAGGATTCAGTTACCAGTTACTTTTACG  1320

Qy   251  ----------LysMetAlaLysLysSerLeuMetAspIleProGlu  263
                    :::|||||||||                    ::: :::
Db  1321  TGTGATGTGAGTTCTACTGTAGAAATCATTAATATGCAAGCCCTTTGCTGGGTACATGAT  1380

Qy   264  SerGlnAsnGluArgAsp-------PheValLeuArgValCysGlyValArgAspGluTyr  280
          ::::                       ::::::|||||||:::::||||||||
Db  1381  GACTTGAATCAAGTAGACATGTTGGCAGCTATGTTCTAAAAGTTTGTGGTCAAGGAAGTG 1440

Qy   281  LeuValGlyGluThrProIleLysProLysPheGlnTrpValArgGlnCysLysLeuLysAsnGly  300
          |||                ::: :::                      ||| :::::::
Db  1441  CTGCAGAATAATCATTGCCTTGGAGTCATGAGCATATTCAAAAACTGTCGAAAATGGGAC 1500

Qy   301  GluGluIleHisLeuValLeu------------  307
          |||||||||||||||                 :::
Db  1501  ACAGAAATTAGACTACAACTCTTGACCTTCAGTGCAATGTGTCAAAATCTGGCCGGAACA 1560

Qy   308  ------AspThrProProAspProAlaLeuAspGluValArgLysGluGluTrp  323
          :::|||||||||||                             ::: :::
Db  1561  GCAGAAGATGATGAAAAACACCCGTGGAT--------------TTAAACAAAACCCTGTAT  1605

Qy   324  ProLeuValAlaAspCysThrGly-------------------------------ValThr  333
          :::                                                    :::
Db  1606  CAAATAGAAAAACCTGCAAAGAACCATGACGAGGAGCACACCCTGTGAAGAACTCTTAGAT 1665

Qy   334  GlyTyrHisGluGln----------LeuThrIleHisGlyLysAspHis---------  346
          ||||| ||                 ||| :::
Db  1666  TCTTATCACACACCAAGTAGAACTGGCTCTTCAAATTGAAAACACCAGCAGTAGAT 1725

Qy   347  --------------------------GluSerValPheThrValSer  353
                                    :::::::
Db  1726  CAAGTAATTAAAGTGTAAGAAAAATCTGTAGTGCTTTAGATGGTGTCGAGACTCTTGCC 1785

Qy   354  LeuTrpAspCysAspArgLysPheArgValLysIleArgGlyIleAspIleProValLeu  373
          :::| ||                        :::::::::::::
Db  1786  ATTACAGAATCAGTAAAGAGCTAAAG------------AGAGCAGTAATCTTCCA-----AGG 1833

Qy   374  ProArgThrAlaAspLeuThrValPheVal---  383
          :::::::|||||||:::::
Db  1834  AGTAAAACTGCTGATGGACTTCTTTGTTGGAGGAAGACACTAGCAGCAGGAGTTCAACT 1893

Qy   384  -----GluAlaAsnIleGlnTyrGlyGlnGlnLeuCysGlnArgArgThr---  399
               |||||||
Db  1894  AGGGGCTCACTTAATCCTGAAAATCCTGTCAAGTAAGCATAAACCAATTAACTGCAGCA 1953

Qy   400  -----SerPro-------  401
               :::||||
Db  1954  ATTTATGATCTTCTCAGACTCCATGCAAATTCTGGTAGGAGTCCTACAGACTGTGCCCAA 2013

Qy   401  ------------------  401
Db  2014  AGTAGCAAGAGTGTCAAGGAAGCATGGACTACAACAGAGCAGCTCCAGTTTACTATTTT 2073

Qy   401  ---LysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle  420
                                                           |||||||
Db  2074  GCTGCTCATGGAATTCAAGTAATGGGTATCAAATTATGAAAAATACTACTGATATGT 2133

Qy   421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyr-----CysGlyLysAla  438
          |||||||||||||||:::::::::::::::                 :::::::
Db  2134  TCACTGTCTCACAATGGAAAGGATCTTTTTAAACCTATTCAATCAAAGAAGGTTGGCACT 2193

Qy   439  ProAlaLeuSerGlyLysThrSerAlaThrAsnProAspProGluSerProGluSerLysGlyLysAla  458
          ::: :::                                                    ::: :::
Db  2194  TACAAGAATTTCTTCATCTTATTAAATGGATGAGAACTAATCATTTTCCTATCCAGATA 2253

Qy   459  GlnLeuLeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGly  478
          :::                                     |||||||::::::
Db  2254  ACTAAACTTCTATATCTTTGGACTTCATCA-----------GTTCCTTTACCTCTTTGTGACTTTAGAC 2313

Qy   479  GluTyrValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsn  498
          :::::::::: :::                           |||||||
Db  2314  AGTGGAAGTTCCCCTGATTCTAATAAGCAGAGAAAGGGACCCAGAAGCTTTGGCAAA---  2370

Qy   499  AlaAspLysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIle  518
                                                  :::::::
Db  2371  -----------------------GGTTCTTACCTCTTTGTGACTTTAGACGGTTTTTAACATGTGGA  2415

Qy   519  LeuLeuAspAsnTyr---CysHisProIleAlaLeuProLysHisArgProThrPro---  536
          :::                                                   ::: :::
Db  2416  ACTAAACTTCTATATCTTTGGACTTCATCA---------------CATACAAATTCTGTTCCTGGACAGTT 2472

Qy   537  -------------AspProGluGlyAspAlaArgValArgAlaGlu-------  546
                       |||||||:::::
Db  2473  ACCAAAAAAGGATAATGTCATCGAAAGATAGTGCTACCAGGTTGATTTTCCTTCCTCTGCA 2532

Qy   547  -----MetProAsnGlnLeuArgLysGlnLeuGlnLeuAlaIleIleIleAlaThrAspLeu  564
          :::
Db  2533  TTTGATATTATTATACAACTCCTCAAGTTGACACAGAAGCATTATACAGCAACACATAACTTA 2592
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Db   3616 TTTAAAGATAAACCACTTGCAGAGTGCTAGGAAATACAATCCCTCGAGAAGAAGAATAT 3675

Qy   922 GlnAlaIleValArgPheValTyrSerCysAlaGlyThrValAlaThrPheVal 941
         |||||||||||||||||||||||||||| ::|| :::||

Db   3676 GAAAAGGCTTCAGAGAACTTTATCTATCCTGTGTCCTGGATCGTGTGGTAGCCACCTATGTT 3735

Qy   942 LeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPhe 961
         ||||||||

Db   3736 TTAGGCATCTGTGATCGACACAATGACAATATAATGCTTCGAAGACACGGGACACATGTTT 3795

Qy   962 HisIleAspPheGlyHisHisLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGlu 981
         ||| :: :::||

Db   3796 CACATTGACTTTGGAAAGTTTTGGGACATGCACAGAGTTTGGCAGCTTCAAAAGGGAT 3855

Qy   982 ArgValProPheValLeuThrProAspPheLeuProValMetGlyThrSerGlyLysLys 1001
         ||||:||

Db   3856 CGGGCTCCTTTGTGCTGACCTCTGATATGGCATATGTCATT---AATGGGGTGAAAAG 3912

Qy   1002 ThrSerLeuHisPheGlnLysPheGlnValCysValLysAlaTyrLeuAlaLeuArg 1021
         ::::|| |||||||||

Db   3913 CCCACCATTCGTTTCAGTTGTTGTGGACTCGTGTCAGGCCTACAACTTGATAAGA 3972

Qy   1022 HisHisThrAsnLeuLeuIleIleLeuPheSerMetMetThrGlyMetProGln 1041
         :::||

Db   3973 AAGCAGACAAACTTTTCTTAACCTCCTTTCACTCATGATCCTTCAGGGTTACCAGAA 4032

Qy   1042 LeuThrSerLysGluAspIleGluTyrIleArgAspAlaAlaLeuThrValGlyLysSerGlu 1061
         ||||

Db   4033 CTTACAAGTATTCAAGATTTGAAATACGTTAGAGATGCACTTCAACCCCAAACTACAGAC 4092

Qy   1062 GluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpThr 1081
         :::|| |||

Db   4093 GCAGAAGCTACAATTTCTTTACTAGGCTTATTGAATCAAGTTTGGAAGCATTGCCACA 4152

Qy   1082 ValGlnPheAsnTrpPheLeuHis 1089
         :::|||

Db   4153 ---AAGTTTAACTTCTTCATTCAC 4173

RESULT 11
US-09-205-658-47
; Sequence 47, Application US/09205658
; Patent No. US2001002961 7A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 3504
;   TYPE: DNA
;   ORGANISM: Caenorhabditis elegans
US-09-205-658-47

Alignment Scores:
Pred. No.:   Length: 3504
Score: 7.99e-110   Matches: 313
Percent Similarity: 1034.00   Conservative: 227
Best Local Similarity: 46.96%   Mismatches: 400
Query Match: 27.22%   Indels: 210
DB: 17.86%   Gaps: 44
          9

US-09-974-573-1 (1-1102) x US-09-205-658-47 (1-3504)

Db   2593 GAAACACTAGAGAATGAATATAAAGGAGAAACTTCTTGATATTCTTCATAAAGACTCATCA 2652
         ::: ||| ::::||| :::|||

Qy   565 AsnProLeuThrAlaGluAspLysGluLeuLeuThrHisPheArgTyrGluSerLeuLys 584
         ||||| ||:|| :::|

Db   2653 CTTGGACTTTCTAAAGAACTAAAAGAAGCTTTTATGGGAGAAACGTTATTATTGCTTCAAA 2712

Qy   585 AspProLysAlaTyrProLysPheSerSerVal------LysTrpGlyGlnGln 601
         ::|||| |||||||| :::|||

Db   2713 CACCCAAATTGTCTTCCTAAAATATTAGCAGAGGCGCCCAAACTGGAAATGGGGTAAT--- 2769

Qy   602 GluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSerAla 621
         ||||| ||||||| :::||

Db   2770 ------CTTGCCAAAACTACTCATTGCTTCACCAG-------TGG------CCTGCA 2808

Qy   622 LeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArg 641
         ||| ::: :::||| :::|||

Db   2809 TTGTACCCCACTAARTGCATTGGAACTTCTGATTCAAAATTTGCTAGCAAGTAAGA 2868

Qy   642 AlaIleAlaValGlnLysGluLeuSerLeuGlu~AspAspAspValLeuHisTyrLeuLeu 661
         :::|||| ||||| :::|

Db   2869 TCCCTAGCTGTGCACCTGGATTGAGGCCATTAGTGATGATGAGCTAACAGATCTTCTTCCA 2928

Qy   662 GlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeu 681
         :::||||||| |||||| :::|||

Db   2929 CAGTTTGTACAAGCTGTGAAATGAAATTACTTGAATAGTTCATTAGTGCAATTCCTT 2988

Qy   682 LeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheTrpPheLeuArgSer 701
         |||:|| :::|||

Db   2989 TTGTCAGGGCATTGGGAAATATCCAGATAGCACACAATTTATATTGGCTTCCTCAAAGAT 3048

Qy   702 GluIleAlaGlnSerArgHisTyrGlnArgGlnAlaValIleLeuGluAlaTyrLeu 721
         :::||

Db   3049 GCCCTG--CATGATGTACAGTTTAGTACCCGATACGAACATGTTTGGGTGCTCCTG 3105

Qy   722 ArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspMet 741
         ::: :::|||| :::

Db   3106 TCAGTAGGAGGAAAACGACTTAGAGAGAACTTCTAAAACAGACGAAACTTGTACAGCTT 3165

Qy   742 LeuGlnLysValThrIleAspIleLysSerAlaGluLysTyrAspValSerSer 761
         ::: :::

Db   3166 TTAGGAGGAGTAGCAGAGAAAAGTAAGGCAGGCAGGTGGATCA------GCCAGA 3213

Qy   762 GlnValIleSerGlnLysGlnLysGlnLnLysGlnLysGluAsnLeuGlnAsnLeuAsnLeuProGln 781
         ||||| ::::|||| ::::||

Db   3214 CAGTTGGT------CTCCAAAGAAGATATGGAACGAGTACAGTCCCTTTTTCAGAAAAAT 3267

Qy   782 SerPheArgValProTyrAspTyrGlyLeuLysAlaGlyAlaLeuValIleLeuValIleGluLysLysCys 801
         :::||||

Db   3268 AAATGCCGGTCCCCTCCTCCAAGCAGTCTAGTGGCAAAAGAATTAAATAATTAAGTCGTGT 3327

Qy   802 LysValMetAlaSerLysLysLysProLeuTrpLeuPheGluPheCysAlaAspProThr 821
         :::|||

Db   3328 TCCTTCTTCAGTTCTAATGCTCTAAAGTCACAATGCTGAATGCTGACCCTCTG 3387

Qy   822 AlaLeuSerAsnGluThrIleGlyIleIlePheHisGlyAspAspLeuArgGlnAsnAsp 841
         ||||| :::

Db   3388 ------GGAGAAGAAATTAATGGTCATGTTTAAGGTTGGTGAAGATCTTCGGCAAGAT 3438

Qy   842 MetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAsp 861
         ||||| ::::||

Db   3439 ATGTTAGCTTACAGATGATAAAGATTATTGGATAAAGAGATCTGGCTTAAAGAGGACTAGAT 3498

Qy   862 LeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysAspLysIleGlyMetIleGluIle 881
         ||||

Db   3499 CTGAGGATGGTAATTTCAAATGTCTCTCAACTGGCAGAGATCGGCAGAGTGTGGAGCTG 3558

Qy   882 ValLysAspAlaThrThrIleAlaLysIleAlaLysIleGlnIleSerThrValGlyAsnThrGlyAla 901
         ::: ::::|||

Db   3559 GTTCCTCGTTCCGATACCCTTCAGGAAAAATCCAAGTGGAA--TATGGTGTGACAGGATCC 3615

Qy   902 PheLysAspGluValGlnLeuSerHisTrpLeuLysGluLysCysProIleGluGluLysPhe 921
         ||||| :::::||

```
Qy   78 AlaLeuGluThrSerValSerAlaAlaAspPheTyrHisArgLeuGlyProAspHisPheLeu   97
          ::::||||    :::||| ||   ||||||                        |||
Db  265 TCGCTAGAAATCAAGCTATCA---GATTCAAACATCAACTT--------------TTCGAA  309

Qy   98 LeuLeuTyrGlnLysLysGlyInTrpTyrGluIleTyrAspLysTyrGlnValValGln   117
          |||          ||::::|| |||||| |||||          |||:::|||
Db  310 TTGATTGCTCCGATGAAGTGGGGAACATATTCCGTAAAGCCACCAGGATTATGTGTTCAGA  369

Qy  118 ThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisVal   137
          |||  ||:::|||                                   :::
Db  370 CAGTTGAATAATTTCGGCGAAATGAAGTTATATTTAACGACGATCAACCCCTGTCGAAA   429

Qy  138 ValGlnArgHisAlaProSerGluGluThrLeuAlaPheGln-------------------   151
          :::::|||||                  :::|||
Db  430 TTAGAGCTCCACGGCCACTTTCCCAATGCTTTTCTACCAACCTGATGGAATAAAACAGG   489

Qy  152 ---------ArgGlnLeuAsnAlaAlaLeuIleGlyLeuGlyTyrAspValThrAspValSer   166
                   :::  |||   |||:::                |||
Db  490 GATAAAGAATTAATGACGTGATATAAGTCATTGTCTAGGATACTCACTGGATAAACTGGAA   549

Qy  167 AsnValHisAspAspGluLeu------GluPhe-------------------ThrArgArg   178
          :::|||  |||   :::           |||                    :::|||||
Db  550 GAGAGCCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTGGGCTCGTCGTACGAAGAAA  609

Qy  179 ArgLeuValThr--------------------------------------------------   182
          |||
Db  610 ACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGCGTTCCCGAAGAACAGTAC   669

Qy  183 --------------------ProArgMetAlaGluValAlaGlyValAlaGlyProLysLeu   195
                              :::          |||:::|||            |||||
Db  670 TTGTGTGTGGTGAATCGTGCCCGAAAGATTGGAGAATCAAAGTCAAGGCTGCCAAGCTG   729

Qy  196 TyrAlaMetHisProTrpValThrSerProLeuProGluTyrLeuLeuLysLysLysIle   215
          |||                                       :::|||
Db  730 AGTTATCAGATGTTTTGGAAAAAGCGTAA-------------------GCGAAATC   768

Qy  216 ThrAsnAsnCysValPheIleValIleValIleArgSerThrThrSerGlnThrIleLysVal   235
          :::                                         |||
Db  769 AATGGAGTTTGC-------------------GAGAAAATGATGAAGATTCAAATTGAATTC   810

Qy  236 SerAlaAspThrProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLys--   255
          :::    ||||||:::|||                   :::|||
Db  811 AATCCGGACGAAATCTCCGAAATCTGCTTCACACGTTTCTCACGAAATGCGAAAA--   867

Qy  256 LysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp------PheValLeuArg   273
                                                          |||
Db  868 --------TTGGGATGTATACGATACCGATCCTGCAGATCGAAGAGGATGGTTTCTTCAA   918

Qy  274 ValCysGlyArgSerGlyTyrLeuValGly--GluThrProIleLysAsnPheGlnTrp   292
          :::||||||                          :::|||
Db  919 TTGGCTGGACGTACCACGTTTGTTACAAATCCAGATCTCAAACTTACGTCTTATGATGGT   978

Qy  293 ValArgGlnCysLeuLysAsn-------------GlyGluGluHis------ValArgLysGlu   305
          :::|||                            :::                |||
Db  979 GTCCGTTCCGAAGCTCAGATCGATGCCCTTGTTCGTCCGCACAATCACTA  1038

Qy  306 ValLeuAsp-----ThrProProAspProAlaLeuAspGlu-------ValArgLysGlu   321
          :::                                             |||||
Db 1039 GTCCTTCAAAGACTATTGTCGCCCCAAAACCACCTACGAACCCATTATGTGAGCGCACAC  1098

Qy  322 GluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluHisThrIle   341
          :::|||                              :::
Db 1099 GAACGAAAACTTGCTCTAGAAGCTCCTCTAGAACGTGCTCAGCCTGTCT-----ATAGATAGCACACCAAAA  1152

Qy  342 HisGlyLysAspHisGluSerValPheThr------------------------------   351
          :::  |||
Db 1153 CAGAGCAAGACAAGTGACATGGTTATGCATGGTTATGGGTTTTCGTCCGCACAGCTTCACTCAAACAA  1212

Qy  352 ValSerLeuTrpAspCysAspArgArgPheArgValLys----------IleArgGlyIle   368
          :::||||||                                         :::|||||
Db 1213 GTTTCACTTTGGGACCTTTGACGCGCAATCTTATGATACCGGCCTGTGAATATTCTGGATTC  1272


Qy  369 AspIleProValLeuProArgThrAlaAspLeuThrValPheGluAlaAsnIleGln   388
          |||    :::|||         |||        :::
Db 1273 GATTTCCCGGCC---------GACGTGGATATGTACGTTCGAATCGAATTCAGTGTATAT  1323

Qy  389 TyrGlyGlnValLeuCysTyrGlnArgThrSerProLysProPheThrGluGluVal   408
          |||    :::|||                   :::
Db 1324 GTGGGGACACTGACGCTGGCATCAAAATCTCACAACA---AAAGTGAATGGTCAATTGCA  1380

Qy  409 LeuTrpAspValTrpLeu---GluPheSerIleLysIleLysAspLeuProLysGlyAla   427
          |||                  :::|||
Db 1381 AAAATGGATAAGGAAATGTACACTTTGATCTATACATGAAGGAGATATGCCACCATCTGCA  1440

Qy  428 LeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAlaLeuSerGlyLysThrSerAla   447
          |||                                                  :::|||
Db 1441 GTACTCAGCATTCGTGTTGTTTGTACGGAAAA-----------------------GTG  1473

Qy  448 GluMetProSerProGluSerLysGlyGlyLysAlaGlnLeuLeuTyrTyrValAsnLeuLeu   467
          :::||||||                                            |||
Db 1474 AAATTAAAAAGTGAAGAATTCGAA----------------GTTGGGTGGGTAAATATGTCC  1518

Qy  468 LeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMetTrpGlnLeu   487
          |||                                                  :::
Db 1519 CTAACCGATTGGAGATGAACTACGACAAGGACAATTTTATTCCATCGTGTGG----------  1572

Qy  488 SerGlyLysGlyGluAspGlnGlnGlySerPheAsnAlaAspLysLeuThrSerAlaThrAsn   507
                                                              :::
Db 1573 ........:::GTCCTGAACCGACTGCCAATCGTAGT  1599

Qy  508 ProAspLysAsn-----------SerMetSerIleSerIleLeuLeuLeuAsp   521
          :::                    |||
Db 1600 AGGATCCGGAGAAAATGGAGCAAGGAGTAGGCACCACGGCGGTTACAATTGAAATCTCA  1659

Qy  522 AsnTyrCysHisProIleAlaLeuPro------------------LysHis   532
          :::||||||                                    |||
Db 1660 AGTTATGGTGGTAGAGTTGGAAATGCCGAGTCAAGGACAATACACATATCTCGTCAGCAC  1719

Qy  533 Arg------------------------ProThrProAspProGluGlyValAspArgValAlaArgValAlaGluMetPro   548
          |||                       :::
Db 1720 CGAAGTACTTCGACGGAAACTTGAATATATTATGGGTGATGACTTGAGTCGTGATCAGA  1779

Qy  549 AsnGlnLeuArgLysAspGlnLeuGluAlaIleLeuIleAlaThrAspProLeuAsnProLeuThr   568
          :::                                                  :::
Db 1780 GATCCAGGAATAAGAAGCTTCAGATGCTTGTCAGGAAGCATGAATCTGGAATTGTATTA  1839

Qy  569 AlaGluAspLysGlu------------LeuLeuTrpIleSerPheArgTyrGluSerLeuLysAsp   585
          :::                        :::|||
Db 1840 GAGGAAGATGAACAACGTGCTCTCGGAATGTGGAG---AGATACATTCAAAAAGCAGGAG  1896

Qy  586 ProLysAlaTyrProLeuPheSer---SerValLysTrpGlyInGlnIleLeuVal   604
          |||                        :::
Db 1897 CCTGATTTGCTCATTGTGCTCTCCGAACTCGGATCGTGTGTGACTAGCGTGAGAACTT  1956

Qy  605 AlaLysThrTyrGlnLeuLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspVal   624
          :::                                                  :::
Db 1957 TCCGAGCTCATGTGATGCTTGAAAA----------TGGAAACCGCCGAGTGTGCAGCC  2007

Qy  625 GlyLeuThrMetGlnLeuLeuGluAspCysAsnPheSerAspGluAsnValAlaIleAla   644
          :::                                                  |||
Db 2008 GCGTTGACT------------TTGCTTGGAAAAGTTGCACGGATGTGATTCGAAAGTTGCA  2061

Qy  645 ValGlnLysLeuLeuGluSerLeuGluAspAspValLeuHis---TyrLeuLeuGlnLeu   663
          |||                                          :::
Db 2062 GTGGAGAAGTTGAATGACGAGCAGCTGAGCCCGGTCACATTCCATCTTTCATATTGCCTCTC  2121

Qy  664 ValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLys   683
          |||                                                  :::
Db 2122 ATACAGGCGTTGAAGTACGAACCGGCCGTGCTCAATCGGAAGTTGGAATGATGCTCTTGACT  2181

Qy  684 ArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIle   703
          |||                                                  :::
Db 2182 AGAGCTCTCGCGATTATCGGAATTGGAATCGACTTTTCTGCCGTGCCGTGAGAGATT  2241

Qy  704 AlaGlnSerArg------------------HisTyrGlnGlnArgPheAlaValIleLeu   717
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RESULT 12
US-09-844-353A-47

; Sequence 47, Application US/09844353A
; Patent No. US2002003758A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Koweek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005
; CURRENT APPLICATION NUMBER: US/09/844,353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857,076
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-844-353A-47

Alignment Scores:
Pred. No.:
Score: 7.99e-110
Percent Similarity: 1034.00   Length: 3504
Best Local Similarity: 46.96%   Matches: 313
Query Match: 27.22%   Conservative: 227
DB: 17.86%   Mismatches: 400
                          9   Indels: 210
                                             Gaps: 44

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Db  1519 CTAACCGGTTGGAGAGATGAACTACGACAAGGACAATTTTATTCCATCTGGG------ 1572
                ||||:||||||                    ||||||||||
Qy   488 SerGlyLysGlyGluAspGlnGlySerPheAsnAlaAspLysLeuThrSerAlaThrAsn 507

Db  1573 -------------------------------------------GCTCCTGAACCGACTGCCAATCGTAGT 1599
Qy   508 ProAspLysGluAsn-----------------SerMetSerIleSerIleLeuLeuAsp 521

Db  1600 AGGATCGAGAAAATGGAGCAAGAGATAGGCACCAACCAGCCGGTTACAATTGAAATCTCA 1659
                    :::                              ||||||
Qy   522 AsnTyrCysHisProIleAlaLeuPro---------------------LysHis 532

Db  1660 AGTTATGTGGTAGAGTTCGAATGCCCAGGTCAAGGACAATACACATATCTCGTCAAGCAC 1719
                ||||:::|||                       :::|||
Qy   533 Arg--------ProThrProAspProGluGluAspAspArgValArgArgAlaAlaGluMetPro 548

Db  1720 CGAAGTACTTGGACGGAAACTTTGAATATTATGGGTGATGACTATGAGTCGTGTATCAGA 1779
Qy   549 AsnGlnLeuArgLysGlnLeuGluAlaIleIleIleAlaThrAspProLeuAsnProLeuThr 568

Db  1780 GATCCAGGATATAAGAAGCTTCAGATGCTTGTCAGGAAGCAGCATGAAATCGGAATTGTATTA 1839
           :::         :::::
Qy   569 AlaGluAspLysGlu--------LeuLeuTrpHisPheArgTyrGluSerLeuLysAsp 585

Db  1840 GAGGAAGATGAACAACGTCATGTCTGGATGTGGAGG---AGATACATTCAAAAGCAGGAG 1896
Qy   586 ProLysAlaTyrProLysLeuPheSer----SerValLysTrpGlyGlnGlyIleValVal 604

Db  1897 CCTGATTGCTCATTGTGTCTCCGACTCGGCATTTGTGTCGGACTGGACTGGTGAGAACTTT 1956
Qy   605 AlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspVal 624

Db  1957 TCCGAGCTCTATGATGCTTGAAAAA-----TGGAAACCGGCGAGTGTGGCAGCC 2007
           :::::::      |||
Qy   625 GlyLeuThrMetGlnLeuGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaAla 644

Db  2008 GCGTTGACT-------TTGCTTGGAAAACGTTGCACGGATCGTGTGATTCGAAAGTTTGCA 2061
Qy   645 ValGlnLysLeuGluSerLeuGluLysValHis----TyrLeuLeuGlnLeu 663

Db  2062 GTTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTCCATCTTTCATATTGCCTCTC 2121
Qy   664 ValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaLeuAArgPheLeuLeuLys 683

Db  2122 ATACAGGCGGTTGAAGTACGAACCGCGTGCTCAATCGGAAGTTGGAATGATGCTCTTGACT 2181
Qy   684 ArgGlyLeuArgAsnLysArgIleGlyHisPheLeuGlnPheTrpPheLeuArgSerGluIle 703

Db  2182 AGAGCTTTCTGCGGATTATCGGAATTGGACATCGACTTTTCTCGGCTCCGGTCGCAGAGATT 2241
Qy   704 AlaGlnSerArg---------------HisTyrGlnArgPheAlaValIleLeu 717

Db  2242 GCTCGTTTGAGAGATTGGATCGTGAAAGTGAAGAAGATATCGCGTATCTCACTTCTGATG 2301
Qy   718 GluAlaTyrLeuArgGlyCysGlyGlyThrAlaMetLeuHisAspPheThrGlnGlnValGln 737

Db  2302 GAAGCTTACCTCCGTGGA---AATGAAGAGACACATCAAGAATCATCACCCGACAAGTTGAC 2358
Qy   738 ValIleAspMetGlnLeuGlnValValThrIleAspIleLysSerLeuSerAlaGluLysTyr 757

Db  2359 ATGGTTGATGAGCTCACCACGAACTCCTTGTCAAAGGAAATGCCAAAA------ 2409
Qy   758 AspValSerSer---------GlnValIleSerGlnLeuLysGlnLeuGluAsn 773

Db  2410 GATGTTGCTACGATGAAACTGCGTGACGAGCTTCGATTAGTCATAAAATGGAAAAT 2469
Qy   774 LeuGlrAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysAla 793

Db  2470 ATGGATTCT-----------CCACTGGATCCTGTGTACAAACTG 2502
           |||:::|:::
Qy   794 GlyAlaLeuValIleGluLysCysLysValMetAlaSerLeuLysLeuProLeuTrpLeu 813

Db  2503 GGTGAAATGATAATCGACAAAGCCATCCTCCTAGGAGTGCAAAACGTCCTTAATGCTT 2562
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; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/857,076
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SEQ ID NO 47
;   LENGTH: 3504
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   TYPE: DNA
;   ORGANISM: Caenorhabditis elegans
US-09-963-693-47

Alignment Scores:
Pred. No.:   Length: 3504
Score: 7.99e-110   Matches: 313
Percent Similarity: 1034.00   Conservative: 227
Best Local Similarity: 46.96%   Mismatches: 400
Query Match: 27.22%   Indels: 210
DB: 17.86%   Gaps: 44
                          13

US-09-974-573-1 (1-1102) x US-09-963-693-47 (1-3504)

Qy   78 AlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeu 97
                :|||||||| :: :||::||||||
Db   265 TCGCTAGAAATCAAGCTATCA---GATTCAAACATCAACTT--------------TTCGAA 309

Qy   98 LeuLeuTyrGlnLysGlyGlnTrpTyrGluIleTyrArgLysTyrAspLysValValGln 117
                   ||| ::|::|| || :|||
Db   310 TTGAATTGCTCCGATGAACTGGGGAACATATTCCGTAAAGCCACAGGATTATGTGTTCAGA 369

Qy   118 ThrLeuAspCysLeuArgTyrTrpLysTrpLysValLeuHisArgSerProGlyGlnIleHisVal 137
                 :||: :||||
Db   370 CAGTTGAATAATTTCGGCGAAATTGAGTTATATTTAACGACGATCAACCCTGTCGAAA 429

Qy   138 ValGlnArgHisAlaProSerGluGluThrGlyLeuAlaPheGln------ 151
                   |||
Db   430 TTAGAGCTCCACGGCACTTCCCAATGCTTTTTCTCACCAACCTGATGGAATAAACAGG 489

Qy   152 ------ArgGlnLeuAsnAlaLeuIleGlyTyrLeuAlaLeuArgHis 166
                                  :::
Db   490 GATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATACTCACTGGATAAACTGGAA 549

Qy   167 AsnValHisAspAspGluLeu---GluPhe 178
                  :|||||| ::|||
Db   550 GAGAGCCTGCGATGAGGAAACTCCGTCAATTTCGTGCTTCTCTCTGGGCTCGTACGAAGAAA 609

Qy   179 ArgLeuValThr---- 182
                 ||||::
Db   610 ACGTGCTTGACACGTGGACTGGAGGGTACCAGTCACTACGGCGTTCCCGAAGAACAGTAC 669

Qy   183 ------------ProArgMetAlaGluValAlaAlaGlyArgAspProLysLeu 195
                        |||
Db   670 TTGTGTGTTGGTGAATCGTGCCCGAAGATTTGGAATCAAAAGTCAAGGCTGCCAAGCTG 729

Qy   196 TyrAlaMetHisProTrpSerLysProLeuProGluTyrLeuLeuLysIle 215
                         :|||
Db   730 AGTTATCAGATGTTTTGGAGAAAAGTAAA------------------------GCGGAAATC 768

Qy   216 ThrAsnAsnCysValPheIleValIleHisArgSerThrThrSerGlnThrThrIleLysVal 235
                  :||::||
Db   769 AATGGAGTTGC---------------------------GAGAAAAATGATGAAGATTCAAATTGAATTC 810

Qy   236 SerAlaAspThrProGlyThrIleLeuGlnSerProPheThrLysMetAlaAlaLys 255
                  :::::||||||||
Db   811 AATCCGAACGAACTCCGAAATCTCGTCTTCACACGTTTCCTACGAAATCGCGAAAA--- 867

Qy   814 GluPheLysCysAlaAspProThrAla---LeuSerAsnGluThrArgIleGlyIleIlePhe 832
                  :: ||| :||
Db   2563 CACTGGAAGACAAAAATCCAAAGAGTGACCTGCACCTTCCGTTCTGTGTCAATGATCTTC 2622

Qy   833 LysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGlu 852
                  :||||||||||||
Db   2623 AAGAATGGAGACGATCTTCGCCAGACAATGCTTGTTCTTCAAGTTCTCCGAAGTTATGGAT 2682

Qy   853 SerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThr 872
              ::|||||||
Db   2683 AACATCTGGAAGGCTGAAAACATTGATTGCTGTTGAACCCGTACGCAGTTCTTCCAATG 2742

Qy   873 GlyAspLysIleGlyMetIleGluIleLeuValLysAspAlaThrThrIleAlaLysIleGln 892
                 :: :::
Db   2743 GGAGAAATGATTATTGGAAGTGTGTCCTAATTGTAAACAATATTCGAGATTCAA 2802

Qy   893 GlnSerThr---ValGlyAsnThrGly------AlaPheLysAspGluValLeuSerHis 909
                 ||| ::
Db   2803 GTTGAACAGGATTCATGAATACAGCAGTTCGGAGTATTGATCCTTCGTTTATGAATAAG 2862

Qy   910 TrpLeuLysGluLysCysProIleGluGlu--------- 919
              |:||||||||::::|||:::
Db   2863 TGGATTCGGAAACAATGCGAATTGAAGATGAAAAGAGAAAAGACTCTACG 2922

Qy   920 --------------------------LysPheAlaAla 924
                                          ::
Db   2923 AAAAATCCCATCGAAAAGAAGATTCGATAATACTCAAGCCATGAAGAAATATTTTGAAAGT 2982

Qy   925 ValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIle 944
              |||:||||:||||:|||||||||||:|||||||:
Db   2983 GTCGATCGGATTCCTATACCTCGTGTGTTGGTAATTCAGTTGCCACGTACATAATGGGAATC 3042

Qy   945 GlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAsp 964
                  |||||||:::
Db   3043 AAGGATCGTCACGTGATATTCTGATGCTCACTGAGACGGGAAAAATATGTCCACATTGAT 3102

Qy   965 PheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleIleAsnLysGluValPro 984
                 :||||||:|||||
Db   3103 TTCGGTCACATTTTGGGACCGGAAAAGACCAAACTTGGGATCCAGCGAGATCGTCAACCG 3162

Qy   985 PheValLeuThrProAspPheLeuPheValMet------GlyThrSerGlyLysLysLysThr 1002
                  ::|:: |||||
Db   3163 TTTATTCTAACCGACACTTTATGACAGTGATTCGATTGAATAAATCTGGATGGAAAT 3222

Qy   1003 SerLeuHisPheGlnLysProValCysValLysAlaLeuAlaLeuArgHis 1022
                 :: |||||||||
Db   3223 TCGCATGAGCTACAAAAATTCAAAACGTTATGCGTGCAAGCCTACGAAGTAATGTGGAAT 3282

Qy   1023 HisThrSerLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
                  ::: :::||||
Db   3283 AATCGAGATTTGTTCGTTTTCCTTGTCACCTTGATGCTCGGAATGGAGTGCCTGACCTG 3342

Qy   1043 ThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrVal--GlyLysSerGlu 1061
                 |||||||:::||
Db   3343 TCGACGAAAGCGGATTGGAATCATTGAAGAAAACCCTCTTCTGCAATGGAGAAAGCAAA 3402

Qy   1062 GluAspAlaLysLysTyrPheLeuValAspGlnIleGluValCysArgAspGlyLysTrpThr 1081
                 :: ::|||:|||
Db   3403 GAGAAGCGAGAAAGTTTTCGCTGGAATCTACGAAGAGCCTTCAATGGATCATGGTCT 3462

Qy   1082 ValGlnPheAsnTrpPheLeuHisLeuVal 1091
                 :: |||||
Db   3463 ACCAAAACGAATTGCCTCTTCCACGCAGTC 3492

RESULT 13
US-09-963-693-47
; Sequence 47, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
;   APPLICANT: Ruvkun, Gary
;   APPLICANT: Ogg, Scott
;   TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

```
Qy  256 LysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp------PheValLeuArg 273
            :||||::    :::::         |||
Db  868 ------TTGGATGTATACGATACCGATGATCCTGCAGATGAAGGATGGTTTCTTCAA 918

Qy  274 ValCysGlyArgAspGluTyrLeuValGly---GluThrProIleLysAsnPheGlnTrp 292
            ::||    ||||
Db  919 TTGGCTGGACGTACCACGTTTGTTACAAATCCAGATGTCAAACTTACGTCTTATGATGGT 978

Qy  293 ValArgGlnCysGluLysAsn------------GlyGluGluIleHis-------Leu 305
        |||||    ||
Db  979 GTCCGTTCGGAACTGGAAAGCTATCGATGCCCTGGATTCGTTGTTCGCCGCAAATCACTA 1038

Qy  306 ValLeuAsp------ThrProAspProAlaLeuAspGlu------ValArgLysGlu 321
                      :::                        |||||
Db 1039 GTCCTCAAAGACTATTGTCGCCCAAAACCACTCACGAACCACCATTATGTGAGAGCACAC 1098

Qy  322 GluTrpProLeuValAspAspCysThrGlyValThrGlyValTyrHisGluGlnLeuThrIle 341
Db 1099 GGACGAAAACTTGCTCTAGACGTGCTCAGCGTGTCT-----ATAGATAGCACACCAAAA 1152

Qy  342 HisGlyLysAspHisGluSerValPheThr-------------------------- 351
            ::: :::
Db 1153 CAGACCAAGAACAGTGACATGGTTATGACTTTTCGTCCGACAGCTTCACTCAAACAA 1212

Qy  352 ValSerLeuTrpAspCysAspArgLysPheArgValLys--------IleArgGlyIle 368
            |||        |||:::
Db 1213 GTTTCACTTTGGGACTGCGACCGGAAGTTCAGGCGTGTCT-----ATATAGGCCGATTC 1272

Qy  369 AspIleProValLeuProArgThrAlaAspLeuThrValPheValGluAlaAsnIleGln 388
                                              |||
Db 1273 GATTTCCCGGCC----------GACGTGATATGTACGTTCGGAATCCAGTGTATAT 1323

Qy  389 TyrGlyGlnValLeuCysGlnAsnArgArgThrSerProLysProProPheThrGluGluVal 408
            |||                                          :::
Db 1324 GTGGGGCAACTGACGCTGGCATCAAAATCTACACA---AAAGTAATGCTCAATTGCA 1380

Qy  409 LeuTrpAsnValTrpLeu---GluPheSerIleLysIleLysAspLeuProLysGlyAla 427
        |||||                :::          |||
Db 1381 AAATGGAATAAGGAAAATGTACACTTTGATCTATACATGAAGGATATGCCACCATCTGCA 1440

Qy  428 LeuLeuAsnLeuGlnIleTyrCysGlyLysGlnAlaProAlaLeuSerGlyLysThrSerAla 447
            :::||||||||||
Db 1441 GTACTCAGGATCATTCGTTGTTTGTACCGGAAAA---------------------GTG 1473

Qy  448 GluMetProSerProGluSerGlyLysGlyAlaGlnLeuLeuTyrTyrValAsnLeuLeu 467
            :::||                      ::|||||||
Db 1474 AAATTAAAAAGTGAAGAATTCGAA------------GTTCGTTGGGTAAAATATGTCC 1518

Qy  468 LeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMetTrpGlnLeu 487
        ||||                                                  |||
Db 1519 CTAACCGATTGGGAGAGATGAACTACGACAAGGACAATTTTATTCCATCTGTGG------ 1572

Qy  488 SerGlyLysGlyGluAspGlnGlyLysSerPheAsnAlaAspLysLeuThrSerAlaThrAsn 507
            :::    :::                          |||:::
Db 1573 ------------------------GCTCCTGAACCGACTGCCAATCGTAGT 1599

Qy  508 ProAspLysGluAsn--------SerMetSerIleSerIleLeuLeuLeuAsp 521
        ||||                                  :::
Db 1600 AGGATCGGAGAAAATGGAGCAAGGATAGGCCACCAGCCGGTTACAATTGAAATCTCA 1659

Qy  522 AsnTyrCysHisProIleAlaLeuPro---------------------LysHis 532
            ::||
Db 1660 AACATCTCGAAGGCTGCAAATATTGATTGCTGTTCGTTTGAACCCGTAGCCAGTTCTTCCAAATG 1719

Qy  533 Arg---------ProThrProAspProGluGlyAspArgValArgAlaGluMetPro 548
        |||                                  ||||
Db 1720 CGAAGTACTTGGACGGAAATTTGAATATTATGGTGATGACTATGAGTCCGTGTATCAGA 1779

Qy  549 AsnGlnLeuArgLysGlyGlnLeuGluAlaIleIleIleAlaThrAspProLeuAsnProLeuThr 568
            :::                |||||||| :::::::
Db 1780 GATCCAGGATATAAGAAGCTTGCAGATGCTTGTCAAGAGAGCATGAATTCTGGAATTGTATTA 1839
```

```
Qy  569 AlaGluAspLysGlu--------LeuLeuTrpHisPheArgTyrGluSerLeuLeuLysAsp 585
            |||||                        :::::
Db 1840 GAGGAAGATGAACACGTCATGTCTGGATGTGGAGG---AGATACATTCAAAAGCAGGAG 1896

Qy  586 ProLysAlaTyrProLysLeuPheSer---SerValLysTrpGlyValGlnGluIleVal 604
            |||                    :::
Db 1897 CCTGATTTGCTCATTGTGCCTCCGAACTCGCCATTGTGTGGCTGACTGATCGTGAGAACTTT 1956

Qy  605 AlaLysThrTyrGlnLeuLeuLysAlaLysArgGluValTrpAspGlnSerAlaLeuAspVal 624
        |||||                                    |||
Db 1957 TCCGAGCTCTATCTGATGCTTGAAAAA-----------TGGAAACCGCCGAGTGTGGCAGCC 2007

Qy  625 GlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValAlaArgAlaIleAla 644
            :::            |||
Db 2008 GCGTTGACT----TTGCTTGGAAAAGCGTTGCACGGATCGTGGATTCGAAAGTTTGCA 2061

Qy  645 ValGlnLysLeuGluSerLeuGluAspAspAspValLeuHis---TyrLeuLeuGlnLeu 663
            :|||||                            ::::||
Db 2062 GTGGAGAGTTGAATGACGAGCAGCTGACCCGGTCACATTCCATCTTTCATATTGCCTCTC 2121

Qy  664 ValGlnAlaValLysPheGluGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLys 683
            ::||||||
Db 2122 ATACAGGCGGTTGAAGTACGAACCCGCGTGCTCAATCGGAAGTTGGAATGATGCTCTTGACT 2181

Qy  684 ArgGlyLeuArgAsnArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIle 703
            :::        |||
Db 2182 AGAGCTCTCGCGGATTATCGAATTGGACATCGACTTTCTCGGCGTCGTCGTCAGAGATT 2241

Qy  704 AlaGlnSerArg--------------------HisTyrGlnArgPheAlaValIleLeuLeu 717
            |||                          :::
Db 2242 GCTCGTTGACGGAAGGATTGTGATCGAAAAGTGAAGATATCCCGTATCCCACTTCTGATG 2301

Qy  718 GluAlaTyrArgLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnInValGln 737
        |||||                                            :::
Db 2302 GAAGCTTACCTCCGTGA---AATGAAGAGCACATCAAGATCATCACCCGACAAGTTGAC 2358

Qy  738 ValIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluGluLysTyr 757
            |||                                          :::
Db 2359 ATGGTTGATGAGCTCACACGAATCAGCACTCTTGTCAAAGGAATGCCAAAA------ 2409

Qy  758 AspValSerSer--------------GlnValIleSerGlnLeuLysGlnLysLeuGluAsn 773
            :::                |||
Db 2410 GATGTTGCTACGGATGAAACTGCGTGACGAGCTTCGATCGATTAGTCATAAAATGAAAAAT 2469

Qy  774 LeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrArgProGlyLeuGluLysAla 793
            :::                              |||
Db 2470 ATGGATTCT------------CCACTGGATCCTGTGTACAAACTG 2502

Qy  794 GlyAlaLeuValIleGluGluLysCysLysValMetAlaSerLysLysProLeuTrpLeu 813
            :::                                      |||||
Db 2503 GGTGAAATGATATCGACAAAGCCATCGTCCTAGGAGTGCAAAAGTCCGTTAATGCTT 2562

Qy  814 GluPheCysLysAlaAspProThrAla---LeuSerAsnGluThrIleGlyIleIleIlePhe 832
            :::                          :::|||||
Db 2563 CACTGGAAGAACAAAATCCAAAGAGTGACCTGACCTTCCGTTCGTTCGTGCAATGATCTTC 2622

Qy  833 LysHisGlyLysAspAspLeuArgGlnMetLeuIleLeuGlnIleLeuLeuArgIleMetGlu 852
            :::                                          ||:::
Db 2623 AAGAATGGAGACGATCTTCGCCAGGACAACATGCTTGTTCTTCAAGTTCTCGAAGTTATGGAT 2682

Qy  853 SerIleTrpGluThrGluAspLeuCysLeuLeuProTyrGlyTyrCysIleSerThr 872
            :::
Db 2683 AACATCTCGAAGGCTGCAAATATTGATTGCTGTTCGTTTGAACCCGTAGCCAGTTCTTCCAAATG 2742

Qy  873 GlyAlaAspLysIleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleIleGln 892
            ::::::                          |||:::
Db 2743 GGAGAAATGATTGGAATTATTGAAGTTGTGCCTAATTGAAAACAATATTCGAGATTCAA 2802

Qy  893 GlnSerThr---ValGlyAsnThrGly------AlaPheLysAspGluValLeuSerHis 909
            :::                              :::
Db 2803 GTTGGACAGGATTCATGAATCAGCAGTTCGGAGTATTGATCCTTCGTTTGATGATAAG 2862

Qy  910 TrpLeuLysGluLysCysProIleGlu-------------- 919
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US-09-974-573-1 (1-1102) x US-10-101-235A-1 (1-627)

```
Qy    536 ProAspProGluGlyAspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeu 555
          ||||||||||||||       :  |||||||||||||||||||||||||||||
Db     48 CCCGAT--AGCCCTGCACGCGGGTTCGACGCAGAAATGCCAACCAGCTTCGCAAGCAATTG 104

Qy    556 GluAlaIleIleAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeu 575
          |||||||                                              ||||||
Db    105 GAGGCGATCATAGCCACTGATCCACTTAAC---------------GACAAAGAAATTGCTC 149

Qy    576 TrpHisPheArgTyrGluSerLeuLysAspProLysAlaTyrProLysLysPheSerSer 595
          ||:||  :||||||||||||||||||||||||||||||||||||
Db    150 TGGCATTTTAGATACGAAGAAGCCTTAAGCACCCAAAGCATATCCTCAGCTATTTAGTTCA 209

Qy    596 ValLysTrpGlyGlnGlnIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGlu 615
          |||||  |||||||||||||        :   |||||||||||||||||
Db    210 GTGAAATGGGGACAGCAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAAGAGGGAA 269

Qy    616 ValTrpAspGlnSerAlaLeuAspValGlyTyrLeuThrMetGlnLeuLeuAspCysAsnPhe 635
          ||  ||  ||||||||||:||||||||||||||||||||||||||||||
Db    270 GTCTGGGATCAAAGTGCTTGGATGTTGGGTTAACATGCAGCTCCTGGACTGCAACTTC 329

Qy    636 SerAspGluAsnValArgAlaIleAlaValLysAsnValGlnLeuSerLeuGluAspAspAsp 655
          |  |||||||       ||||||||||||||||||||||||||||||||||||
Db    330 TCAGATGAAAATGTAAGAGCCATTGCAGTTCAGAAACGTGAAATTTGAAGGAGACGATGAT 389

Qy    656 ValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSer 675
          |||    |||||||||| :      ||||||||||||||||||||
Db    390 GTTCTGCATTACCTTCTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGC 449

Qy    676 AlaLeuAlaArgPheLeuLeuLysArgGlyLeuGlnAsnLysArgIleGlyHisPheLeu 695
          |||||||||         ||||||||||||  ||||||||||||||||||
Db    450 GCCCTTGCCAGATTTCGCTGAAGCGTGGTTTAAGAACAAAGAATTGGTCACTTTTTTG 509

Qy    696 PheTrpPheLeuArgSerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaVal 715
          ||     |||||||||||||||||||||||||:  ||||||
Db    510 TTTTGGTTCTTGAGAAGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGAGGTTCGCTGTG 569

Qy    716 IleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAsp 731
          ||:||   :|||||||||
Db    570 ATTCTGGAAGCCTATCTGAGGGGCTGTGGCACAGCCATGCTGCACGAC 617
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RESULT 15
US-09-917-800A-477
; Sequence 477, Application US/09917800A
; Patent No. US2002011946 2A1
; GENERAL INFORMATION:
;   APPLICANT: Mendrick, Donna
;   APPLICANT: Porter, Mark
;   APPLICANT: Johnson, Kory
;   APPLICANT: Castle, Arthur
;   APPLICANT: Elashoff, Michael
;   APPLICANT: Gene Logic, Inc.
;   TITLE OF INVENTION: Molecular Toxicology Modeling
;   FILE REFERENCE: 44921-5038-US
;   CURRENT APPLICATION NUMBER: US/09/917,800A
;   CURRENT FILING DATE: 2001-07-31
;   PRIOR APPLICATION NUMBER: US 60/222,040
;   PRIOR FILING DATE: 2000-07-31
;   PRIOR APPLICATION NUMBER: US 60/222,880
;   PRIOR FILING DATE: 2000-11-02
;   PRIOR APPLICATION NUMBER: US 60/290,029
;   PRIOR FILING DATE: 2001-05-11
;   PRIOR APPLICATION NUMBER: US 60/290,645
;   PRIOR FILING DATE: 2001-05-15
;   PRIOR APPLICATION NUMBER: US 60/292,336
;   PRIOR FILING DATE: 2001-05-22
;   PRIOR APPLICATION NUMBER: US 60/295,798
;   PRIOR FILING DATE: 2001-06-06
;   PRIOR APPLICATION NUMBER: US 60/297,457
;   PRIOR FILING DATE: 2001-06-13
;   PRIOR APPLICATION NUMBER: US 60/298,884
;   PRIOR FILING DATE: 2001-06-19

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Db   2863 |||||||:::::||||   |||||||:::
          TGGATTCGGAAACAATGCGGGAATTCGAAGATGAAAAGAAGAAGAAAAGGACTCTACG 2922

Qy    920 --------------------------------------LysPheGlnAlaAla 924
                                                  |||  :::
Db   2923 AAAAATCCATCGAAAGAAGAAGGAGATATAATACTCAAGCCATGAAAATATTTGAAAGT 2982

Qy    925 ValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIle 944
          ||:|||       ::::::|||:|||  ||||||||||| ||:::::::::||||
Db   2983 GTCGATCGATTCCTATACTCGTGTGTTGGATATTCAGTTGCCACGTACATAAATGGGAATC 3042

Qy    945 GlyAspArgHisAspAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAsp 964
          |||||||||:||||||:::||      |||   |||||:::  ||||
Db   3043 AAGGATCGTCACAGTGATATATCTGATGCTCACTGAGATGGAAAATATGTCCACATTGAT 3102

Qy    965 PheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgValPro 984
          ||||||||||:::|||   |||||||:||:||:   ||||||||
Db   3103 TTCGGTCACATTTTGGACACGGAAGACCAAACTTGGGATCCAGCCGAGATCGTCAACCG 3162

Qy    985 PheValLeuThrProAspPheLeuPheValMet------GlyThrSerGlyLysLysThr 1002
          |||  |   ||||||:||:||||||    |||||||||||:   ::::::
Db   3163 TTTATTCTAACCGAACACTTTATGACAGTGATTCCATCGGGTAAATCTGTGGATGGAAAT 3222

Qy   1003 SerLeuHisPheGlnAspValCysValLysAlaTyrLeuAlaLeuArgHis 1022
          |||:||     ||||:|||||||   :::|||||||  ||||
Db   3223 TCGCATGAGCTACAAAAATTCAAAACGTTATGCGTGAAGCCTACGAGTAATGTGGAAT 3282

Qy   1023 HisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
          |||:::||||||    ||:::::||||
Db   3283 AATCGAGATTTGTTCGTTTCTTGATGCTCGGGAATGGAGTTGCCTGAGCTG 3342

Qy   1043 ThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrVal---GlyLysSerGlu 1061
                    :::  ||||||||||||||  |||
Db   3343 TCGACGAAAGCGGATTTGGATCATTTGAAGAAAAACCCTCTTCTGCAATGGAGAAAAGCAAA 3402

Qy   1062 GluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpThr 1081
          |||:::||:|::   ||:||||||||||||:||    :::   |||
Db   3403 GAAGAAGCGGAGAAAGTTTTTCGCTGGAATCTACACGAAGAAGCCTTCAATGGATCATGGTCT 3462

Qy   1082 ValGlnPheAsnTrpPheLeuHisLeuVal 1091
          |||:::   :||||
Db   3463 ACCAAAACGAATTGCTCTTCCACGCAGTC 3492
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RESULT 14
US-10-101-235A-1
; Sequence 1, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;   APPLICANT: Rockman, Howard A.
;   APPLICANT: Naga Prasad, Sathyamangla V.
;   APPLICANT: Laporte, Stephane A.
;   APPLICANT: Barak, Larry S.
;   APPLICANT: Caron, Marc G.
;   TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
;   FILE REFERENCE: 033072-064
;   CURRENT APPLICATION NUMBER: US/10/101,235A
;   CURRENT FILING DATE: 2002-03-19
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
;   LENGTH: 627
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-235A-1

Alignment Scores:

Pred. No.:	1	Length:	627
Score:	1.54e-100	Matches:	186
Percent Similarity:	944.00	Conservative:	1
Best Local Similarity:	95.41%	Mismatches:	3
Query Match:	94.90%	Indels:	6
DB:	16.30%	Gaps:	2
	13		

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; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 477
; LENGTH: 5990
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477

Alignment Scores:
Pred. No.:           2.91e-96
Score:               922.00
Percent Similarity:  45.21%
Best Local Similarity: 26.88%
Query Match:         15.92%
DB:                  10

Length:       5990
Matches:      286
Conservative: 195
Mismatches:   366
Indels:       218
Gaps:         37

US-09-974-573-1 (1-1102) x US-09-917-800A-477 (1-5990)

Qy      90  ArgLeuGlyProAspHisPheLeuLeuLeuTyrGlnLysLysGlyGlnTrpTyrGluIle  109
                ::|||                ||:|:||||
Db    1083  CAGCTTCCCCAAAGAGTATCTTCTA--------------------------------AGTATA  1115

Qy     110  TyrAspLysTyrGlnValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHis  129
                |||||||||||||                ||||||
Db    1116  TGCGGTTCTGAGGAATTTTACAGATCACTGTCTAGGGAGCCACAAAATATTTCAG       1175

Qy     130  ArgSerProGly----------GlnIleHisValValGlnArgHisAlaProSerGluThr  147
                :::||||       ||:|||||               :::
Db    1176  AAAAGTAAAATCTGTCATTCAACTCCAT--CTCCAGAGAGCAGGACACTCCAGGAAAA  1232

Qy     148  LeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyrArgValThrAspValSerAsn  167
                |||:||||||||                |||||
Db    1233  TTAATCCCGGAAGAGGGAT------------------------GATGACCGCAGTCGG  1265

Qy     168  ValHisAspAspGlu----LeuGluPheThrArgArgArgLeuValThrProArgMetAla  186
                :::|::||       ||||||||||
Db    1266  GTCCATCTGAACCAACTTCTAGAATTTACA----------------------------  1295

Qy     187  GluValAlaGlyArgAspProLysLeuTyrAlaMetHisProTrpValThrSerLysPro  206
                ||||||||||
Db    1296  -----------------------------------------CATATTTCG---------  1304

Qy     207  LeuProGlyTyrLeuLeuLysLysIleThrAsnAsnCysValPheIleValIle-----  224
                ||||||              :::||
Db    1305  ------------AAAATATCCAGACAACAATGCCTCTCCAAGTAATGAAAAGC       1343

Qy     225  --------------HisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAsp  238
                    ||||              :::              :::
Db    1344  TACAACCTCCATGTCGAGCCACCTGTGAAAACCCCAGGAGATGTG-------------GAG  1391

Qy     239  AspThrProGlyThrIleLeuGlnSerPhePheThr-----  250
                :::||||              |||
Db    1392  GAGAAACCT----------CTGTCATCCATGTTTCCTGTGGCCGACACCCTCCTCAGCCA  1442

Qy     251  .------------LysMetAlaLysLysLysSerLeuMetAspIleProGlu  263
                           :::              ||
Db    1443  CATGGAATGACACATTATTGAAGATGTTAGAAACATATGCAGTGTTCTGGGGTGTATTGAA  1502

Qy     264  SerGlnAsnGluArgAspPheValCysGlyValCysArgAspGluTyrrLeuuValGly  283
                |||              :::|||
Db    1503  ACCAAACAAGTTCAGATGCAGTA----------------AAAGAACTAACTCAATTCTG  1547

Qy     284  GluThrProIleLysAspCysLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly--------  300
                :::              ::
Db    1548  CAGAGACCATCACAGAATTTTCATCAGAATTCAGAGACTTCAAAAAAAGGCTTCATAGAG  1607

Qy     301  -----------GluGluIleHisLeuValLeuAspThrProProAspPro  313
                           ||||||              :::::
Db    1608  AACGTGACATGCGGAACTGTCGAGGTCCCCATCAGCTGGTTGACGTGTACTGCAGTAGC  1667
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Qy     314  AlaLeuAspGluValAlaArgLysGluGluTrpProLeuValAspAspCysThrGlyValThr  333
                :::              |||              |||:::
Db    1668  TTTTGTACAGATTTCCGGCTCGCGGCCGCCACCT--------------------GGAGGCGTCTCC  1712

Qy     334  ------------GlyTyrHisGluGlnLeuThrIleHisGlyLysAspHisGluSerVal  349
                           ||||||              :::::
Db    1713  CGCGGACCACGCTGGGCTCCACTCCCACCTGAG-CTTCACGGT------------------GTG  1756

Qy     350  PheThrValSerLeuTrpAspCysAspArgLysPheArgValLysLysArgGlyIleIleAsp  369
                |||              |||
Db    1757  TTCCCTGCA--------CAATGTTCAGAAACTTGGCACACAGTACA-------------  1798

Qy     370  IleProValLeuProArgThrAlaAspLeuPheVal-GluAlaAsnIleGlnTy  389
                              :::|||::              :::
Db    1799  ------------------AGCATTTCATTTCCTGCTGGCTCACATA       1828

Qy     389  rGlyGlnGlnValLeuCysGlnArgArgThrSer-----------ProLysProPh  404
                ||:|::              :::
Db    1829  TGCTGGGAAGAAGCTGTGCCAAGTGAAAAGCTGCGAATCCCTGCCAGTCACAAAGTCATT  1888

Qy     404  eThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLeuLysIleLysAspLeuPr  424
                :::::              :::::              ::::
Db    1889  CTCTTTTTCGGTGAACTGGAATGAAATAATCAATTTCCCTTGAGATAAAGTCACTTCC  1948

Qy     424  oLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaLeuLeuSerGlyLy  444
                |||              |||
Db    1949  AAGAGAAATCCATGCTCGTTATAAAGCTGTTT----------------GGGGAT  1984

Qy     444  sThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyrTyrVa  464
                ||||||              :::
Db    1985  TGACAGTGCC-------------ACCCACAGCCGCAAATCTGCTGGCCTGGAC  2023

Qy     464  lAsnLeuLeuLeu-----------IleAspHisArgPheLeuLeuArgHi  477
                |||              |||
Db    2024  CTGCCTTCCACTATTCCAAAAGAAAAGTCTCCGCTGGGGTCTAGGCTTCTC--------  2075

Qy     477  sGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyLysGlyLysGlyLysGlySerPh  497
                |||
Db    2075  ---------------------------------------------  2075

Qy     497  eAsnAlaAspLysLeuThrSerAlaThrAsnProAspLysGluAsnSerSerIleSe  517
                :::              :::
Db    2076  -------------AGCATGACACTACAGAGTGAGCCTCCTATAGAA---------  2122

Qy     517  rIleLeuLeuAspAsnTyrCysHisProIleAlaLeuProLysHisArgProThr-----  535
                :::              |||
Db    2123  AGTATGGGATGGGAGCCAGCCTACCCCACTGACCCTGCAGATAGATTTTCCAGTCGCCAC  2182

Qy     536  --------ProAspProGluGlyValAspArgVal---ArgAlaGluMetProAs  549
                       ||:||              :::
Db    2183  GTGGGAGTACGTGAAACCTGAGACTGAAGAGAACAAGACTGACCACCAAGAGCCCTCAAG  2242

Qy     549  nGlnLeuArgGlySerGlnLeuGluAlaIleIleIleAlaThrAspProLeuAsnProLeuThrAl  569
                :::              :::
Db    2243  AGAGTGTTTAAAACACATACCGCCAGACCTCCCAAAGACAGCCTCCCTGCTACTTTCTGT  2302

Qy     569  aGluAspLysGluLeuLeuTrpHisPheArgGluTyrGluSerLeuuLysAspProLysAlaTy  589
                :::              :::
Db    2303  GGAAAAGAGGAGGATATTTGTCGGTTTTATCGTTTCACTCGCAACAATGAGAACTCCTCT  2362

Qy     589  rProLysLeuPheSerSerValLysTrpGlyValGlnGlnIleLeuValAlaLysThrTyrGl  609
                |||              :::
Db    2363  CCCTCTGCTTCGTTCCTCTTGGTTGGGATGATGGAAATGCATGC                2422

Qy     609  nLeuLeuAlaLysArgGluValValTrpAspGlnSer---AlaLeuAspValGlyLeuThrrMe  628
                :::
Db    2423  CGTCTTGAGAAGG------------TGGACATTTTCCCATCCGTTGGAA--------GCTCT  2464

Qy     628  tGlnLeuLeuAspCysAsnPheSerArgSpGluAsnValArgGlnAlaAlaAlaValGlnLysLe  648
                :::
Db    2465  TGGCCTTTGACTTCCAGTTTCCAGACACCAAGACAATTCGTCGAAGTTGCCGTTCACAGTT  2524
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Qy    648  uGluSerLeuGluAspAspValLeuHisTyrLeuGlnLeuValGlnAlaVally  668
                :::::|||   ||||  :::::|||||       |||||
Db   2525  AGACAACTTCTGACCGATGAGCTGCTGGACTCCCCACAGTAGTTCAGGCTGTCAA  2584

Qy    668  sPheGluProTyrHisAspArgAlaLeuAlaArgPheLeuLysArgGlyLeuArgAs  688
               :::::|||   ||||   ||||||   :::::|||||::::
Db   2585  GTTTGAGTGGAGTCTGAAAGTCCCTGGTGGAGATCCCTTCATCGAACCCTTGCAAAG  2644

Qy    688  nLysArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHi  708
            :|||:::||   ||||||   |||
Db   2645  CATCCGAGTGGCTCACCGCCTGTTCTGGTTCCTGCGGGAT-----GCACAAGTGAAGA  2698

Qy    708  sTyrGlnIleArgPheAlaValIleLeuGluGluAlaTyrLeuArgGlyCys--GlyThrAl  727
               :::  :::  :::|||    ||||:::  |||  ||
Db   2699  CTACTTTAAAAGCTGGTACCAGGAGCTTTTGGCCGGCTCTCCAGTTCTGTGCAGGAGAAGC  2758

Qy    727  aMetLeuHisAspPheThrGlnGlnValGlnValIleAspMetLeuGlnLysValThrIl  747
            :::||||::::|||      :::::|||   |||:::|||
Db   2759  CCTGATCGAAGAGCTTTCAAAGACAGAAACTTGTCAAACTCCTGGGTGATATTGGAGA  2818

Qy    747  eAspIleLysSerLeu--SerAlaGluLysTyrAspValSerSerGlnValIleSerGl  766
            :::::||||::::  :::|||  ::::::|||   :::::|||
Db   2819  AAAAGTGAAGTCGGCTGGCTGGCGATGCTCAGAGAAGGATGTGCTAAAGAAGGAGATTGGCAG  2878

Qy    766  nLeuLysGlnLysGluGlnLeuAsnLeuGlnAsnLeuProGlnSerPheArgValPr  786
            :||::::::|||  ||||::::|||   :::  ||
Db   2879  TCTAGAAGAATTCTTAAAGATATAAAGACTTGCCATCTT----------------CC  2920

Qy    786  oTyrAspProGlyLeuLysLysLysAlaLeuGlyAlaLeuValIleLysLysCysValMetAlaSe  806
            :::::|||   ||||:::  :::|||  ||||::::|||
Db   2921  TCTGAACCCGGCCCTGTGCGTAAAAGGAATTGATCGGGATGCATGTTCATATTTCACATC  2980

Qy    806  rLysLysLysProLeuTrpLeuGluPheLysCysLysAlaAspProThrAlaLeuSerArgAsnGl  826
            :::  ::::|||   |||||::::|||
Db   2981  TAATGCCTTGCCATTGAAGATCACTTTCATCAATGCTAATCCA-------ATGGGCCAA  3031

Qy    826  uThrIleGlyIleLeuPheLysHisGlyAspLeuArgGlnArgAspMetLeuIleLeuGl  846
               ::::|||  :::|||  :::|||  :::::|||
Db   3032  AAAATCAGTGTATTTTAAGGCCCGGCAGATCTTCGGCAGGATATGTTGTTCTGCA  3091

Qy    846  nIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuPr  866
               ||||  :::|||   |||||::::|||   ||||:::::|||
Db   3092  GATTATTCAGTGATGGACAACGTTTGGCTTCAGGAGGGCCTCGATATGCAAATGATCAT  3151

Qy    866  oTyrGlyCysIleSerThrGlyAspLysLysIleGluMetIleGluIleValLysAspAlaTh  886
            :::|||  ||||::::|||   :::::|||   |||:::||
Db   3152  TTATGGATGTCTAGCCACAGGAAAGGCTCAAGGATTCATAGAGATGGTGCCTGATGCTGT  3211

Qy    886  rThrIleAlaLysIleGlnSerThrValGlyAsnThrGlyAlaPheLysAspGluVa  906
            :::::|||   :::  :::::::|||
Db   3212  AACGCTTGCCAAGATCCATCTGCACTCT---GGGCTGATAGGACCCCCGAAAGAAAAACAC  3268

Qy    906  lLeuSerHisThrLeuLysGluLysCysSerProIleGluGluLysPheGlnLysAlaAlaValGl  926
               :::  :::|||||   :::::|||   :::  :::::|||
Db   3269  CATCAAGAAGTGGTTCAGTCAGCACAACCACTTAAAGGAAGATTATGAAAAGGCCTTGAG  3328

Qy    926  uArgPheValTyrSerCysAlaGlyTyrCysValValThrGlyValGlnAlaThrPheValLeuGlyIleGlyAs  946
               :::  ||||:::::|||   ||||:::::|||
Db   3329  GAACTTTTTTACTCTTGTGCTGGCTGGTGTGTGCACATTCATCTTGGAGTCTGTGA  3388

Qy    946  pArgHisAsnAspAsnIleMetIleSerGluThrGlyThrGlyLysAsnLeuPheHisIleAspPheGl  966
            :::||||::::  :::::|||   ||||:::::|||
Db   3389  CCGACATAATGACAATATCATGTCTGACAAGTCAGGCCACATGTTTCATATTGACTTTGG  3448

Qy    966  yHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgValProPheVa  986
            ||||::::|||   :::::|||   ||||:::::|||
Db   3449  ATAATTCTTGGGTCACGCGCACAAACATTTGGCGTATAAAAAGGGACCGAGCGCCTTTCAT  3508

Qy    986  lLeuThrProAspPheLeuValMetGlyThrSerGlyLysLysThrSerLeuHisPh  1006
            :::  :::  :::|||   :::|||
Db   3509  TTTTACTTCAGATGGAGTACTTTATT--ACCGAGGGTGGGAAAAACACACACCATTT  3565

Qy   1006  eGlnLysPheGlnAspValCysValLysAlaValLysTyrLeuAlaLeuArgHisHisThrArgHisAsnLeu  1026
```

```
Db   3566  TCAAGACTTCGTGGAACTTGGCTGCTGCAGAACCTCCCTACAACATTGTGAGGAGGCACAGCCAACT  3625
                |||||      |||      ||       :::::|||||||
```

```
Qy   1026  uLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGl  1046
            :::|||      :::::|||   ||||||:::::||
Db   3626  GCTCCTGAGCCTTCTAGAAATGATGCTGCATGCCGGCGCTTCCTGAGCTGAGGGGGATTGA  3685
```

```
Qy   1046  uAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysSerLy  1066
            :|||:::::|||||   :::||||      :::::|||
Db   3686  AGACCTGAAATACGTACACGACAATCTCCGGCCACAAGACACCAGACCTGGAAGCCACACAAG  3745
```

```
Qy   1066  sTyrPheLeuAspGlnIleGluValCysArgGlyTrpProValGlnPheAsnTr  1086
            :::::|||      ||   :::      :::::|||
Db   3746  TCATTTTACCACGAAGATAAAGCAGAGTCTGGAG---TGCTTCCCAGTTAAACTGAATAA  3802
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Qy   1086  pPheLeuHis  1089
            ::::|||
Db   3803  CCTGATCCAC  3812
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Search completed: February 15, 2004, 09:17:53
Job time : 1163 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    February 15, 2004, 01:39:44 ; Search time 40 Seconds
                                    (without alignments)
                         2649.447 Million cell updates/sec

Title:          US-09-974-573-1
Perfect score:  5790
Sequence:       1 MELENYEQPVVLREDNRRRR..........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:     283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR 76:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                 SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	5222	90.2	1050	1	A57134	1-phosphatidylinos
2	1465.5	25.3	1068	1	A43322	1-phosphatidylinos
3	1460.5	25.2	1068	1	I38110	1-phosphatidylinos
4	1354.5	23.4	1070	1	A54600	1-phosphatidylinos
5	1319	22.8	1043	2	T43502	1-phosphatidylinos
6	1297	22.4	1570	2	T18272	1-phosphatidylinos
7	1283	22.2	1088	2	T13950	1-phosphatidylinos
8	1233	21.3	1858	2	T18273	1-phosphatidylinos
9	1136.5	19.6	1585	2	T18274	1-phosphatidylinos
10	1076.5	18.6	1658	2	T42642	phosphoinositide 3
11	1031	17.8	1164	2	S71792	phosphatidylinosit
12	1021	17.6	1634	1	JC5500	phosphoinositide 3
13	876	15.1	1506	2	JC5985	phosphoinositide 3
14	873.5	15.1	1876	2	T13801	phosphoinositide 3
15	720.5	12.4	816	1	A59003	phosphoinositide 3
16	714.5	12.3	801	2	T52538	1-phosphatidylinos
17	701.5	12.1	664	2	PC4002	phosphatidylinosit
18	701.5	12.1	1607	2	T21982	hypothetical prote
19	693.5	12.0	887	1	S57219	1-phosphatidylinos
20	672	11.6	814	2	T07761	phosphatidylinosit
21	669	11.6	812	2	T07745	phosphatidylinosit
22	657.5	11.4	814	2	B96630	Phosphatidylinosit
23	649.5	11.2	875	1	A36369	1-phosphatidylinos
24	646	11.2	873	2	T25442	hypothetical prote
25	626	10.8	897	2	T43628	phosphatidylinosit
26	562	9.7	1020	2	T18260	1-phosphatidylinos
27	508	8.8	732	2	T08420	1-phosphatidylinos
28	435.5	7.5	2028	2	T52022	1-phosphatidylinos
29	432	7.5	2051	2	F96529	probable Phosphati

30	410	7.1	1466	2	S65741	1-phosphatidylinos
31	408.5	7.1	133	2	PC4348	phosphoinositide 3
32	404	7.0	2121	2	T27406	hypothetical prote
33	402	6.9	854	2	A55404	1-phosphatidylinos
34	397.5	6.9	131	2	PC4346	phosphoinositide 3
35	397.5	6.9	131	2	PC4345	phosphoinositide 3
36	390.5	6.7	1877	2	T40550	probable phosphati
37	380	6.6	1900	2	S45530	probable 1-phospha
38	364	6.3	525	2	F96547	probable phosphati
39	361.5	6.2	131	2	PC4347	phosphoinositide 3
40	328.5	5.7	828	2	JC5706	1-phosphatidylinos
41	326	5.6	1121	2	T52631	1-phosphatidylinos
42	315	5.4	379	2	T07007	probable 1-phospha
43	314.5	5.4	1093	2	T18275	1-phosphatidylinos
44	277	4.8	1066	2	A49335	1-phosphatidylinos
45	274.5	4.7	604	2	F89453	protein F35H12.4 [

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                              ALIGNMENTS

RESULT 1
A57134
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) gamma isoform - human
N;Alternate names: p110-gamma protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A57134
R;Stoyanov, B.; Volinia, S.; Hanck, T.; Rubio, I.; Loubtchenkov, M.; Malek, D.; Stoyanov
  Wetzker, R.
Science 269, 690-693, 1995
A;Title: Cloning and characterization of a G protein-activated human phosphoinositide-3
A;Reference number: A57134; MUID:95350661; PMID:7624799
A;Accession: A57134
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 11050 <STO>
A;Cross-references: GB:X83368
C;Genetics:
A;Gene: GDB:PIK3CG
A;Cross-references: GDB:370920
A;Map position: 3q26.3-3q26.3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match        90.2%;  Score 5222;  DB 1;  Length 1050;
Best Local Similarity   90.2%;  Pred. No. 0;
Matches 990; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

Qy    35 MELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPD 94
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     1 MELIPIEFVLPTSQRKCKSPETALLHVAGHGNVEQMKAQVWLRALETSVAADFYHRLGPH 60

Qy    95 HFLLLYQKKGQWEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQL 154
          |||||||||||||||||||||||||||||||||||||:::||||||||:|||||||||
Db    61 HFLLLYQKKGQWEIYDKYQVVQTLDCLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQL 120

Qy   155 NALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKK 214
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKK 180

Qy   215 ITNNCVFIVIHRSTTSQTIKVSADDTPGTIIQSFFTKMAKKKSLMDIPESQNERDFVLRV 274
          ||:|:||||||||||||||||:||||||||:|||||||||||||||||||||:||||||||
Db   181 IANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRV 240

Qy   275 CGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTG 334
          ||||||||||||||||||||:||||||||||:||||||||||||||||||||||||||||
Db   241 CGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTG 300

Qy   335 YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVL 394
          ||||||||||||||:|||||||||||||||||||||||||:|:||||||||||||||||
Db   301 YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVL 360
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Qy    23  MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
              :  : :::   :      :: : :: :    :    :
Db     1  MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLITIKGHELFKEA   53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
             :   : :            ::     ::                      -----LKVI
Db    54  RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI  102

Qy   139  QRHAPSEETLAFQRQLNALIGYDVDTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
            :        :  :                 :
Db   103  EPVGNRBEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy   193  PKLYAMIPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL  245
             :                  :
Db   162  RAMYVYPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKNHDCVPEQVI  221

Qy   246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN  299
                :                   :  :   :
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy   300  GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL  354
                                                             :  :
Db   280  GRMPNLML-------MAKESLYSQLFM--DCFTMPSYSRRISTATPYMNGE---TSTKSL  327

Qy   355  WDCDRKFRVK---------IRGIDIPVLPRTADLIVFVEBANIQYGQQVLCQRRTSPKPF  404
            :           :
Db   328  WVINSALRIKILCATYVNVNIRDID---------KIYVRTGIYHGGEPLCDNVNTQRVP  377

Qy   405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
                                           :      :
Db   378  CSNPRWNEWLNVDIYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCPLAWG  425

Qy   465  NLLLIDHRFLLRHGEVYLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC  524
            ::: ::   ::  ::
Db   426  NINLFDYTDTLVSGKMALNLWFVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS  481

Qy   525  HPIALPKHRPTPDPEGDRV----------RAEMPNQLR---KQLEAIIATDPLN  565
Db   482  SVVKFPDMSVIEHAWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS  541

Qy   566  PLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG  625
            :          :::
Db   542  EITBEQEKDFLWSHRHYCVTIPEILPKLLSVKWNSRDEVAQMYCL-----VKDWPPIKPE  596

Qy   626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR  684
            : ::::::  :::         :
Db   597  QAMBLLDCNYPDMVRGPAVRCLEKYLTDDKLSQYILQVVIQLVQVLKYEQYLDNLLVRFLLKK  656

Qy   685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILBAYLRGCTAMLHDFTQQVQVIDMLQK  744
            ::::::: ::: :: :::
Db   657  ALPNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN  714

Qy   745  VTIDIKSLSAERYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALVIEKC  801
             : :::        :: ::
Db   715  LI-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEEC  769

Qy   802  KVNASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQLIRIMESIW  855
             : :::::::: ::         :::::::::::::::::::
Db   770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW  824

Qy   856  ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE  913
            :: ::: :::::: :::::::::::::::::::::::::::::::::
Db   825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883

Qy   914  KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK  973
            :          ::::::::::::::::::::::::::::::  ::::::::::::::::
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVDDGGQLFHIDFGHFLDHKK  942

Qy   974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCKAYLALRHHTNLLILF  1031
            :::::::::::::: :::: :::::::::   :::::::: :::::::::::::::: ::
Db   943  KKFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFNLF  1002

Qy  1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091
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Qy   395  CQRRTSPKFFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPES  454
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  CQRRTSPKFFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPES  420

Qy   455  KGKAQLLYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSM  514
            |||| ||||||||||||||||| |||||||||| ||||||||||||||||||||||||||
Db   421  KGKVRLLYVNLLLIDHRFLLRRGEYVLHMWQISGKGEDQGSFNADKLTSATNPDKENSM  480

Qy   515  SISILLDNYCHPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  574
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   481  SISILLDNYCHPIALPKHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  540

Qy   575  LWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCN  634
            ||||||||| |||||||||||||||||||||||||||| |||||||||||||||||||||
Db   541  LWHFRYESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCN  600

Qy   635  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  694
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  660

Qy   695  LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSA  754
            ||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||||
Db   661  LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSA  720

Qy   755  EKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLE  814
            ||||||||||||||||||||||  ||| |||||||||||||| |||||||||||| ||||
Db   721  EKYDVSSQVISQLKQKLENLQNSQLPESFRVPYDPGLKAGALAIEKCKVMASKKKKPLWLE  780

Qy   815  FKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCISTGD  874
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  FKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCISTGD  840

Qy   875  KIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAG  934
            |||||||||||||||||||||||||||||||| ||||| | ||||||||||||||||||
Db   841  KIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAG  900

Qy   935  YCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV  994
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   901  YCVATFVLGIGDRHNDNIMTETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV  960

Qy   995  MGTSGKKTSLHFQKFQDVCKAYLALRHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDA  1054
            ||||||||| ||||||| |||||||||||||||| |||||||||||||||||||||||
Db   961  MGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDA  1020

Qy  1055  LTVGKSEEDAKKYFLDQIEV  1074
            |||||| |||||||||||||
Db  1021  LTVGKNEEDAKKYFLDQIEV  1040
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RESULT 2
A43322
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A43322
R;Hiles, I.D.; Otsu, M.; Volinia, S.; Fry, M.J.; Gout, I.; Dhand, R.; Panayotou, G.; Rui
Cell 70, 419-429, 1992
A;Title: Phosphatidylinositol 3-kinase: structure and expression of the 110 kd catalytic
A;Reference number: A43322; MUID:92354059; PMID:1322797
A;Accession: A43322
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-1068 <HIL>
A;Cross-references: GB:M93252; NID:g163519; PIDN:AAA30698.1; PID:g163520
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:110292)
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match   25.3%;   Score 1465.5;   DB 1;   Length 1068;
Best Local Similarity 33.5%;
Matches 382;   Conservative 204;   Mismatches 405;   Indels 149;   Gaps 39;
Pred. No. 2.3e-91;

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Db    1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062
           |||||::|||:||||  |||    ||||||||||||||||||||||:||  ||| ::||:|

RESULT 3
I38110
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) alpha isoform - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I38110; S44127
R;Volinia, S.; Hiles, I.; Ormondroyd, E.; Nizetic, D.; Antonacci, R.; Rocchi, M.; Waterf
Genomics 24, 472-477, 1994
A;Title: Molecular cloning, cDNA sequence, and chromosomal localization of the human pho
A;Reference number: A55636; MUID:95229146; PMID:7713498
A;Accession: I38110
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1068 <RES>
A;Cross-references: EMBL:Z29090; NID:g472990; PIDN:CAA82333.1; PID:g472991
C;Genetics:
A;Gene: GDB:PIK3CA
A;Cross-references: GDB:370915; OMIM:171834
A;Map position: 3q26.3-3q26.3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match             25.2%;  Score 1460.5;  DB 1;  Length 1068;
Best Local Similarity   33.3%;  Pred. No. 5.1e-91;
Matches    381;  Conservative  206;  Mismatches  400;  Indels  157;  Gaps  40;

Qy    23 MKPRSTAASLSSMELIP-------IEFVLFTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
            |: :|| | :::|          :: |:   |:   ||||||||||  | : :|||||||
Db     1 MPPRPSSGELWGIIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA 53

Qy    79 LETSVSADFYHRLGPDHFLLLYQKKGQWEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
                        :     |:||||:||::|||: |||:||||||||: :||||||||||
Db    54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------- 192
              :  :                                      | :|  || |
Db   103 EPVGNREEKI-LNREIGFAIGMFVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193 PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
             |:       : |      || |:||| :         |:::|   ||  | :|::
Db   162 RAMYVYPPHVESSPELPKHIYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246 QSFFTKVAKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQVVRQCLKN 299
                  :                    |::|||||:|::|||||||: |:|||||||||:|
Db   222 AEAIRK--KTRSMLLSSEQLKLCVLEYGQKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy   300 GEBIHLVLDTPPDALDEVRKE----EWPLVDDCTGVTGYHEQLT----IHGKDHBSVF 350
                                                                 :: :|:
Db   280 GRM--------PNLKMMAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE------TS 323

Qy   351 TVSLMDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQGQVLCQRRTS 400
           |||: || :| :            :: ||||| || | |::| |: |:|| || ||:|:
Db   324 TKSLWVINRALRIKILCATYVNLNIRDID--------KIYVRTGIYHGGEPLCDNVNT 373

Qy   401 PKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
               | :  ||    |:     |     ||| | |::|  : |:|          |:|
Db   374 QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C-----SVKGRKGA-------KEEHCP 421

Qy   461 LYYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520
           | :::|:| :|:|| :|| :     ||  :  :|    |:|::  || :||  | :|
Db   422 LAWGNINLPDYTDTLVSGMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477

Qy   521 DNYCHPIALPKHRPTPDPEGDRV-------------RAEMPNQLR---KQLEAIIAT 561
             || | :|      |   |           :  |    :||||: | :|||||||||:
Db   478 DWFSSVVKFPDMSVIEEHANWSVSREAGPSYSHAGLSNRLARDNELRENDKEQLKAISTR 537

Qy   562 DPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGGQEIVAKTYQLLAKREVWDQSA 621
           |||:       ::|:: :|         |||:::|| :| |      |  :|: |  || |
Db   538 DPLSEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy   137 VQQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
```

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Db   622 LDVGLITMQLLDCNFSDENVRAIAVQKLES-LEDDVLHYLLQLVQAVKFEPYHDSALARF 680
           |  |::||||  : || : |||| |||::  | ||||:|:||::||||| |  ||||||
Qy   593 IKPEQAMELLDCNYPDMVRGFAVRCLEKYLTDDKLSQYILQLVQVKYEQYLDNLLVRF 652
         ::| ||:|:|| ||||:| :|| ||| ||  |||: ||:||||::|:|||||||||||

Db   681 LLKRGLRNKRIGHFLEWFLRSEIAQSRHYQQRFAVILEAYLRGGCTAMLHDFTQQVQVID 740
           |||  |:||||||| ||||::|||:||:|  ||  |::| |||  :||||  ||  |:|
Qy   653 LLKKALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVBAME 710
         ||| ||:|||||||  ||:|||  |:||:|| ||:|||:||  :|:||| | ||| |

Db   741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQN---LNLPQSFRVPYDPGLKAGALV 797
           :||:|||||||| |:|  ||::|:||||||:||:|     | |||:||  |  || ||||
Qy   711 KLINL?-DI--LKQERKDETQKV--QMKFLVEQMRPDFMDALQGLLSPLNPAHQLGNLR 765
         |:::|  ||  |||:|||  ||   :||||:|||  :| | |::|: |||||| ||:|

Db   798 IEKCKVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIM 851
           ||:| | :|| |||::||| |||:|       |||||: :||||||||||:||||||||
Qy   766 LKECRIMSSAKRPLWLNWE--NPDIMSELLFQNNE----IIFKNGDDLRQDMLTLQIIRIM 820
         ||:|:||::||:||||| :  ||||| ||| |:|     ||||:|||||||||:|||:|||

Db   852 ESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
           |:|:|||||||||||||||:||||:||||:||| |:||||||:||:||   |||:|| |
Qy   821 ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879
         |:||:| |||| :||||| | || ||:|||:||| | |: | | | || || |||||| |

Db   910 WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGN.LFHIDFGHIL 969
           ||||| ||:||:|||:|| |||| | |||| |||||| |||||:|::||||||||||| |
Qy   880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVAFFILGIGDRHNSNIMVKDDGQLFHIDFGHFL 938
         |||:|:| ||:||||:|:| |||||||||| :|||||||:|||: |||||||||||||:|

Db   970 GNYKSFLGINKERVPVPVLTPDFLFVMGTSGKK--TSLHFQFQDVCVKAYLALRHHTNLL 1027
           |:|:|:||||:||||:||||| ||||||||||    ||||| |||||||| | |  |||
Qy   939 DHKKKKFGYKRERVPFVLTQDFLIVISKGAQDCTKREFERFQEMCKAYLAIRQHANLF 998
         |:|||||| ::||||:||| |||:|:|||| |   || |||::| ||||| || ||| |

Db  1028 IILFSMWLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGWTVQFNWF 1087
           | |||: |  |||||:|||: ||||||| | | :||: :: |: ||  ||||||  | |
Qy   999 INLFSMWLLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058
         |::||||| |||||| || ||||||:|||| |||:||| |||::|:||| |||||  | |

Db  1088 LHLIV 1091
           :|: |
Qy  1059 FHTI 1062
         ||:|
```

```
RESULT 4
A54600
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain beta isoform - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A54600
R;Hu, P.; Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
Mol. Cell. Biol. 13, 7677-7688, 1993
A;Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase
A;Reference number: A54600; MUID:94067128; PMID:8246984
A;Accession: A54600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1070 <HU1>
A;Cross-references: GB:S67334; NID:g455759; PIDN:AAB29081.1; PID:g455760
A;Note: sequence extracted from NCBI backbone (NCBIN:140879; NCBIP:140880)
C;Genetics:
A;Gene: GDB:PIK3CB; PIK3C1
A;Cross-references: GDB:136233
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match            23.4%;  Score 1354.5;  DB 1;  Length 1070;
Best Local Similarity  31.8%;  Pred. No. 8.5e-84;
Matches   361;  Conservative  202;  Mismatches  407;  Indels  165;  Gaps  37;

Qy    30 ASLSSMELIPIEFVLFPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH 89
           ::|: :|||: |:|| |  |   :|: ::  :|      |:::|||::|: : ||| |
Db    22 SQIASDGSIPVDFLLPTG-----IYIQLEVPREATISYIKQMLWKQVHYPM------ 68

Qy    90 RLGPDHFLLLYQKKGQWEIYDKYQVVQTLD------C----LRYWKVLHRS--PGQIH 136
            : |||| | |:|||| |||||:| :|| |       |     ||::|: |   | | |
Db    69 ------FNLLMDIDSYMFACVNQTAVYEELEDETRRLCDVRPFLPVLKLVTRSCDPGE-- 120

Qy   137 VQQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
```

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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43502
R;Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D.A.; Wood, C.; Gray, P.W.; Cooper,
J. Biol. Chem. 272, 19236-19241, 1997
A;Title: P110delta, a novel phosphatidylinositol 3-kinase catalytic subunit that associa
A;Reference number: 222519; MUID:97382246; PMID:9235916
A;Accession: T43502
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1043 <CHA>
A;Cross-references: EMBL:U86587; NID:g2331237; PIDN:g2331238; PIDN:AAC25676.1
A;Experimental source: spleen
A;Note: highly expressed in lymphocytes and lymphoid tissues
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match             22.8%;   Score 1319;  DB 2;  Length 1043;
Best Local Similarity   31.9%;   Pred. No. 2.1e-81;
Matches  354;  Conservative 206;  Mismatches 404;  Indels 144;  Gaps  40;
```

```
Qy       38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRIG-PD  94
               : .  :  : : :  :  :  ::     :      ::       . : :: :. :  :
Db       20 VVVDFLLPTG----------YLNFPVSRNANLSTIKQVLWHRAQYEPL---FHMLSDPE  66

Qy       95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
              :: :      :      :      :  ::    :  :  :  : :    .  :
Db       67 AYVFTCVNQTAEQQELEDEQR--RLCDIQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy      154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPLP---- 208
             .       :  :  :  : : :    ::   :  :   : ::      :::
Db      117 ISLLIAKGLHEFDSLRDPEVNDFRTKM--RQFCEEAAAHRQLGMVEWLQYSFPLQLEPS 174

Qy      209 ------EYILKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSLMD 260
                    :  ::  :: ::       : :  :  :  :   :  :   :  :    :::
Db      175 ARGWRAGLLRVSNRALLVNVKFEGSEBSFFTQVSTKDMPLALMACALRKKATVRFQPLVE 234

Qy      261 IPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEBIHLVL----------D 308
            :    : :  :  : :  :  :   : :    :   : :  :
Db      235 QPE------EYALQVNGRHEVLYGNYPLCHFQYICSCLHSGLTPHLTMVHSSSILMRDEQ 289

Qy      309 TPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRKFRVK-IRG 367
                  :        :  :  :    :  :   :  :         ::      :
Db      290 SNPAPQVQKPRAKPPP----------------------IPAKKPSS--VSLWSLEQPFSIELIEG 330

Qy      368 IDIPVLPRTAD--LTVFVEANIQYGQVLCRRTSPK-PFTEEVLWNVWLEFSIKIKDLP 424
             : ::  :       :  :    : :  : :    :   :  :  :  ::  : :  :
Db      331 RKV-------NADERMKLVVQAGLFHGNEMLCKTVSSSEVNVCSEPWKQRLEFDISVCDLP 385

Qy      425 KGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEYVLHM 484
             :  :  :    :   : :      :  ::   :   : :      : ::  :   :  ::
Db      386 RMARLCFALYAVVVEAKKGARSTKK----KSKKADCPIAWNLMLFDYKDQLKTGERCLYM 441

Qy      485 WQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC-HPIALP--------KHRP 534
                      : : :  :  :  :  :  :  :   : : :   : :
Db      442 W--PSVPDEKGELLNPAGTVRGNPNTESAAALVIYLPEVAPHPVVFPALEKILLELGRH-- 497

Qy      535 TPDPEGDRVR-AEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPKL 592
               ::  :     :   :  :::   ::   : :    :: : :  :   :     : :
Db      498 ----------GERGRITEEELQLREILERRGSGE----LYEHEKDLVWKMRHEVQEHFPEALARL 548

Qy      593 FSSVKWGQQEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLE 652
             ::         : :    : :  :         : :  :    :  :   : :  :  :
Db      549 LLVTKWNKHEDVAQMLYLLCS---WPE--LPVLSALELLDSSFPDCYVGSFAIKSLRKLT 603

Qy      653 DDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFLFWLRSEIAQSRHYQQ- 711
             :::::    : :  :   :   :  :    : :  : :  :   : : :    :  :
Db      604 DDELFQYLLQLVQVLKYESYLDCBLTKFLLGRALANRKIGHFLFWHLHSEM----HVPSV 659

Qy      712 --RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVT--IDIKSLSAEKYDVSSQVISQL 767
                :   :         :    : :   : :     :       :   :      :
Db      660 ALRFGLIMEAYCRG-STHHMKVLMKQGEALSKLKALNDFVKVSSQKTTKPQTKEMWHMCM 718

Qy      768 KQK--LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSN 825
```

```
Db       121 ---------------KLDSKIGVLIGKGLHEPDSLKDPEVNEFRRKVRKFSEEKILSLVGLSW 168
                              : : :  :  :  ::  :  :            :  ::   : :
Qy       193 -PKLYAMHPWVTSKPLPEVLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249

Db       169 MDWLKQTYPPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE-- 225
             :  :     :::  :  :    :   :    :       ::    :  :    :  :
Qy       250 TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEBIHLVLDT 309

Db       226 LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVFGDHPLIQFQYIRNCVMNRALPHFIL-- 283
              :   : :  : :    :       : :   ::   : :   :  :      :  : :
Qy       310 PPPDALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------ 354

Db       284 ---------------VECCKIKKMYEQEMIAIEAAINRNSSNLPLPKKTRIISHV 326
                              :::            :  :    :  :   :     :   :
Qy       355 WDCDRKFR-VKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPK-PFTEEVLWNV 412

Db       327 WENNNPFQIVLVKG--NKLNTEETVKVHVRAGLFHGTBLLCKTIVSSEVSGKNDHIWNE 383
             :      :  :       :  : :  :  ::   :  :    :   :     :  :  ::
Qy       413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP---ESKGKAQLLYY----VN 465

Db       384 PLEFDINICDLPRMARLCFAVY-AVLDKVKTKKSTKTINPSKYQTIRKAGKVHYPVAWVN 442
               :::  : :: :    :   :     : :  :    : :   :  :  :    :
Qy       466 LLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKL------TSATNPDKENSMSIS 517

Db       443 TMVFDFKGQLRTGDIILLHSW----------SSF-PDELEEMLNPMGTVQTNPYTENATALH 492
             : :  :  :    :  : ::              :     :      :  :   :    :
Qy       518 ILL-DNYCHPIALP---------KHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA 569

Db       493 VKFPENKKQPYYYPPFDKIIEKAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE 552
             :    :  :      : : :          :  : :   :    :      : :  :
Qy       570 EDKELLWHFRYESLK-DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM 628

Db       553 NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA--QLQALLQIWPK--LPPREAL 607
             :   : :  : :  :  : :  : :  :  :         : :  :   : ::
Qy       629 QLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRN 688

Db       608 ELLDFNYPDQYVREYAVGCLRQMSDEELSQYLLQLVQVLKYEPFLDCALSRFLLERALGN 667
             :::::       :  :     :       : ::     :   : :    :    :  : :
Qy       689 KRIGHFLFWFLRSEIAQSRH---YQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKV 745

Db       668 RRIGQFLFWHLRSEV----HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKLKTL 722
             ::::  :::  :::          :   :  ::::  :     : :  :   : :  :
Qy       746 T---IDIKSLSAEKYDVSSQVISQLKQK----LENLQNLNLPQSFRVPYDPGLKAGALVI 798

Db       723 NSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQS--------PLNPCVILSELYV 773
             :::  :  :  : : :  :  : :        : :              :  : ::  :
Qy       799 EKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESETMETE 858

Db       774 EKCKYMDSKMKPLMLVY---NNKVFGEDSVGVIFKNGDDLRQDMLTIQMLRLMDLLWKEA 830
             ::::  :: : ::: :        : ::  : :: : :::::::: ::  :    :
Qy       859 SLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCP 916

Db       831 GLDLRMLPYGCLATGDRSGLIEVVSTETIADIQLNSSNVAAAAFNKDALLNMLKEYNS 890
             ::::  ::::  : :: : ::: : : :::  :    : :    :   : : :::
Qy       917 IEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL 976

Db       891 GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTGQLFHIDFGHILGNFKSKF 949
             :    :  ::: : ::::::::  :::::::::::::::   : :::::::::::::  :
Qy       977 GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLLILFSMMLM 1036

Db       950 GIKRERVPFILTYDFIHVIQQGKTGNTEKFGRRFRQCCEBDAYLILRRHGNLFITTFALMLT 1009
             ::  ::::: :  :   :   : :     :   :  :         : : :   :  ::
Qy      1037 TGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEYCRDKGWTVQFNWFLHLV 1091

Db      1010 AGLPELTSVKDIQYIKDSLALGKSEEEALKQFKQKFDEALRESWTTKVNWMAHTV 1064
```

```
RESULT 5
T43502
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - mouse
N;Alternate names: p110delta protein
C;Species: Mus musculus (house mouse)
```

```
Db  847 SIRBIKXPFRVKVMGSTRIPLSCIKDIDSSSVVSISLYHGIECFSKAFTQPIPPPPAF  906
             :|:       :   |       ||:     :::: |
Qy  405 ---TEEVLWNVLEF-SIKIKDLPKGALLNLQIYCGKRAPALSGKTSAEMPS----PESKG  456

Db  907 LAETLSVDWCEWLVFTNIDYSNLPVDARLSISVYS------ANETVDDVEEIKNLDEATK  960
             |:|        : :|      :  ||:|::::
Qy  457 KAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSI  516

Db  961 KLTPIGWINVMITDFKYQLRQGMVELSLW------PSDFSNFLGTCSNNPSSSQSVGL  1012
             |         :|:|          :
Qy  517 SILLDNYCHPIALPKHRPTPDPEGDRVRAEMP----NQLRKQLEAIIATDPINPLTAED  571

Db 1013 TLEFEEFNLPVLFP--RKTKFSTSVSVIEQPPTNINSNEMREFFEQITALDDPLSDLKQEK 1070
             ::|:|:||||:    :|:|:      :  ::|  :   ::::|||::    ::  ||:|
Qy  572 KELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL  631

Db 1071 YNQLWTLRHYSILFPQVLPRLMLSVPWTQATAVDEAISLLDR--WPK--LKPYESLELL  1125
             :| |  |:|| :|   |  | :   || :    |:| :|:|    ||:   ||  ||||
Qy  632 DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKPEPYHDSALARFLLKGLRNKRI  691

Db 1126 DAKHANRKVREFAVTCLEDLSEDELLDILLQLVQVLKYEPFHDSKLSRFLIRKAILNRNI 1185
             | :|::|:||:|||  |||| :|| || |||||||:|||||||| | ||| |: |||||
Qy  692 GHFLFWFLRSEIAQSRHYQQRFAVILEAYILRGCGTAMLHDFTQQVQVIDMLQKVTIDIKS 751

Db 1186 GHSFFWYLKSDLHDS-NLSERFGILLESYLYACGAHRI-ELLKQMEVINNLTEVAKKIKP 1243
             || ||| |:  ::    |:|:| |:|| ||| || |:  |||:|  | ||| | |||||
Qy  752 LSAEKYDVSSQVISQLKQKLENLQNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPL  811

Db 1244 LKDQ------------DRREFMIKEFESLEWPKRFHLTLNPRFESNGLIINKSKYMDSKKLPL 1294
             | |:            ||  || |||||||||| || | || ||| || |||| ||||||
Qy  812 WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIQIIRIMESIWETESLDLCLLPYGCIS  871

Db 1295 RLSFTNTDMNA---DPIEVIFKAGDDLRQDMLTLQMIRLMDKIWQKEGLDLKLLSPYGCIS 1351
             |  |   |: |    | :|||| ||||||||| ||:|||| |||| || ||| || ||||
Qy  872 TGDKIGMEIVKDATTIAKIQOSTVG-----NTGAFKDEVLSHWLKEKCPIEEKFQAAVE  926

Db 1352 TGDMIGMIEVVLNSETTAKIQKSEGGGAFRFGVSFQQLILQH---NKSDME--YQKAVD  1406
             ||| |||||:|  | |||||| |      |::| :::|:::|    ||  |   | |:|
Qy  927 RFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLPFHIDFGHILGNYKSFLGINKERVPFV  986

Db 1407 TFILSCAGYCVATYVLGIGDRHNDNLMVTKGGRLFHIDFGHFLGNYKKKFGFKRERAPFV  1466
              |: |||||||| |||||||||||:|: | | | |||||| ||||| | | | || ||
Qy  987 LTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLJILFSMLMTGMPQLTSKE  1046

Db 1467 FTPDFCVVM---GGKESFKFSQFVNYCCTGYNIVRKNAKLFMNLFAMMVSTGIPELQSME  1523
             :||||  :|   | |:|:|| ||| |   ||||:|:||| :|| | | |||| ||:| |
Qy 1047 DIEYIRDALTVGKSEEDAKKYFLDQI-EVCRDKGWTVQFNWFLH  1089

Db 1524 DLNYLKESFSIELSDAKCAREKFVALIHESLATK--TTQLNNFFH  1565
```

RESULT 7
T13950
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13950
R;Leevers, S.J.; Weinkove, D.; MacDougall, L.K.; Hafen, E.; Waterfield, M.D.
EMBO J. 15, 6584-6594, 1996
A;Title: The Drosophila phosphoinositide 3-kinase Dp110 promotes cell growth.
A;Reference number: Z17828; MUID:97133288; PMID:8978685
A;Accession: T13950
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1088 <LEE>
A;Cross-references: EMBL:Y09070; NID:g1707447; PIDN:CAA70291.1; PID:g1707448
C;Genetics:
A;Cross-references: FlyBase:FBgn0015279
A;Map position: 3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match   22.2%;   Score 1283;   DB 2;   Length 1088;

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Db  719 RQETYMEALSHL-------QSPLDPSTLLEEVCVEQCTFMDSKMKPLWIMYSSEBRAGSSAGN 772
             :|:        :       |||
Qy  826 ETIGIIFKHGDDLRQDMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDA  885

Db  773 --VGIIFKNGDDLRQDMLTIQMIQLMDVIWKQEGLDLRMTPYGCLPTGDRTGLIEVVLHS  830
              :||:|| |||||||||: |:| |||:|||| ||||:||||||| ||| ||:|||:|:|
Qy  886 TTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERPVYSCAGYCVATFVLG  943

Db  831 DTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIEEFTLSCAGYCVATYVLG  889
              ||| ||  :|  | |||| ||:|| |||:| |  ||   || || ||||||||| |||
Qy  944 IGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTS 1003

Db  890 IGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRERVPFFILTYDFVHVIQQGKTNNS  949
             |||||:|||||:|| |||||||||:|||:|:||||:|||||| ||| ||::|:| || | |
Qy 1004 LHFQKFQDVCVKAYLALRHHTNLLILFSXMLMTGMPQLTSKEDIEYIRDALTVGKSEED  1063

Db  950 EKFERFRGYCERAYTILRRHGLLFLHLFALMRAAGLPELLSCCSKDIQYLKDSLAIGKTEBE 1009
             :||||| ||| ||  | || |||:||:|| ::      |     | | ||:||| ||||::
Qy 1064 AKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091

Db 1010 ALKHFRVKFNEALRESWKTKVNWLAHNV  1037
```

RESULT 6
T18272
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18272
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18272
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1570 <ZHO>
A;Cross-references: EMBL:U23476; NID:g733519; PID:g733520; PIDN:AAA85721.1
C;Genetics:
A;Gene: PIK1
C;Keywords: phosphotransferase

Query Match   22.4%;   Score 1297;   DB 2;   Length 1570;
Best Local Similarity   30.9%;   Pred. No. 1.3e-79;
Matches 347; Conservative 203; Mismatches 406; Indels 168; Gaps 37;

```
Qy   40 IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH--RLGPDHFL   97
             :|:|                     ::|     : :|
Db  536 ILFLMPNQSKK-------ILQVKGSDTIENLKERIISDYLFNNSNNNNNNNCKYGADSYL  588

Qy   98 LL-------------YQXKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
             ||              :|:| ||:||||| : :|  | |::|
Db  589 ILDFNDNPMERSLVLNKSDYILDXRAQ--GLIPLKLKVIEKSTIILDSDPSDELSPSEYEII 646

Qy  139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDLEFTRRRLVTPRMAEVAGRDPKLYAM  198
             |: |    | |:|: | |:|:|||:|||||:|||||||||||
Db  647 RKLIPIGTDTW---------------RGEEVEYFRR--VTSRLR-------YEA  675

Qy  199 HPWTS----------KPLPEYLLKKITNNCVFIVIHRSTT--SQTIKVSADDTPGTILQ  246
             :|                | ||||||:||| |:|:||  :   |:|
Db  676 LPLIKGSIOSTLLVRLSPLP----IPIVGNKILISIFLPITQVTKTLDLELNETADQFTN  731

Qy  247 SFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLV  306
             :|||| |:|:::|      :||||:|||||||||| |:||||||||||||||||||
Db  732 RLFTKNYSK----HLP-NVNSNHFILKVVGSSDFIHGPHDIRTFESIRNHIIQGTKPQLT  786

Qy  307 LDCTPPDPALDE---VRKEEWP----LVD-DCTGVTGYHEQLT------IHGKDHESVFTV  352
             |   |  |            :    ::|
Db  787 LIQRPKPELDPQPFKPRFDYPPELIIDHSCSNAINCNNNNTNSTNNNNINFDNWDQITHI  846

Qy  353 SLWDCDRKPRVKIRG---IDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS---PKPF--  404
             :|:
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C;Accession: T18273
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1858 <ZHO>
A;Cross-references: EMBL:U23477; NID:g733521; PID:g733522; PIDN:AAA85722.1
C;Genetics:
A;Gene: PIK2
C;Keywords: phosphotransferase

Query Match  21.3%;  Score 1233;  DB 2;  Length 1858;
Best Local Similarity  29.6%;  Pred. No. 3.7e-75;
Matches  338;  Conservative 178;  Mismatches 364;  Indels 364;  Gaps 31;

Qy  157 LIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKIT 216
         ||| :  :     :  :   :        |   : |          ::|  |: :||||
Db  768 LIGTSFTRVLDGQEVVSF-RRDFAQFRLSNFTSTRNDLSQM-IYVSSEPLLTIPNKIT 825

Qy  217 NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQ-NERDFVLRV 274
                     :  :  |      :   :  ::     :  : :    ::| :|  ::||:
Db  826 -----IMVLLPGDGKIIK-RVDCCPNSSVGDVKKEIFKKPAMIDRVHTQGKTQDDFVLKV 879

Qy  275 CGRDEYLV------------------------GETPIKNFQWVRQCLKNGEEIHLVLDTPPDPA 314
         :|:|||:                          :::      :|  |:|  :
Db  880 TGFREYILCIHELGNLTSRQRFYPTSSGGDFSLMDYDYIRQCVGKNQTVELSLTNNSILS 939

Qy  315 LDEVRKEEWPLVD---DCTGVTGYHEQL------------------THGKDHESVFTV--- 352
         |::|  : |  | |   : :  || | |                    :|:|:||  |
Db  940 LNQV-SEKVSFIDKILETSDFPDYDEDLDSINSNSFPDLKQSIQQQQQQQTVINIKET 998

Qy  353 -------------------------------------------------------- 352
                                                                  
Db  999 NKENKDSNKENKDSSSNNNNNNNNNNNNNNNNNGNNNGNNGNSNNNNSNI 1058

Qy  353 SLWDCD----------------------------------RKFVKIRGIDIPVLPR 375
         :   :                                  : :|:||||||||||:
Db 1059 SRGSIDSEGNGSGSGNGSEQPTLIGVQNFSLPNNSKLPINIVKRLFRVNIAGLRNLNFNN 1118

Qy  376 TADL----------------------------------------BEVLW 410
         | :|                                        : ||
Db 1119 NEDARNKFADGKNNQPNVFVMAELYYGGELL----------TNP-VFTPIAQLASYGDGSVEPPNW 1173

Qy  411 NVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLID 470
          : ||: ::|   |:     :  :    : : |   ::  :  : | :|   : :|| :|
Db 1174 EKGIAFTIPIRYLPRARARASFTVY--VTTISEALESQM--DEVVSKSIPIGWSNCLLMN 1228

Qy  471 HRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSAATNPDKENSMSISILLDNYCHPIA-- 528
          ::| :|| : | |  :|| |  | :      :|   :   : | :  :   :| |  |
Db 1229 HKGMLRMGPTAFRLWDDGRRANPIG----------TCVDNQAAKQPIILLVEFSSFIRPIVYV 1281

Qy  529 ------------------------------------LPKHRPTPDPEGDRVRAEMPNQL 551
                                             |  :  |  |::  ::| :|  |
Db 1282 DTALQSMVNDSSISSNGVESPSIVSFSSSAASSSPLPS--SPLPSPVGLK---KLDLDE 1337

Qy  552 RKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLL 611
          ::|:| :|:|||  |::|||| :|  |  || : |||  |  :|:|   | : | ::||
Db 1338 ARRLKALMDSDPLVQLSAEDKKLVGYRHIYKSKPKALAKFLLSVNWIDPPDGVTDAY--- 1394

Qy  612 AKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQIVQAVKFEP 671
          :|:   :  :  : | ::| ||| ||:|| || :|  :  |::|::| | :|  :|:||
Db 1395 --RQMNDWALLKPVQALEILDAKFADEHVRNFAIKIINSFSDAEFSDFLLQLTQVLKYEP 1452

Qy  672 YHDSALARFLLKRGLRNK-RIGHFLFWFLRSRSIAQSRHYQQRFAVILEAYLRGCGTAMLH 730
         ||:|  :  :||:  :| ||||| ||||: :  :  ||: |||| ||| ||| ||||  :
Db 1453 YHNSDLTHILIQRALSNRSRIGHFFFWFLKSEM-HTPEIEBRYGLLLEGYLRSCGTHR-Q 1510

Qy  731 DFTQQVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPG 790
         | ::| : : |: ::  :  :  :|    |:  : ::|:| |        |  :|:||:
Db 1511 DLIKQNQYLKSLHTVAMAVKQTNGSS-------------ERKKVLMEGLSKKFPDTFQLPLDPR 1562
```

```
Best Local Similarity  33.1%;  Pred. No. 6.4e-79;
Matches  315;  Conservative 189;  Mismatches 333;  Indels 114;  Gaps 28;

Qy  194 KLYAVHP--WVTSKPLPEYLLKKITNNCVFIVIVHRSTTSQ---TIKVSADDTPGTIIQSF 248
         :| |:|   :  :  :  : : :  ::  ::|:|      :    : ||::|||   :  :
Db  189 RLLYEHPLRLANSTKMPE-LIRERHPTRTFLIVVKNENDQSTFTLSVNEQDTPFSLTEST 247

Qy  249 FTKMAKKKSLMDIPESQNER--DFVLRVCGRDEVIVGETPIKNFQWVRQCLKNGEEIHLV 306
                  :::| :  ||    |::|:|.||:|:   : :|  ::  :|  :| :  ::
Db  248 LQKMNRSQMKM------NDRTSDYILKVSGRDEYLLGDYPLIQFLYIQEMLSD------- 294

Qy  307 LDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQL----------THGKDHESVFTVSLW 355
          |   : |:        :  :   ::        :          |::|::| :|:|
Db  295 -SAVPNVLQSVYRLE-------SYINHNEQAMVTKRPLPKKRTVH--LHKSI--SSLW 342

Qy  356 DCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKP---FTEEVLMNV 412
         |  : |::.: ::  :   :| | :   :|:| | : :| :|::: :      |||::|:
Db  343 DMGNYFQLTIHSISNVNFDKTRALKVGVHVCLYHGDKKLCAQRSTDSPNGNFDTFLFNDL 402

Qy  413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTS-----AEMPSPESKGKAQLLYYVNLL 467
          ::| ::   : :   ::: :  : : :| ::       : :  | :::::  : : | :
Db  403 VMDFPIQMRNLPRMTRLCIVIFEVTKMSRSKKSSNNKDIALKDVPYNKNP--LAWVNTT 459

Qy  468 LIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSA---------TNPDKENSMSIS 517
          :|| : | :| : | |  : :   | ::  ::   :          |::  :: :::
Db  460 IFDHKDILRTGRHTLYTWTY-----------ADDIQSVEVFHPLGTIEPNRKEECALVD 508

Qy  518 I-LLDNYCHPIALPKGHRPTPDPEGDRVRAEMPNQLR-------------KQLEAIIAT----D 562
           | | :| | :     :  :     :  ::  ::|             ::| :: | |
Db  509 LTFLSSGTGTVRYPSEEVVLQYAADR---EQVNRLQRQLAGPEKPIKELKELMANYTGLD 565

Qy  563 PLNPLTAEDKELLWHFPRYESLKD-PKAYPKLFSSVKWGCQEIVAKTYQLLAKREVWDQSA 621
          : :| : :  :: | | | : :  |:|     :  : |   :    | :| :|   ::
Db  566 KIYEMVDQDRNAIWERRNDILRELPEELSILLHCVYWKERDDVADMWYLLKQ---W--PL 620

Qy  622 LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFL 681
          : : : : |  :  | :.:| |  | ::|::|:||:|||||||| | | |::|  : ||
Db  621 ISIERSLELELDYAYPDPAVRRFAIRCLHFLKDEDLLLYLLQLVQAIKHESYLESDLVVFL 680

Qy  682 LKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGGTAMLHDFTQQVQVIDM 741
         |:: ||:::|||: ||:|||: : |   | ||  :| |:| |    : :|:: :: ::|
Db  681 LERALRNQRIGHYFFWHLRSEM-QTPSMQTRFGLLLLEVVLKGC-KHHVAPLRKQLHVLEK 738

Qy  742 LQKVTIDIKSLSAEKYDVSSQVISOLKQKLENLQNLN-LPQSFRVPYDPGLKAGALVIEKC 801
         |:: :: :  :  ||     :: ::|:: :   ::   |: |||      | : || ::|
Db  739 LKQGSLIAKKGSKEK------VKTMLQDFLRDQRNSAVFQNIQNPLNPSFRCSGVTPDRC 792

Qy  802 KVMASKKKPLMLEFKCADPTALSNETIGIIFKHGDLIQILRIMESIWETESLD 861
         |||:|: :||::.| | :  : :   ::|||:|| |:|:: : : :|  : :|
Db  793 KVMDSKMRPLWVVFENADVNA---SDVHIIFKNGDDLRQDMLTIQMLRVMDQLWKRDGMD 849

Qy  862 LCLLPYGCISTGDKIGMIBIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEE 919
           :: : | || :  |||::| |:::| :|   ::   :    ::  |:||||: :  :|
Db  850 FRMNIYNCISMEKSLGMIEVVRHAETIANIQKEKGMFSATSPFKKGSLLSWLKEHNKPAD 909

Qy  920 KFQAAVERFVYSCAGYCVATPVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGIN 979
         | : |::.| :||||||||| ||| .|||:|||| ::| ||||||||||||::| :||:
Db  910 KLNKAINEFTLSCAGYCVATYVLGVADRHSDNIMVKRNGQLFHIDFGHILGHFKEKLGVR 969

Qy  980 KERVPFVLTPDFLFVMGTS-GKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSMMLMTG 1038
          ||||||| |||::|:      |: : :  |:|:| :| :::| :  ::|: |:|::|
Db  970 RERVPFVLTHDFVYVINKGFNDRESKEFCHFQELCERAFIVLRKRHGCLILSLPSMMISTG 1029

Qy 1039 MPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
          | :|| :|::|:|::::| :   |::  |  : : :   :|| :: ::  |
Db 1030 LPEILSSEKDLDYLRETLVLDYTEBKAREHFRAKFSEALANSWKTSLNWASH 1080
```

RESULT 8
T18273
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

```
Qy    791  LKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRI  850
                :|.||: |:|||||||||||||| ||: .|. : :: ||||||:|.||
Db   1563  WEAKGLIIDKCRYMDSKKLPLWLVFENVEPHA---KPLIVIFKVGDDLRQDIITLQVLRI 1619

Qy    851  MESIWETESLDLCLLPYGCISTGDKIGMIBIVKDATTIAKIQQSTVGNTGAFKDE-VLsH  909
Db   1620  MDKFWKNSGMDLRLQPYKCIATGDGIGMLEVLNANTIANINKD-AGGTGALLEEKTLVN  1678

Qy    910  WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL  969
Db   1679  WLKECNKTEAEYNKAVETFILSCAGYVVATYVMGIGDRHSDNIMITKLGHLFHIDFGHFL 1738

Qy    970  GNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHTNLLII  1029
Db   1739  GNYKKKYGPKRERAPPIFTQYMAIV---GGKDSENFKRFVTTCCSAYNILRKNTDLFIN  1795

Qy   1030  LFSWMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
Db   1796  LFQLMLSTGIPELQVAEDIDYLRKALAPGLSDEEAAEEFTKNISVALNTK-TVLLNDIFH 1854
```

RESULT 9
T18274
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18274
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cel. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18274
A;status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1585 <ZHO>
A;Cross-references: EMBL:U23478; NID:g733524; PID:g733523; PIDN:AAA85723.1
C;Genetics:
A;Gene: PIK3
C;Keywords: phosphotransferase

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Query Match        19.6%;   Score 1136.5;   DB 2;   Length 1585;
Best Local Similarity   28.2%;   Pred. No. 1.1e-68;
Matches  337;   Conservative 214;   Mismatches 413;   Indels 231;   Gaps   41;

Qy      2  ELENYEQPVVLRE----DNRRRRRMKP----RSTAASLS---SMELIPIE--------F   42
Db    411  KLENEREKILKERNEIDNLKKKNHLSKGYFMRACNASNDDGLEEEDIPLQDEHWETNVI  470

Qy     43  VLPTSQRNTKTPETALLHV---------AGHGNVEQMKAQVWLRALETSVSADFYH   89
Db    471  VLLPCRHHVKVPGSSSSSIDSIRQLAWASGKMQGHLNLEKDEKFFTLRWCNKDVVFDQDT  530

Qy     90  RLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPCQIHV-VQRHAPSEETL  148
Db    531  PLG--HLI------------------QYNLNYNNPTQKPNIKLELVLEDEL  562

Qy    149  AFQRQLNALIGYDVTDVSNVH------DDELEFTRR-----RLVTPRMAEVAGRDPKL  195
Db    563  CKER---LVDLQSLEINNGRPSIWKSHIDDVLSFNRKLRELAMLAKFQSNVPAAR---  614

Qy    196  YAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKK  255
Db    615  --LTPYPPPKTIPEFFV----IRVHLFKNQTKSLRCANNHTAFSLMTILSEKLKN  663

Qy    256  KSLMDIPESQNERDPVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLV----------  306
Db    664  TTPFD-----PTQYRFLITGINQYVDPNVFLLSVEYIVEKIKRKGEIDLTMVELLSLGL  717

Qy    307  ---------------LDTPPDP------ALDEVRKEEWPL--VDDCTGVTGYH  336
Db    718  IIQQQQQQQQQQQQQQIENIDDENILKLNNGILNVLSKIEKPIREKDNCISSLTVT  777
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Qy    337  EQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVL-PRTADLITVPVEANIQYGQQVLCQ  396
Db    778  ENLQVRLLHAHEIFASK------ASEIIGTDSP------SIQLFIEAAVFGGELLAT  823

Qy    397  RRTSPKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQYCGKAPALSGKTSAEMPSPESKG  456
Db    824  QSSKLVSFQDTVWNEWVNIPLAVSNIPNGARMCLGL---------NARYRG  866

Qy    457  KAQLLYVNLLLIDHRFLLR-HGEYVLHMWQLSGKGBDQGSFNADKLTSATNPDKENSMS  515
Db    867  DIFNIGWCHRLFDSKGILNTPAPFSLLLW---PGKINPIGTC-VDNLES------KDQAII  918

Qy    516  ISILLDNYCHPIALPKHRPTPDPEGDRV----RKQLEAIIATDPL  564
Db    919  IAPEFKDY----VVPK--TIHYEDLLELISKDENGNELPVVTMEEMDRVEQIIIQDPL  971

Qy    565  NPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQ-SALD  623
Db    972  YSLNKEERLLIWKSRYFCHTKPQALSKLLQSVEWTNYKQVGEAFQLL--KIWPTLSAVD  1028

Qy    624  VGLTMQLLDCNFSD-ENVRAIAVQKLESLEDDDVLHYLLQLQVAVKFEPYHDSALARFLL  682
Db   1029  --ALELLDPKFADCVEIREYTVKCLDQMSDYELEIYILQLVQAIKHDVFHNSVLSLFLI 1085

Qy    683  KRGLRNKRI-GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM  741
Db   1086  GRVWQNMQVLGHPFWHIRADI-DNQEVCERRFRVLSSGFLRYAPTQLMESFKREITTLRI 1144

Qy    742  LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFR----VPYDPGLKAGALV  797
Db   1145  LENLAKRVKEVPYEK--------RKQYVEN--NLREEQSFPTELFVPFDPSIRIINII  1192

Qy    798  IEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLIQILRIMESIWET  857
Db   1193  PEKCKSMDSAKVPLWVTFKNADPFA---PPLQMIAKTGDDLRQDIITLQLLRLMDHMWKS 1249

Qy    858  ESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPI  917
Db   1250  QDLDLHMTIYRCIATGMGTGLIEVVPNSETARIQAGAGGVSGAFKQTPIANWLKNHNQT  1309

Qy    918  EEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLG  977
Db   1310  ENSYQKAVSKFTLSCAGYCVATYVLGIGDRHNDNIMVDIHGHLFHIDFGHFLGNFKTFAG 1369

Qy    978  INKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHTNLLILLFSNMLMT 1037
Db   1370  FQREKAPFVLTPDFVVVI----GGKDSPNFAPFVDICCKAFNIIRSNAHVFINMFELMLST 1426

Qy   1038  GMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKG-WTVQFNWFLHLV  1091
Db   1427  GIPELRSENDIVYLRDKFRLDLTDAEASEYFKKLIH--ESIGTLTTTINFAIHIM  1479
```

RESULT 10
T42642
phosphoinositide 3-kinase (EC 2.7.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T42642
R;Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
J. Biol. Chem. 271, 13892-13899, 1996
A;Title: Cpk is a novel class of Drosophila ptdins 3-kinase containing a C2 domain.
A;Reference number: Z17659; MUID:96278830; PMID:8862856
A;Accession: T42642
A;status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1658 <MOL>
A;Cross-references: EMBL:U52193; NID:g1272421; PID:g1272422; PIDN:AAC52604.1
A;Experimental source: strain balb c
C;Genetics:
A;Gene: cpk
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
C;Keywords: phosphotransferase

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Query Match          18.6%;  Score 1076.5;  DB 2;  Length 1658;
Best Local Similarity 28.0%;  Pred. No. 1.4e-64;
Matches 330;  Conservative 198;  Mismatches 381;  Indels 269;  Gaps 39;

Qy  108  EIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLN--ALIGYDVTDV 165
Db  259  QISPKSEDINKFD----W--LDLDPWDAVLLEERSPS---CHLERKVNGKSLSGATVTRS 309

Qy  166  SNVHDDELEFTRRRLVTPRMAEVAGRDP------------------------K 194
Db  310  QSLIIRTAQFTKAQ------GQVSQKDPNGTSSLPTGSSLLQEFEVQNDEVAAFCQSIMK 363

Qy  195  LYAMHPWVTSKPLPEYLLKKIT---NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT- 250
Db  364  LKTKFPYTDHCTNPGYLLSPVTVQRNMC------GENASVKVSI-BIEGLQLPVTFTC 414

Qy  251  ---KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNGE 301
Db  415  DVSSTVEIIIMQALCWHDDLNQVDVGSYILKVCGQEEVLQNNHCLGSHEHIQNCRKWDT 474

Qy  302  EIHLVLDT--------PPDPALDBVRKE------EWPLVDDCTG------VTGYHEQL 339
Db  475  EIKLQLLTLSAMCQNLARTAEDDEAPVDLNKYLYQIEKPYKEVMTRHPVBELLDSYHYQV 534

Qy  340  TI---HGKDHESVFTVSLWDCDRKFRVKIRGIDIPV-------LPR--TADLT- 380
Db  535  ELALQTENQHRAVDQVI--KAVRKICSALDGVETPSVTEAVKKLKRAVNLPRNKSADVTS 592

Qy  381  ----------------VFVEANIQYGQQVL----------------CQRRT 399
Db  593  LSGSDTRKNSTKGSLNPENPVQVSMDHLTTAIYDLLRLHANSSRCSTGCPRGSRNIKEAW 652

Qy  400  ---------------------------SPKPFTEEVL 409
Db  653  TATEQLQFTVYAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGTYKNFFYLIK 712

Qy  410  WNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKAQLLYYVNLL 467
Db  713  WDELIIFPIQISQLPLESVLHGTLFGVLNQSSGSSPDSNKQRKGPEALGK-----VSLT 766

Qy  468  LIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPI 527
Db  767  LFDFKRFLTCGTKLLYLWTSSHTNSIPGAI----------PKKSYVMERIVLQVDF--- 812

Qy  528  ALPKHRPTP--------DPEGDR--VRAE----MPNQLRKQLEAIIATDPLNPLTA8DKEL 574
Db  813  ------PSPAFDIIYTSPQIDRNIIQQDKLETLESDIKGKLLDIIHRDSSFGLSKEDKVF 866

Qy  575  LWHFRYESLKDPKAYPKLFSSV--KWGQQEIVAKTYQLLAAKREVWDQSALDVGLIMQLL 631
Db  867  LWENRYYCLKHPNCLPKILASAPNWKWAN---LAKTYSLLHQ--W--PPLCPLAALELL 918

Qy  632  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRI 691
Db  919  DAKFADQGVRSLAVSWMEAISDDELADLLPQFVQALKYEIYLNSSLVRFLLSRALGNIQI 978

Qy  692  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGGGTAMLHDFTQQVQVIDMQKVTIDIKS 751
Db  979  AHSLYWLLKDAL-HDTHFGSRYEHVLGALLSVGGKGLREELSKQMKLVQLLGGVABKVRQ 1037

Qy  752  LSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKPL 811
Db 1038  ASGS---TRQVV-LQKSMERVQSFFLRNKCRIPLKPSLVAKELNIKSCSFFSSNAMPL 1091

Qy  812  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETBSLDICLLPYGCIS 871
Db 1092  KVTMWNADPL--GEEINVMFKVGEDLRQDMLALQMIKIMDKIWLKEGLDLRMVIFRCLS 1148

Qy  872  TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEKFQAAVERFVYS 931
Db 1149  TGRDRGMVELVPASDTLRKIQVE-YGVTGSFKDKPLAEWLRKYNPSEEYEKASENFIYS 1207

Qy  932  CAGYCVATFVLGIGDRHNDNIMISTGNLPHIDFGHILGNYKSFLGINKERVPFVLTPDF 991
Db 1208  CAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRDRAPFVLTSDM 1267

Qy  992  LFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPOLTSKEDIEYI 1051
Db 1268  AYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPELTSIQDLKYV 1326

Qy 1052  RDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
Db 1327  RDALQPQTTDAEATIFFTRLIESSLGSIAT-KFNFFIH 1363
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RESULT 11

S71792

phosphatidylinositol-3-OH kinase AGE-1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 01-Dec-2000
R;Morris, J.Z.; Tissenbaum, H.A.; Ruvkun, G.
Nature 382, 536-539, 1996
A;Title: A phosphatidylinositol-3-OH kinase family member regulating longevity and diapa
A;Reference number: S71792; MUID:96320556; PMID:8700226
A;Accession: S71792
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1164 <MOR>
A;Cross-references: EMBL:U56101
R;Williams, L.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21038
A;Accession: T31476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-263,'YEMR',270-285,'L','Q',289-307,324-328,'LESY',332-1164 <WIL>
A;Cross-references: EMBL:AL110499; PIDN:CAB57914.1; CESP:B0334.8
A;Experimental source: clone Y62F5A
R;Swinburne, J.
submitted to the EMBL Data Library, October 1995
A;Reference number: T18707
A;Accession: T18707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1089-1164 <WI2>
A;Cross-references: EMBL:Z66519; NID:g1044812; PIDN:CAA91377.1; GSPDB:GN00020; CESP:B033
C;Genetics:
A;Experimental source: clone B0334
A;Gene: CESP:B0334.8
A;Map position: 2
A;Introns: 22/2; 117/3; 307/3; 748/2; 835/2; 960/2; 1077/2; 1121/3
C;Superfamily: phosphatidylinositol 3-kinase

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Query Match          17.8%;  Score 1031;  DB 2;  Length 1164;
Best Local Similarity 27.1%;  Pred. No. 1e-61;
Matches 316;  Conservative 221;  Mismatches 406;  Indels 222;  Gaps 43;

Qy   78  ALETSVSADFVHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
Db   68  SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEBVIFNDDQPLSK 122

Qy  138  VQRHAPSEETLAFQ------------------------RQLNALIGYDVTDVSNVHDDEL-EF------TRR 178
Db  123  LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 182

Qy  179  RLVT------------------PRVAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215
Db  183  TCLTRGLEGTSHYAPPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK------AEI 235

Qy  216  TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKM-AKKKSLMDIPESQNERDFVLRV 274
Db  236  NGVC-----EKMMKIQIEFNPETPKSLLHTFLSRTNAIKLDVVTDTDDPADEGWFRSEL 289

Qy  275  CGRDEVILVGETPIK-------------NFQWVR------QC--LKNGEEIHLVLD 308
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A;Reference number: JC5500; MUID:97289668; PMID:9144573
A;Accession: JC5500
A;Molecule type: mRNA
A;Residues: 1-1634 <BRO>
A;Cross-references: GB;Y11312; NID:g2808446; PIDN:CAA72168.1; PID:g2076604
A;Experimental source: breast cell
C;Comment: This enzyme is involved in receptor signal transduction, in a signalling com
vival.
C;Genetics:
A;Gene: GDB;PIK3C2B; C2-PI3K; PI3K-C2beta
A;Cross-reference: GDB;9837703; OMIM:602838
A;Map position: 1q32-1q32
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
C;Keywords: phosphotransferase
F;156-162,169-174/Domain: SH3 #status predicted <SH3>
F;1037-1320/Domain: catalytic #status predicted <CAT>
F;1498-1612/Domain: protein kinase C C2 region homology <KC2A>

Query Match   17.6%;   Score 1021;   DB 1;   Length 1634;
Best Local Similarity   28.0%;   Pred. No. 8.4e-61;
Matches 304;   Conservative 178;   Mismatches 391;   Indels 212;   Gaps 29;

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Db  290 AGRTTP-VTNPDVKLTSYDVRLQQNIFVQLKILNFQGVRSERRLRCPGFVVRRQSLVLKDY 348
             :   |:.   .:                      ||||
Qy  309 TPPPDALDE--VRKEEWPLVDDCTGVTGVYHEQLTIHGKDHESVFT--------VSLWD 356
             ||||                 :.:.:             :           ||||||
Db  349 CRPKPLYEPHVRAHERKIALDVLSVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWD 406
            ||:| :                      ::: :: .:   ::::  .::
Qy  357 CDRKFPRVK---IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVW 413
            :.:|  |      .|    :    |  :.  |::.:  |::  |    :: |
Db  407 LDANLMIRPVNISGFDFPA---DVDMYVRIEFSVVGTLTLASKSTT-KVNAQFAKWNKE 462
            |   .::|.|:    :    |       :.  |.:|  :: :    :::::
Qy  414 L-EFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHR 472
            |       ||:          :      :|::   ||
Db  463 MYTFDLYMKDMPPSAVLSIRVLYGK---------VKLKSEEFE-----VGWVNMSLTDWR 508
            |||  : :.       ::  :.                |::
Qy  473 FLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKEN------SMSISILLDNYCHP 526
                                                     ||
Db  509 DELRQGQFLFHLW-----------APEPTANRSRIGENGARIGTNAAVTIEISSYGGR 555
            ::|  :   |                 :   |          :   :.:|
Qy  527 IALP-------KHR---PTPDDEGDRVRAEMPNQLRKQLRAIIATDPLNPLTAEDKE 573
                       :|:          |::      |:|          .:|  :.:|||
Db  556 VRMPSQGQYTYLVKHRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEDDEQ 615
            :        :: :|                          ::.  |:     ||:
Qy  574 ---LLWHFRYESLKDPKAYPKLFS-SVKWGQQEIVAKTYQLLARKEVWDQSALDVGLTMQ 629
               :::|||:  |              |:.:| | :  |:::    :
Db  616 RHVWMWR--RYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEK---WKPPSVAAALT-- 669
            ||   |||                 ||    :.|: ||     ||||||
Qy  630 LLDCNFSDENVRAIAVQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRN 688
            ||.|  .|:.|::|.|:  |:|  ||       |:|:.:  ||:  ||||||.::||||
Db  670 LLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMLLTRALCD 729
            ||                  ::|                 :   |  :. || |
Qy  689 KRIGHFLFWFLRSEIAQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDML 742
            ||:|  |||  |:|:|||          :::| | :|.|  ||  :      :.:|
Db  730 YRIGHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDEL 788
            .:|.|  |:|:|                 :: | |:::  |
Qy  743 QKVTIDIKSLSAEKYDVSS---QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVI 798
              :: :|.|:            ||::        ::    .|:|||:||.|:|  |::|
Db  789 TRISTLVKGMPK---DVATMKLRDELRSISHKDMERMDS---------PLDPVVKLGEMII 836
            |::|  ||:|           ::  | :::::::                  | ::|||:
Qy  799 EKCKVMASKKKPLWLEFKCADPTA-LSNETIGIIPKGHDDLRQDMLILQILRIMESTWET 857
            :| :|  :|||||||:    |    ||.|||    |||||:|||||| |:||:|||:|||
Db  837 DKAIVLGSAKRPLMLHWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNINKA 896
            ::     ||  ||:|:  ||||:|:||||| |  ::|||||||||:||:||:|||::|:|
Qy  858 ESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEK 914
            :|||:|||||||||.||||||:|:|||||:||||||:  |||||   ||||||||||||:
Db  897 ANIDCCLNFYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQ 956
            |:| |  |:|||| ||:||||||:|  |||||||||| ||:|||  |||||:|||||||:
Qy  915 CPIEE-----------------------KFQAAVERFVYSCAGYCVATFVLGIGDRHN 949
            |||:                        ||||||:|| ||||||||||||:|||||||
Db  957 CGIEDBKKKSSKKDSTKNPIEKKIDNTQAMKKYFSVDRFLYSCVGYSVATYIMGIKDRHS 1016
            |.|:| |||.|.|: ||||:|||:|  .|||| :|::|:|||||| |||||::|||||:|
Qy  950 DNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQ 1007
            ||:|:||||||||||||||||||:| |||:||:|||:|||||| ||  ||||||||:|||
Db 1017 DNLMLTEDGKYFHIDFGHILGHGKLG!QRDRQPFILTEHFMTVIRSGKSVDGNSHLQ 1076
            |||| |||||||||||||||||.|:   ||:| |||| ||:|:|||||||||.|||||
Qy 1008 KFQDVCVKAYLALRHHTNLLILFSMMLMTGMPOLTSKEDIEVIRDALTV-GKSEEDAKK 1066
            ||:|||||||||||||||:||:|:|:|::||||:||||||:||||||:  |||||.||
Db 1077 KFKTLCVEAYEVMNNRDLFVSLFTLMLGMELPELSTRADLDHLKKTLFCNGSKEEARK 1136
            ||||| |:||:|:||||||||:|| ||||:||| |:||||||||::| ||.||||:|
Qy 1067 YFLDQIEVCRDKGWTVQFNWFLHLV 1091
            ||  |:||| |:||.||:|||||||
Db 1137 FFAGLYEEAFNGSWSTKTNWLFHAV 1161
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RESULT 12
JC5500
phosphoinositide 3-kinase (EC 2.7.1.-) - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: JC5500
R;Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, M.J.
Biochem. Biophys. Res. Commun. 233, 537-544, 1997
A;Title: Identification and cDNA cloning of a novel mammalian C2 domain-containing phosp

Query Match stats (second alignment):

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Qy  159 GYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAM--HPWVTSKPLPEYLLKKIT 216
            .:::.:| :          ::  :    .    |:    |  ::                ::
Db  322 GHELFEVSEERDEVAAFCHMLDILR---SGSDIQYFLTGYVWSAVTPSPEHLGDEV- 376
Qy  217 NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPSQNERDFVLRVCG 276
            ::: |:|                                   :|            ::
Db  377 NLKVTVLCDRLQEALTFTCNCSSTVDLLI--YQTLCYTHDDLRNV---DVGDFVLXPCG 430
Qy  277 RDEYLVGETPIKNFQWVRQCLK----- 298
            ||:|  |            ::|  ::
Db  431 LEEFLQNKHALGSHEYIQYCRKFDIDIRLQLMEQKVVRSDLARTVNDDQSPSTLNVLVHL 490
Qy  299 -----------NGEEIHLVLDT------- 309
               :|::|||:|
Db  491 QERPVKQTISRQALSLLFDTYHNEVDAFLLADGDFPLKADRVVQSVKAICNALAAVETPE 550
Qy  310 --------------DPALDEVRKEEWPLV- 330
               .|||||||||||:
Db  551 ITSALNQLPPCPSRMQPKIQKDPSVLAVRENREKVVEALTAAILDLVELYCNTFNADFQT 610
Qy  331 GVTGYHEQLTIHGKDH---ESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANI 387
            |::                   |::||                .      :      ::
Db  611 AVPGSRKHDLVQEACHFARSLAFTV-YATH---------------IPIIWATSYEDFYLSCSL 658
Qy  388 QYGQQVLC------QRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYC--GKAPA 440
            |:|                                                      .:||
Db  659 SHGGKDMCSPLQTRRAHPSKYLFHLIVWDQQICFPVQVNRLPRETLLCATLYALPIPPPG 718
Qy  441 LSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNAD 500
            .:::                   :                   .:
Db  719 SSEEANKQRRVPEALG------WVTTPLFNFRQVLTCGRKLLGLWPATQE------NPS 765
Qy  501 KLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEGDRVR-----AEMPNQLRKQL 555
            |||                                                   ::
Db  766 ARWSAPNHQPDSVILQIDFPTSAFDIKF----TSPPGDKFSPRYEFGSLREEDQRKL 819
Qy  556 EAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKRE 615
            :   :    ::|  |::|        :||:||::||:||:::                   :
Db  820 KDIMQKESLYWLTDADKKRLWEKRYYCHSEVSSLPLVLASAPSWEWACLPDIYVLLKQ-- 877
Qy  616 VW-----DQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEP 671
            |            :|:|||:|:                                    :|
Db  878 -WTHMNHQDALG------LLHATFPDQEVRRMAVQWIGSLSDAELLDYLPQIVQALKYEC 930
Qy  672 YHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHD 731
            ||:|||            |::||                                     :
Db  931 YLDSPLVRFLLKRAVSDLRVTHYFFWLLKDGLKDSQ-FSIRYQYLLAALLCCCGKGLREE 989
Qy  732 FTQQVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQLENL-QNLNLPQSFRVPYDPDG 790
            |                                          ::|
Db  990 FNRQCWIVNALAKLLAQQVR----EAAPSARGI---LRTGLBEVKQFFALNGSCRLPLSPS 1043
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Qy    791  LKAGALVIEBCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRI   850
           |||||| |: : |||  |:||||||||||||||||||:||||
Db   1044  LLVKGIVPRDCSYPNSNAVPLKLSFQNVDPL---GENIRVIFFKCGDDLRQDMLTLQWIRI  1100

Qy    851  MESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHW   910
           |||||||||||||||||||||||||||||||||:||||||||: |:||||||:|||||
Db   1101  MSKIWVQBGLDMRMVIFRCFSTGRGRGMVEMIFNAETLRKIQVEH-GVTGSFKDRPLADW  1159

Qy    911  LKEKCPIEKFQOAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILG   970
           |:||| |||||||||||||||||||||||:|||||||||||||||:||||||||||||
Db   1160  LQKHNPGEDEYEKAVENFIYSCAGCCVATYVLGICDRHNDNIMLKT~GHMFHIDFGRFLG  1219

Qy    971  NYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKPQDVCVKAYLALRHHTNLLIIL  1030
           |:|| ||:||  ||| |||:||:||: |:||::|| ||  |  ||::|| |:|:||: |
Db   1220  HAQMFGNIKRDRAPPVFTSDMAYVI-NGDGDKPSSRFHDFVDLCCQAYNLIRKHTHLFLNL  1278

Qy   1031  FSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHL  1090
           |||||||||||||||||||||||||||||||||||||||||||||||||: :|||||||
Db   1279  LGLMLSCGIPELSDLEDLKYVYDALRPQDTEANATTYFTRLIIESSLGSVAT-KLNFFIHN  1337

Qy   1091  VLGIK  1095
           :|: |
Db   1338  LAQMK  1342


RESULT 13
JCS985
phosphoinositide 3-kinase C2gamma - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 30-Apr-1999
C;Accession: JCS985
R;Misawa, H.; Ohtsubo, M.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Yoshimura, A.
Biochem. Biophys. Res. Commun. 244, 531-539, 1998
A;Title: Cloning and charaterization of a novel class II phosphoinositide 3-kinase conta
A;Reference number: JCS985; MUID:98189216; PMID:9514948
A;Accession: JCS985
A;Molecule type: mRNA
A;Residues: 1-1506 <MIS>
A;Cross-references: DDBJ:AB008791
A;Experimental source: liver
C;Comment: This protein exclusively expressed in the liver,and a N-terminal truncated fc
C;Genetics:
A;Map position: 6
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
F;978-1239/Domain: catalytic #status predicted <CAT>

Query Match    15.1%;   Score 876;   DB 2;   Length 1506;
Best Local Similarity  25.4%;   Pred.No. 5.6e-51;
Matches  277;   Conservative 195;   Mismatches 407;   Indels 210;   Gaps  34;

Qy     58  LLHVAGHGN--VEQMKAQVWLRALETSVSADFY--HRLGPDHFLLLYQKKGQWYEIYDKY  113
           ::   ||    :   :  |   ||  |:  | |      :  ::   :|||   |::
Db    300  LLLLMPHANYLVKDIIAEILLLCANEPLSPKEYLLSVCGSEEFLQMDHSLGS-HKIFQK-  357

Qy    114  QVVVQTLLDCLRYKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDE-  172
           :  ::   :  |    |:   | :|        :   |::  |  |  ||  |::|:
Db    358  ---------------NKSVIQLH-LQKNRDTPGKLSRKSE---------DDHSPFHLNQL  392

Qy    173  LEFTRRRLVTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRST--TS  230
           |||        : |: |     | :  | :|| ||:|||::   |:|    :
Db    393  LEFT------------------HIW------------KISRQCLSTVMKKYNLHVB  418

Qy    231  QTIKVSADDTPGTIILQSFFTKMAKKKSLMDIPESQNERDFVLRVCG------------  276
           |: :: |  ||   | |  |||      :  |    |  | |: |
Db    419  HLLKPQKD----MEEKHLSSMVSGNQHTSQPHVNNVLEEVKNICSVLGCIETKQVSDAV  473

Qy    277  RDEYLVGETPIKNFQWVRQCLKNG--EBIHLVLDTPPDALDEVRKEEWPLVD-----DC  329
           | :  ||| | :  |   :||         |:|  ||| |  |: |:|:|
Db    474  KELNLILQRPSQNFHQNSETSKKGFIERV-------------TAELSRSIYQLIDVYCSSFC  522

Qy    330  T-------GVTGYHEQLTIHGKDHESVFTVSLMDCDRKFRVKIRGIDIPVLPRTADLT  380
           ||:                ::   ::
```

RESULT 14
T13801
phosphoinositide 3-kinase (EC 2.7.--) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13801; T13351
R;MacDougall, L.K.; Domin, J.; Waterfield, M.D.
Curr. Biol. 5, 1404-1415, 1995
A;Title: A family of phosphoinositide 3-kinases in Drosophila identifies a new mediator
A;Reference number: Z17766; MUID:96362138; PMID:8749393
A;Accession: T13801
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1876 <MAC>
A;Cross-references: EMBL:X92892; NID:g2113837; PIDN:CAA63465.1; PID:g2113838
R;Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
J. Biol. Chem. 271, 13892-13899, 1996
A;Title: Cpk is a novel class of Drosophila ptdIns 3-kinase containing a C2 domain.

```
Db    523  TDFQPVHTPGGVSHVHAGL---QSHLSFTVCSLHNVPETWAHSYKAFSF---------  568

Db    381  VFVEANIQYGQQVLCQ-RRTSPKPTTEE----VLMNVWLEFSIKIKDLPKGALLNLQIYC  435

Db    569  ---SCWLTYAGKKLCQVKSCRPLPVTKSFSLLVNWNBIINFPLEIKSLPRESMLVIKLF-  624

Qy    436  GKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEYVLHMWQLSGKGEDQG  495

Db    625  ----------------------AWTCLPLFPRQE  648

Qy    496  SFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPD------PEGDRVRA---  545

Db    649  SVLGSRLFSVTLQSEPPIEMIAPGWDGSQPSPLTIQIDFPDAGWEYLKPESEENRTDHE  708

Qy    546  EMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVA  605

Db    709  EPPRECLKHIAKLSQKKSPLLSEEKRRYLWFYRLYCNNENSSLPLVLGASPGWDEETVS  768

Qy    606  KTYQLIAK---REVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYLLQ  662

Db    769  EMHAILRRWTFSHPWE-------AlGLLISRFPPDQDIREVAVQQЈDTLLTDELLDCLPQ  820

Qy    663  LVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLR  722

Db    821  LVQAVKFEWNLESPLVELLPRRPLQSIRVAнCLYWLLRD--AQGEAYFKSWYQELLAALQ  878

Qy    723  GC-GTAMLHDFTQQVQIDMLQKVTIDIKSLS--ABKYDVSSQVISQLKQKLENLQNLNLP  780

Db    879  FCAGEALNEELSKEQKLVKLLGDIGEKVKSASDPQRKDVLKKBIGSLEEFFKDIKTCHL-  937

Qy    781  QSFRVPVYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Db    938  ---PLNPALCIKGIDRDACSYFTSNASPLKITFINANP--MGKNISVIFKAGDDLRQ  989

Qy    841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900

Db    990  DMLALQIIQVMDNAWLQEGLDMQMITYGCLSTGRAQGFIEMVPDAVTLAKIHLHS-GLIG 1048

Qy    901  AFKDEVLSHWLKEKCPIEEKFQOAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Db   1049  FLKENTIKKKWFSQHNHLKBDYEKALRNFFYSCAGWCVVTFLGVCDRHNDNIMLTKSGHM 1108

Qy    961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKPQDVCVKAYLAL 1020

Db   1109  FHIDFGKFLGHAQCTFGGIKRDRAPFLFTSEMEYFI-TEGGKNIQHFQDFVELCCRAYNIV 1167

Qy   1021  RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Db   1168  RGЈSQLILSLLEMLHAGLPELRGIEDLKYVHNNLRPQDTDLEATHSFTKKIKESLE-CF 1226

Qy   1081  TVQFNWFLH 1089

Db   1227  PVKLNNLIH 1235
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A;Reference number: Z17659; MUID:96278830; PMID:8662856
A;Accession: T13351
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-295,'P',297-331,'R',333-576,'T',578-641,'S',643-1876 <MOL>
A;Cross-references: EMBL:U52192; NID:gi1272419; PID:gi1272420; PIDN:AAC47117.1
C;Genetics:
A;Gene: PI3K 68D; cpk
A;Cross-references: FlyBase:FBgn0015278
A;Map position: 3L
C;Keywords: phosphotransferase

Query Match        15.1%;   Score 873.5;  DB 2;   Length 1876;
Best Local Similarity 32.2%;  Pred. No. 1.2e-50;
Matches  238;  Conservative  129; Mismatches 298;  Indels  75;  Gaps  22;
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2003
C;Accession: AS9003
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: bi
A;Reference number: AS9003; MUID:96009592; PMID:7565716
A;Accession: AS9003
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-816 <ZHO>
A;Cross-references: GB:U23480; NID:g733480; PIDN:AAA85726.1; PID:g733530
C;Superfamily: phosphatidylinositol 3-kinase Vps34 type
C;Keywords: phosphotransferase

Query Match        12.4%;   Score 720.5;  DB 1;   Length 816;
Best Local Similarity 26.1%;  Pred. No. 8.4e-41;
Matches  216;  Conservative  163; Mismatches 288;  Indels  161;  Gaps  28;
```

(sequence alignment data)

```
RESULT 15
AS9003
phosphoinositide 3-kinase (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
```

Sun Feb 15 18:14:38 2004

Search completed: February 15, 2004, 02:07:49
Job time : 50 secs

```
          GenCore version 5.1.6
     Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:   February 15, 2004, 01:29:38 ; Search time 91 Seconds
                                         (without alignments)
                              3124.989 Million cell updates/sec

Title:         US-09-974-573-1
Perfect score: 5790
Sequence:      1 MELENYEQPVVLREDNRRRR..........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:   830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_23:*
             1: sp_archea:*
             2: sp_bacteria:*
             3: sp_fungi:*
             4: sp_human:*
             5: sp_invertebrate:*
             6: sp_mammal:*
             7: sp_mhc:*
             8: sp_organelle:*
             9: sp_phage:*
            10: sp_plant:*
            11: sp_rodent:*
            12: sp_virus:*
            13: sp_vertebrate:*
            14: sp_unclassified:*
            15: sp_rvirus:*
            16: sp_bacteriap:*
            17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5538	95.6	1102	4	Q8IV23	Q8iv23 homo sapien
2	5534	95.6	1102	4	Q9BZC8	Q9bzc8 homo sapien
3	5476.5	94.6	1113	11	Q9EQL1	Q9eql1 mus musculu
4	1468.5	25.4	1068	13	O42391	O42391 gallus gall
5	1450.5	25.1	1083	15	O39483	O39483 avian sarco
6	1363	23.5	1064	11	Q8BTI9	Q8bti9 mus musculu
7	1339	23.1	1047	11	Q8BS14	Q8bs14 mus musculu
8	1335	23.1	260	11	Q8C5Q7	Q8c5q7 mus musculu
9	1329	23.0	1037	11	Q8CI98	Q8ci98 mus musculu
10	1329	23.0	1043	11	Q8CJ28	Q8cj28 mus musculu
11	1290	22.3	1068	4	O00334	O00334 homo sapien
12	1283	22.2	1088	5	P91634	P91634 drosophila
13	1103.5	19.1	852	13	Q9PTE5	Q9pte5 xenopus lae
14	1076.5	18.6	1658	11	Q61182	Q61182 mus musculu
15	1074	18.5	1686	4	O00443	O00443 homo sapien
16	1040.5	18.0	1509	11	Q61194	Q61194 mus musculu
17	873.5	15.1	1876	5	Q9VTN5	Q9vtn5 drosophila
18	820.5	14.2	318	11	Q9CTK7	Q9ctk7 mus musculu
19	758	13.1	286	4	Q9BTS4	Q9bts4 homo sapien
20	713.5	12.3	887	11	O88763	O88763 rattus norv
21	708.5	12.2	887	5	Q8NEB9	Q8neb9 homo sapien
22	701.5	12.1	1607	5	Q20187	Q20187 caenorhabdi
23	698.5	12.1	887	4	Q15134	Q15134 homo sapien
24	683	11.8	847	11	Q8R3S8	Q8r3s8 mus musculu
25	667	11.5	808	10	Q8GUA6	Q8gua6 medicago tr
26	660	11.4	813	10	Q8H1S8	Q8h1s8 brassica na
27	659.5	11.4	291	11	Q91XL6	Q91xl6 rattus norv
28	647	11.2	949	5	P91635	P91635 drosophila
29	645	11.1	949	5	Q9W1M7	Q9w1m7 drosophila
30	628	10.8	901	5	Q9TXI7	Q9txi7 caenorhabdi
31	626	10.8	897	5	Q9XZR0	Q9xzr0 caenorhabdi
32	597	10.3	650	5	Q9TXI6	Q9txi6 caenorhabdi
33	550.5	9.5	499	10	Q8RXR0	Q8rxr0 arabidopsis
34	510	8.8	273	5	Q9BIU5	Q9biu5 leishmania
35	508	8.8	732	10	O04269	O04269 chlamydomon
36	489	8.4	99	11	Q8C403	Q8c403 mus musculu
37	472.5	8.2	1016	3	Q9Y8E4	Q9y8e4 pichia angu
38	435.5	7.5	2028	10	O81129	O81129 arabidopsis
39	432	7.5	2051	10	Q9SXA1	Q9sxa1 arabidopsis
40	418.5	7.2	2043	6	O02811	O02811 bos taurus
41	418	7.2	1889	10	Q94H07	Q94h07 oryza sativ
42	412.5	7.1	608	10	Q8L5D9	Q8l5d9 oryza sativ
43	410	7.1	1466	6	Q28925	Q28925 bos taurus
44	410	7.1	2044	5	Q9UPG2	Q9upg2 homo sapien
45	409	7.1	1433	5	Q8SQY7	Q8sqy7 encephalito

ALIGNMENTS

```
RESULT 1
Q8IV23
ID   Q8IV23            PRELIMINARY;      PRT;   1102 AA.
AC   Q8IV23;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide-3-kinase, catalytic, gamma polypeptide.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035683; AAH35683.1; -.
KW   Kinase.
SQ   SEQUENCE   1102 AA;  126453 MW;  EF2B1A0E1CBEF406 CRC64;

Query Match             95.6%;  Score 5538;  DB 4;  Length 1102;
Best Local Similarity   95.3%;
Matches 1050;  Conservative   20;  Mismatches   32;  Indels    0;  Gaps    0;

Qy         1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
             |||||||:|||||||| |||||||||| |||||||||||||||||| |:|||||||||||
Db         1 MELENYKQPVVLREDNCRRRRRMKPRSAAASLSSMELIPIEFVLPTSQRKCCKSPETALLH 60

Qy        61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
             |||||||||||||||||||||||:|||||||||| |||||||||||||||||||||||||
Db        61 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 120

Qy       121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
             ||||||  ||||||||:||||| |||| ||||||| |||||||||||||||||||||| |
Db       121 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 180

Qy       181 VTPRMAEVAGRDPKLYAMHPVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95505661; PubMed=7624799;
RA   Stoyanov B., Volinia S., Hanck T., Rubio I., Loubtchenkov M.,
RA   Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nurnberg B.,
RA   Gierschik P., Seedorf K., Hsuan J.J., Waterfield M.D., Wetzker R.;
RT   "Cloning and characterization of a G protein-activated human
RT   phosphoinositide-3 kinase.";
RL   Science 269:690-693(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Michalke M., Schaefer M., Stoyanov B., Wetzker R., Nuernberg B.;
RT   "Regulation of a G-protein-activated phosphoinositide-3-kinase.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF327656; AAG61115.1; -.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase; Transferase.
SQ   SEQUENCE 1102 AA;   126481 MW;   402BB67E8DD2191A CRC64;

Query Match
Best Local Similarity   95.6%;   Score 5534;   DB 4;   Length 1102;
                        95.2%;   Pred. No. 0;
Matches 1049;   Conservative 21;   Mismatches 32;   Indels 0;   Gaps 0;

Qy    1 MELENYEQPVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH  60
        |||||| || ||||| |||||||||| ||||||||||||||||||||||    ||||||
Db    1 MELENYKQPVVLREDNCRRRRRMKPRSAAASLSSMELIPIEFVLPTSQRKCKSPETALLH  60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
        |||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||
Db   61 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 120

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        ||||||  |||||||||||||  ||| ||||||| |||||||||||||||||||||| |
Db  121 CLRYWKATHRSPGQIHVVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 180

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSADDT 240
        ||||||||  |||||||||||||||||||||||||||||||||||||||||||||  ||
Db  181 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 240

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        ||  ||||||||||||||||||||| | ||||||||||||||||||||||||||| ||||
Db  241 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 300

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 EEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQGQVLCQRRTSPKPFTEVLWNVWLEPSIKI 420
        ||||||||||||||| |||||||||||| |||||||||||||||||||||||||||||||
Db  361 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQGQVLCQRRTSPKPFTEVLWNVWLEPSIKI 420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGAQLLYYVNLLLIDHRFLLRHGEY 480
        ||||||||||||||||||||||    ||| ||  ||||  |||||||||||||||| |||
Db  421 KDLPKGALLNLQIYCGKAPALSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 480

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
        ||||||   |||||||||||||||||||||||||||||||||||||||||    ||||||
Db  481 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKQPTPDPEG 540

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWIHFRYESLKDPXAYPKLFSSVKWGQ 600
        ||||||||||||||||||||||||||| |||||||| |||||||||| ||||||||||||
Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPJTAEDKELLWHFRYESLKHPXAYPKLFSSVKWGQ 600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
        |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661 LQLVQAVKPEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LQLVQAVKPEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy  721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSLAEKYDVSSQVISQLKQKENLQNLNLP 780
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||| ||
Db  721 LRGGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSLAEKYDVSSQVISQLKQKENLQNSQLP 780

Qy  781 QSFRVPYPDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
         ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  781 ESFRVPYPDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        |||||| ||||||  | |||||||||||||||||||||||||||||||||||| |||||
Db  901 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 960

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLIPDFLFVMGTSGKKTSLHPQKFQDVCVKAYLAL 1020
        |||||||||||||||||||||||||| |||||||||||||| || | ||| |||||||||
Db  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1020

Qy 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
        |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081 TVQFNWFLHIVLGIKQGEKHSA 1102
        ||||||||||||||||||||||
Db 1081 TVQFNWFLHIVLGIKQGEKHSA 1102
```

RESULT 2
```
Q9BZC8
ID   Q9BZC8       PRELIMINARY;     PRT;   1102 AA.
AC   Q9BZC8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Phosphoinositide-3-kinase gamma catalytic subunit (EC 2.7.1.137).
GN   PI3CG.
OS   Homo sapiens (Human).
```

```
Db    481 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 540

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
            |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 600

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
            |||||||||||:||:||||||||||||||||||||||||||||||||||||||||||||
Db    601 QEIVAKTYQLLARREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSXHYQQRFAVILEAY 720

Qy    721 LRGGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSABKYDVSSQVISQLKQKLENLQNLNLP 780
            |||||||||:|||||| :|:|||||||||||||||:||||||||||||||||||:||:||
Db    721 LRGGCGTAMLQDFTQQVHVIEMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLP 780

Qy    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
            :||||||||||||||.|||||||||||||||||||||||:||||||||||||||||||||
Db    781 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQ 840

Qy    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTG 900

Qy    901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
            |||||||.||||||.|.||||||||||||||||||||||||||||||||||||||:||||
Db    901 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 960

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
            ||||||||||||||||||||||||||||||||||||||||||:|||||||:||||||||
Db    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1020

Qy   1021 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
            |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   1021 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1080

Qy   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
            ||||||||||||||||||||||
Db   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
```

RESULT 3
Q9EQL1

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ID   Q9EQL1       PRELIMINARY;       PRT;    1113 AA.
AC   Q9EQL1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphatidylinositol 3-kinase gamma isoform.
GN   PIK3CG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chakravarti S., McColl S.R.;
RT   "Cloning of a murine ortholog of PI 3-kinase gamma.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF208345; AAG41122.1; -.
DR   MGD; MGI:1355576; Pik3cg.
DR   InterPro; IPR001263; PIK3CG.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
SQ   SEQUENCE   1113 AA;   127538 MW;   6729FE8BA5D35691 CRC64;
```

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Query Match             94.6%;  Score 5476.5;  DB 11;  Length 1113;
Best Local Similarity   93.2%;  Pred. No. 0;
Matches 1037;  Conservative 31;  Mismatches 34;  Indels 11;  Gaps 1;
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```
Qy      1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEPVLPTSQRNTKPETALLH 60
            ||||||||||||||||:|||||||||:||.|||||||||||:|||||||:..:|||||||
Db      1 MELENYEQPVVLREDNLRRRRRMKPRSAAGSLSSMELIPIEFVLPTSQRISKTPETALLH 60

Qy     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
            ||||||||||||||||||||||||:|:|||||||:|:|||||||||||||:||:||||||
Db     61 VAGHGNVEQMKAQVWLRALETSVAAEFYHRLGPDQFLLLYQKKGQWYEIYDRYQVVQTLD 120

Qy    121 CLRYWKVLHRSPGQIHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
            ||.|||:.|.||||||||.||.|||||||:||..:|||||||||:||||||||||||||
Db    121 CLHYWKLMHKSPGQIHVVQRHVPSEETLAFQKQLTSLIGYDVTDISNVHDDELEFTRRRL 180

Qy    181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
            ||||||||||||.|||||||||||||||:||.|||:|||:||||||.|||||||||||||
Db    181 VTPRMAEVAGRDAKLYAMHPWTSKPLPDYLSKKIANNCIFIVIHRGTTSQTIKVSADDT 240

Qy    241 PGTILQSFFTKMAKKKSLMDIPSQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
            |||||||||||||||||||:|.||||:|||||||||||||||||||||:||||||||||
Db    241 PGTILQSFFTKMAKKKSLMNISESQSEQDFVLRVCGRDEYLVGETPLKNFQWVRQCLKNG 300

Qy    301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
            :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy    361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLWNVWLEFSIKI 420
            ||||||||||||||||.||||||||||||.||||||||||||||:||||||||||||:||
Db    361 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVLCQRRTSPKPFABEVLWNVWLEFGIKI 420

Qy    421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEY 480
            ||||||||||||||..|:|..||.:||||.|.|||||||||||||||||||||||||:|
Db    421 KDLPKGALLNLQIYCCKTPSLSSKASAETPGSESKGKAQLLYYVNLLIDHRFLLRHGDY 480

Qy    481 VLHMWQLSGKGEDQGSFNADKLTSAINPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
            ||||||:||:.|:|||||||||||||||||||||||||||||||||||||||||||||||
Db    481 VLHMWQISGKAEBQGSFNADKLTSAINPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
            |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 600

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
            |||||||||||:||:||||||||||||||||||||||||||||||||||||||||||||
Db    601 QEIVAKTYQLLARREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSXHYQQRFAVILEAY 720

Qy    721 LRGGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSABKYDVSSQVISQLKQKLENLQNLNLP 780
            ||.|||||||:||||| :|:|||||||||||||||:||||||||||||||||||:||:||
Db    721 LRGCGTAMLQDFTQQVIEMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLP 780

Qy    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
            :||||||||||||||.|||||||||||||||||||||||:||||||||||||||||||||
Db    781 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQ 840

Qy    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTG 900
```

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Qy    54 RKYPL-----YQLLQDSSYIFVSVTQEAEREFFDETRRLCDLRLFQPF-----LKVI 102
            ::        :::                      ::       : :::  |||||
Db   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPK---- 194

Qy   103 EPVGNREEKI-LNREIGFAIGMPICEFDMVKDPEVQDFRRNILNVCKEAVDLRDANAPHS 161
            :::          ||:            :::   :::                   :::
Db   195 --LYAMHPWTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245

Qy   162 RALYVCPPNVESSPELPKHIYNKLDKGQIIVIWIVTVSPNNDKQKYTLKINHDCVPEQVI 221
            ::|::: :|:  |:  |: |  :||:||| |: ::| :: :::|||::|  || :::
Db   246 QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299

Qy   222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYLLEKYPLSQYKYIRSCIML 279
            :: :::        ::   ::   :  :  :: ::  ::    :::          :::
Db   300 GEEIHLVLDTPDPALDEVRKE---EWPLVDDCTGVTGYHEQLT-----IHGKDHESVF 350

Qy   280 GRMPNLMLI-------------MAKESLYTQLPL--DTFTMPSYSRRISTATPYMNGE---AT 323
            ::      :::::         |::        ||:  :::      ::     ::
Db   351 TVSLWDCDRKFPVK---------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTS 400

Qy   324 AKSLWTINSALRIRILCATYVNVNIRDID-----KIYVRTGIYHGGEPLCDNVNT 373

Db   401 PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460

Qy   374 QRVPCSNPRWNEWLSYDMYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCP 421
            ||            ::  :   :: |   |:::::|:    :||:||          :::
Db   461 LYYVNLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520

Qy   422 LAWGNINMFDYTDTLVSGKMALNLWAVPHGLED-LLNPIGVT-GSNPNKS-TPCLELEF 477
            :: ::   :::  :::|::        :  :::       ::        :::

Db   521 DNYCHPIALPKIRPTPDPEGDRVRAEM---------------PNQLR----KQLEAIIAT 561
            ::       :            ::::                          :::::
Qy   478 DWFSNPVKFPDMTVIEBHANWTISRELGFNVYSAGLSNRIARDNELRESDKEQLRAICTR 537

Qy   562 DPLNPLTAEDKSLLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVMDQSA 621
            ||:|:   ::  :::||:::||            :: |:||::::::      :::
Db   538 DPLSBITEQEKDFLWSHRHYCVNTPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy   622 LDVGLIMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF 680
            |:||  ::|:|||  |::  |: :||::  |:||::|  |:|:||: |: ||::|  :::
Db   593 IKPEQAMELLDCNYPDDMVRAFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNCLVRF 652

Qy   681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCTAMLRDFTQQVQVID 740
            |||  |:::| ||| ||::|    :::: :: | ::::: ||| |    :::|  ::::
Db   653 LLKKALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LSRQVBAME 710

Qy   741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQN---LNLPQSFRVPYDPGLKAGALV 797
            |::|: :|:|||:||:||    :::  :::::|||   :::||:||:  ||:: :::
Db   711 KJINLT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFISPLNPAHQLGNLR 765

Qy   798 IEKCKVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGGDDLRQDMLILQILRIM 851
            ::|| :: | : :|:|| |   :: |:      ||:||:|::||::|:||||:::|:|:::
Db   766 LEECRIMSSAKRPLWLNWE---NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy   852 ESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
            |:|| |:||:|||||||| ||||:||:|:||:|:    ::::| |:|: :  |:|:|:::
Db   821 ENIWQNQGLDLRMLPYGCLSIGDCVLIEVVRSSHTIMQI-QCKGLKGALQFNSHTLHQ 879

Qy   910 WLKEKCPIEEKFQAAVERFVSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
            |||:|||||||:||| ||||||||||||||||||||:||:||||||||:|||||||||
Db   880 WLKDKNK-GEMYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFL 938

Qy   970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL 1027
            ||   :||:  || |||||||:|||||| :|    :|||||| |  : :|  ::|: :::
Db   939 DHKKKKFGYKRERVRPFVLTQDFLIVISKGAQBCTKTREFERFQEMCYKAYLAIRQHANLF 998
```

```
RESULT 4

ID   O42391     PRELIMINARY;     PRT;     1068 AA.
AC   O42391;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Phosphoinositide 3-kinase catalytic subunit.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97334438; PubMed=9188528;
RA   Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,
RA   Teichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
RT   "Transformation of chicken cells by the gene encoding the catalytic
RT   subunit of PI 3-kinase.";
RL   Science 276:1848-1850(1997).
DR   EMBL; AF001076; AAB62534.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_Kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
SQ   SEQUENCE   1068 AA;   124287 MW;   9912A96B3397735E CRC64;
```

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Query Match             25.4%;    Score 1468.5;   DB 13;   Length 1068;
Best Local Similarity   33.2%;    Pred. No. 5.6e-105;
Matches   380;   Conservative 211;   Mismatches 396;   Indels 157;   Gaps 40;

Qy    23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
            ::|| :  ::::::  :      :|||: ||:|  :|: ||:||||||:|:::::|::
Db     1 MPPRPSSGELWGIIHLMPPRILVECLLPNGMIVT------LECLREATLLTIKHELFKEA 53

Qy    79 LETSVSADFYHRLGPDHFLLLYGKKGQWYEIYDKYQVQVTLDCLRYWKVLHRSPGQIHVV 138
            ::  :::|    |||||| ||:||: |||||:||     ::|  | ||::|||||||||
Db  1088 LHLIV 1091
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Db     1059 FHTI 1062


RESULT 5
ID   O39483       PRELIMINARY;       PRT;    1083 AA.
AC   O39483;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag-v-phosphoinositide 3-kinase catalytic subunit fusion protein
DE   (Fragment).
GN   GAG-V-P3K.
OS   Avian sarcoma virus 16.
OC   Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX   NCBI_TaxID=60029;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97334438; PubMed=9188528;
RA   Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,
RA   Teichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
RT   "Transformation of chicken cells by the gene encoding the catalytic
RT   subunit of PI 3-kinase.";
RL   Science 276:1848-1850(1997).
DR   EMBL; AF001075; AAB62532.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2_1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
FT   NON_TER       1       1
SQ   SEQUENCE   1083 AA;  125869 MW;  371EF7055A78ACE8 CRC64;

Query Match             25.1%;  Score 1450.5;  DB 15;  Length 1083;
Best Local Similarity   34.9%;  Pred. No. 1.4e-103;
Matches  359;  Conservative  189;  Mismatches  345;  Indels  135;  Gaps  36;

Qy      135 IHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPK 194
                :|:: |:  ::|:  |  :      ::|:          |  |  ||| :
Db      114 LKVIEPVGNREEKI-LNRKIGFAIGMPICEFDMVKDPEVQDFRRNILNVCKEAVDLRDAN 172

Qy      195 -----LYAMHPWVTSKP-LPEYLLKKITNNCVFIVI-----HRSTTSQTIKVSADDTP 241
                 ::| | : :          ||:||: :|:  ||     ||:| |:|: : |||
Db      173 APHSRALIYCVCPPNVESSPELPKHIYNKLDKGQIIVIWVIVSPNNDKQKYTLKINHDCVP 232

Qy      242 GTILQSFFTKMAKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQ 295
                |:    ||:| | ::|::           :|:|:| |:| ||| ||| | ::|
Db      233 EQVIAEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYLLEKYPLSQYKYIRS 290

Qy      296 CLKNGEEIHLVLDTPPDPALDEVRKE-------EWPLVDDCTGVTGYHEQLT-----IHGKDH 346
                 |::         :  :||         :  |   ||:: ||: :||        ::|
Db      291 CIMLGRMPNIML--------MAKESLYTQLPL--DTFTMPSYSRRISTATPYMNGE-- 336

Qy      347 ESVFTVSLWDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQ 396
                ::|  ::|:| | ||:          | |: ||: |  | : || :|:  :|| ::
Db      337 -ATAKSLWTINSALRIRILCATYVNVNIRDID--------KIYVRTGIYHGGEPLCD 384
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Qy      397 RRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKG 456
                : :  |  : :|| ::: |: :| :|:|  :| ||: | |  :
Db      385 NVNTQRVPCSNPRWNEWLSYDMYIPDLPRAARLCLSI-C----SVKGRKGA------KE 432

Qy      457 KAQLLYYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSI 516
                : :|: :: :::  |    |:   |:| ::| :   |   :|  ||  :::::
Db      433 EHCPLAWGNINMFDYTDTLVSGKWALNLWAVPHGLED--LLNPIGVT-GSNPNK-GTPCL 488

Qy      517 SILLDNYCHPIALPKHRPTPDPEGDRVRAEM----------PNQLR---KQLEA 557
                |: |  || |:|:|: |  |: :||:|:|||          | :|:   :|| |
Db      489 ELEFDWFSNPVKFPDMTVIEBHANWTISRELGFNYSYAGLSNRIARDNELRESDKEQLRA 548

Qy      558 IIATDPLNPLTAEDKELLWHPRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVN 617
                |:|  : || |::|:|::  : ||  :|  || |::  : :| ||::  : ::|:|:
Db      549 ICTRDPLSEITEQEKDFIWSHRHYCVKTPEILPKLLLSVKWNSRDEVAQMYCL----VK 603

Qy      618 DQSALDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSA 676
                : |:|:|| ||||:| ||     ||   ||:  :|:|:|::  :|:||:|||: :  |
Db      604 DWPPIKPBQAMELLDCNYPDPMVRAFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNQ 663

Qy      677 LARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPFAVILEAYLRGCGTAMLHDFTQQV 736
                | | :|:||:|::|:| |  |:| ::|: :: :|  :|: | :|: | | : :|| :|:|
Db      664 LVRFLLKKALTNQRIGHPFFWFLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LSRQV 721

Qy      737 QVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKA 793
                |:::|:: ::: :  : :| :|  | :::::|::::         ||::|||:|:| |
Db      722 EAMEKLINLT-DI--LKQEKKDBTQKV--QMKFLVEQMRRPFMDALQGFISPLNPAHQL 776

Qy      794 GALVIECKVMASKKKPLWLEPKCADPTALS------NETIGIIFKHGDDLRQDMLILQI 847
                | ::::|||:  :|| :|:|::           : ::: |||  | :|||:||::|:
Db      777 GNLRLEECRIMSSAKRPLMLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQI 831

Qy      848 LRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDE 905
                :|:|| :|| ||::||:||||| : :|:|| ||| :  | |::: ||  |||  : :|
Db      832 IRIMENIWQNQGIDLRMLPYGCLSIGDCVGLIEVRSSHTIMQI--QCKGGLKGALQFNSH 890

Qy      906 VLSHWLKEKCPIEKFQAAVERRFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDF 965
                ||   ::| |:|::  :   :|:|::|||| |||  :|:|||: ||:|: : ||||:|||
Db      891 TLHQWLKDKNK-GEMYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDF 949

Qy      966 GHILGNYKSFLGINKERVPFVLTPDELFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHH 1023
                |||:||::| |:|:||||||||| |:|| |||:|:   ::|: |:|:: | ||||:|:|:
Db      950 GHFLDHKKKKFGYKRERVPFVLTQDLLIVISKGAQECTKTREFERFQEMCHKAYLAIRQH 1009

Qy     1024 TNLIIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAXXKYFLDQIEVCRDKGWTVQ 1083
                ||| |:|||:|| || || ::| ::|:|:  :|:| |:||| |  |:|:|: |||||| |
Db     1010 ANLFINLFSMMLGSGMPELQSPDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTK 1069

Qy     1084 FNWFLHLV 1091
                | ::|:
Db     1070 MDWIFHTI 1077
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RESULT 6
ID   Q8BTI9       PRELIMINARY;       PRT;    1064 AA.
AC   Q8BTI9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphatidylinositol 3-kinase catalytic subunit.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
```

```
Db  441  MW--PSVPDEKGELLNPAGTVRGNPNTESAAALVIYLPEVAPHPVYFPALEKILELGRH-  497
         ||               :::: ||                     ||:
Qy  534  PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPKL  592
              ::                  :::   : |||::::|:|: ::  |:|: ::|: ||
Db  498  ------GERGRITEEQL--QLRBILERRGSGELYEHEKDLVNKMRHEVQEHFPEALARL  549

Qy  593  FSSVKWGGQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLE  652
           :||:   ||::  |  :: |       ::::  ::::|    |: ::  ::|:||
Db  550  LLVTKWNKHEDVAQLSQMYLLCSWPE--LPVLSALELLDFSFPDCYVGSFAIKSLRKLT  607

Qy  653  DDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQ-  711
         || :|:||||||||:|::||  :  ||||| ||:|||||||||| |||||   :| |
Db  608  DDELFQYILLQLVQVLKYESYLDCELTKFLLGRALANRKIGHFLFWHLRSEM---HVPSV  663

Qy  712  --RFAVILEAYLRGCGTAMLHDFTQQVQIDMLQKVT--IDIKSLSAEKYDVSSQVISQL  767
           ||  ::|||  | ||::     :|:|:    :    ||:|:|:|:  |||||:||:|
Db  664  ALRFGLIMEAYCRG-STHHMKVLMKQGEALSKLKALNDFVKVSSQKTTKPQTKEMMHMCM  722

Qy  768  KQK--LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSN  825
         :|:   |::: || ||  :  ::   :    ::|| : | :|||||:::    :    ||
Db  723  RQETYMEALSHL------QSPLDDSTLLSEVCVBQCTFMDSKMKPLWIMYSSEEAGSAGN  776

Qy  826  ETIGIIFKGHGDDLRQDMLILQIILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDA  885
          |:|||||  |||||||: :||:| :|:|:::   :|||| | |||  ||: |:||:|:  
Db  777  --VGIIFKNGDDLRQDMITLQMIQLMDVLWKQEGLDLRMTPYGCLPTGDRTGLIEVVLHS  834

Qy  886  TTIAKIQ--QSTVGNTGAPKDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLG  943
          |||:||   ::  ::|  :|: | ||| | | :  :|| | |  |||||| |: ||||
Db  835  DTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIREFTLSCAGYCVATVVLG  893

Qy  944  IGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTS  1003
         ||||| |||||  :| |||||||| ||| |:: || |:||| |  |||   | :| :|
Db  894  IGDRHSDNIMIRESGQLFHIDFGHGFLGNFKTKFGINRRVPFLTYDFVHVIQQGKTNNS  953

Qy 1004  LHFQKFQDCVKAYLALRHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEED  1063
          :|: : |  :|| :|:||  ||  :: :  ::  |||  ::| | |:| ::|:|:::
Db  954  EKFRFRGYCERAYTILRRHGLLFLHLFALMRAAGLPELSCSKDIQYLKDSLALGKTEEE  1013

Qy 1064  AKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091
         | | | : ::  : |  |::| |||| |
Db 1014  ALKHFRVKFNEALRESWKTKVNWLAHNV  1041
```

RESULT 8
Q8C5Q7
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ID   Q8C5Q7      PRELIMINARY;      PRT;    260 AA.
AC   Q8C5Q7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide-3-kinase (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK077772; BAC37000.1; -.
FT   NON_TER        1      1
SQ   SEQUENCE   260 AA;  29624 MW;  91C63B59663BCC5 CRC64;

Query Match             23.1%;  Score 1335;  DB 11;  Length 260;
Best Local Similarity   97.7%;  Pred. No. 1.5e-95;
Matches  254;  Conservative   4;  Mismatches   2;  Indels   0;  Gaps   0;
```

```
Qy  843  LILIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAF  902
         ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db    1  LILIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTGAF  60

Qy  903  KDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFH  962
         ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  KDEVLNHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFH  120

Qy  963  IDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDCVKAYLALRH  1022
         ||||||||||||||||||||||||||||||||||:||||||||||||||:|||:||||||
Db  121  IDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGSSGKKTSPHFQKFQDVVVRAYLALRH  180

Qy 1023  HTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTV  1082
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  HTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTV  240

Qy 1083  QFNWFLHLVLGIKQGEKHSA  1102
         ||||||||||||||||||||
Db  241  QFNWFLHLVLGIKQGEKHSA  260
```

RESULT 9
Q8CI98
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ID   Q8CI98      PRELIMINARY;      PRT;    1037 AA.
AC   Q8CI98;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphatidylinositol 3-kinase catalytic delta polypeptide.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035203; AAH35203.1; -.
KW   Kinase.
SQ   SEQUENCE   1037 AA;  119130 MW;  4446B78B5F37A0E2 CRC64;

Query Match             23.0%;  Score 1329;  DB 11;  Length 1037;
Best Local Similarity   32.1%;  Pred. No. 3.8e-94;
Matches  356;  Conservative  203;  Mismatches  407;  Indels  142;  Gaps  40;
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Qy   38  IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRLG-PD  94
         :  :: ||| :  ||  |  | |    || :| : |  |: ||:    :||:||::|  |
Db   12  VVVDFLLPTG--------VYLNFPVSRNANLSTIKQVLWHRAQYEPL---FHMLSDPE  58

Qy   95  HFLL-LYQKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ  153
         : ||  : ||: | :  ::   :||  ||:     |:||:|:|:|| : :|:  | |:
Db   59  AYVFTCVNQTABQQELEDEQR--RLCDIQPFLPVL------RLVAREGDRVKKL-INSQ  108

Qy  154  LNALIGYDVTDVSNVHDDELEFTRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPLP----  208
         :  ||| : : : ||  :||:: |:|  :::  :  |:  :|  : |:: :| |
Db  109  ISLLIGKGLHEFDSLRDPEVNDFRTKM--RQFCEEAAAHRQQLGWEWLQYSFPLQLEPS  166

Qy  209  ---EVILLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSLMD  260
            :::||  :  | |:: :    |::|  ||||:|:: |||:|: :| |:|   ||| :|
Db  167  ARGWRAGLLRVSNRALLVNVKFEGSBEESFTFQVSTKDMPLALMACALRKKATVRPQPLVE  226

Qy  261  IPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGBEIHIVL---------D  308
         | :  :| | |||| ||:|||:| ||: ::| | | |  | ::
Db  227  QPE-----EYALQVNGRHEYLYGNYPLCHFQYICSCLHSGLTPHLTMVHSSSILAMRDEQ  281

Qy  309  TPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHSSVFTVSLWDCDRKFRVK-IRG  367
         : | ::|  ::| ||: :   |  ||::|| :|| :|||||:| ||| ||||||: |
Db  282  SNPAPQVQKPRAKPPP--------------------IPAKKPSS---VSLWSLEQPFSIELIEG  322

Qy  368  IDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTBEVLMNVWLEFSIKIKDLP  424
         | ||:|| :    |||:|:||||||||||||||:||| |||:|||:|:|||:||||||||
Db  323  RKV-----NADERMKLVVQAGLFHGNEMLCKTVSSSEVNVCSEPVWKQRLEFDISVCDLP  377
```

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OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97133288; PubMed=8978685;
RA   Leevers S.J., Weinkove D., MacDougall L.K., Hafen E., Waterfield M.D.;
RT   "The Drosophila phosphoinositide 3-kinase Dp110 promotes cell
RT   growth.";
RL   EMBO J. 15:6584-6594(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
CC       1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
DR   EMBL; Y09070; CAA70291.1; -.
DR   EMBL; AE003731; AAF55792.1; -.
DR   FlyBase; FBgn0015279; Pi3K92E.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase; Transferase.
SQ   SEQUENCE   1088 AA;  127005 MW;  ABDEF07902AB81C CRC64;
```

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Query Match             22.2%;  Score 1283;  DB 5;  Length 1088;
Best Local Similarity   33.1%;  Pred. No. 1.6e-90;
Matches  315;  Conservative 189;  Mismatches 333;  Indels 114;  Gaps 28;
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```
Qy    194 KLYAMHP--WVTSKPLPEYLLKKITNNCVPIVIHRSTTSQ--TIKVSADDTPGTILQSF 248
              :|| ||  ||:    |:||:  |:||::  ||:|||||:|  :|| ||| ::|||||
Db    189 RLLYEHPLRLANSTKMPE-LIRERHPTRTFLIVVKNENDQSTFLSVNEQDTPFSLTEST 247

Qy    249 FTKMAKKKSLMDIPESQNER--DFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLV 306
              |  | :|| :||  :||:   |::|:   |:::      |||:|  |||  | :::|
Db    248 LQKMNRSQMKM------NDRTSDYILKVSGRDEYLLGDYPLIQFLYIQEMLSD------- 294

Qy    307 LDTPPDALDEVRKEWPLVDDCTGVTGYHEQL---------TIHGKDHESVFTVSLW 355
              |   :|   |:  |||: :  |::|:||:|         | :|:|||::|||| :||
Db    295 -SAVPNVLQSVYRLE------SVINHHNEQAMVTKRPLPKKRTVH--LHKSI--SSLW 342

Qy    356 DCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKP---FTEEVLWNV 412
              |   |||:|  | |::| :|  | ::::|||  || ||:|:||:| :    ::||::||
Db    343 DMGNYFQLTLHSISNVNFDKTRALKVGVHVCLYHGDXKLCAQRSTSPNGNFDTFLFNDL 402

Qy    413 WLEFSIKIKDLPKGALLNLQYCGKAPALSGKTS----AEMPSPESKGKAQLLYYVNLL 467
              | : :|:||:|||  |:||:|  :||:| :|:       ::||:|:|: ||||||:||
Db    403 VMDFDIQMRNLPRMTRLCIVIFEVTKMSRSKKSSNNKDIALKDVPYNKNP---LAWVNTT 459

Qy    468 LIDHRFLLRHGEYLHMWQLSGKGEDQGSFNADKLTSA---------TNPDKENSMSIS 517
              :| |||:|:|| |:: :||:||:| ||||| ||:: |:         :|||||||||:|
Db    460 IFDHKDILRTGRHTLYTWTY------------ADDIQSVEVFHPLGTIEPNRKEBCALVD 508

Qy    518 I-LLDNYCHPIALPKHRPTDPEGDRVRAEMPNQLR---------KQLEAIIAT---D 562
              | :|||| :||| |  | | :||:|::| | ||:|         ||||:   |   |
Db    509 LTFLSSGTGTVRYPSEEVVLQYAADR--EQVNRLQRQLAGPEKPIKELKELMANYTGLD 565

Qy    563 PLNPLTABDKELLWHFRYESLKD-PKAYPKLFSSVKWGQQEIVAKTYQLLAKREWDQSA 621
              ||:||: |::||| :|  :|: |  || | :| :|: | ::||:||::|   ||  ||
Db    566 KIYEMVDQDRNAIWERRNDILRELPELSILLHCVVWKERDDVADMWYLLKQ--W--PL 620

Qy    622 LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFL 681
              :| :| ::|  |:|  | |  ||:| ||:|:|| |:|||||:|  :|||:|    |:||
Db    621 ISIERSLELLDYAYPDPAVRRFAIRCLHFLKDEDLLLYLLQLVQLVLGGTAMLHDFTQQVQVIDM 680

Qy    682 LKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM 741
              |:|||:|:|||  |||:|:|||  ||  |||:|  || |  :||  :|  ||:| :  ::|
Db    681 LERALRNQRIGHYFFWHLRSEM-QTPSMQTRFGLLLEVVLKGC-KHHVAPLRKQLHVLEK 738

Qy    742 LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNPQGSFRVPYDPGLKAGALVIEKC 801
              |:|  |||: | |:|   ||:|: :|:|:|:||:|    |::  | |  :|||:|||:|
Db    739 LKQGSLIAKKGSKEK-----VKTMLQDFLRDQRNSAVFQNIQNPLNPSRCSGVTPDRC 792

Qy    802 KVMASKKKPLWLEFKCADPTALSNETIGIIFKHGGDLRQDMLILQILRIMESIWETESLD 861
              |||:|:|:|||:||: |  | ||||:|||||:||||:|:|||:|||||||||:|||||:|
Db    793 KVMDSKMRPLWVFENADVNA---SDVHIIFKNGGDLRQDMLTLQMLRVMDQLWKRDGMD 849

Qy    862 LCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEE 919
              |:|||||:| |||:|:||||||| : :|||:   ||||||||: || |||| :|:|  ||
Db    850 FRMNIYNCISMEKSLGMIEVVRHAETIANIQKEKGMFSATSPFKKGSLLSWLKEHNKPAD 909

Qy    920 KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGIN 979
              | :||:| |:|:|| |||:|||| |:|| ||:||:|  || :|||||:|:||  :||::|
Db    910 KLNKAINEFTLSCAGYCVATVLGVADRHSDNIMVKRNGQLFHIDFGHILGHILSLFSMMISTG 969

Qy    980 KERVPFVLTPDFLFVNGTS-GKKTSLHFQDVCVKAYLALRHHTNLLILFSMMLMTG 1038
              |:||||| |::||:| |   ||||:|:|:|  ||:|| :|||||:||||||||:|:|
Db    970 RERVPFVLTHDFVYVINKGFNDRESKEFCHFQELCERAFLVLRKHGCLILSLFSMMISTG 1029

Qy   1039 MPQLTSKEDIEYIRIDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
              : :|:::: |:|:::|:::|:|:||  |::|||:|:||||||||::||:|||
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Db   1030 LPELSSEKDLDYIRETLVLDYTEEKAREHFRAKFSEALANSWKTISLNWASH 1080

RESULT 13
Q9PTE5
ID   Q9PTE5          PRELIMINARY;      PRT;   852 AA.
AC   Q9PTE5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphoinositide 3 kinase catalytic subunit (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Distal nephron;
RA   Al-Khalili O.K., Tran T., Eaton D.C.;
RT   "Molecular cloning of Xenopus laevis phosphoinositide 3 kinase
RT   catalytic subunit mRNA.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Distal nephron;
RA   Al-Khalili O.K., Eaton D.C.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF204924; AAF15300.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
FT   NON_TER       1       1
FT   NON_TER     852     852
SQ   SEQUENCE   852 AA;  98705 MW;  15C1F3CCDDE28884 CRC64;

Query Match             19.1%;  Score 1103.5; DB 13;  Length 852;
Best Local Similarity   33.1%;  Pred. No. 1e-76;
Matches  298;  Conservative 162;  Mismatches 310;  Indels 129;  Gaps  34;

Qy     135 IHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPK 194
               |:||||| |:  :|:|:  |:  :::
Db      16 LKVVBPVGNREEKI-LNREIGFAIGMPVCEFDMVKDSEVQDFRQNVLNVCKDSVELRDAN 74

Qy     195 -----LYAMHPWV-TSKPLPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTP 241
                     :||  :   |||  |||::|||    ::|:::|
Db      75 GPISRALVYVYPPNVESSSELPKHIESKLDKGQIIVWIWVISPNNEKQKYSLKINHDCVP 134

Qy     242 GTILQSFFTKMAKKKSLMDIPES-----QNERDFVLRVCGRDEYLVGETPIKNFQWVRQ 295
                ::  :  |::|    |::|::|         |||   :|:|| |||||
Db     135 EHVIAEAIRK--KPRSMLLSTEQLKLCVLEYQGKYILKVCGCDEYLLEKYPLSQYKYIRS 192

Qy     296 CLKNGEEIHVLDTPPDPALDEVRKEEWPIVDDCTGVTGYHEQLT-----IHGKDHESVF 350
                ::             ||| :: :||        :|:|    :|:
Db     193 CIMLGRMPNLML------MAKESLYNQIPV--DIFTMPSYSRRISTAAPYMNGETSAK-- 242
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Qy     351 TVSLWDCDRKPRVK--------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS 400
               :||| |                :|||:|:| |  | |  ||| | ||::|||
Db     243 --SLWAINSTLRIKILWATYVNVTIRDID---------KIYVRTGIYHGVEPLCDNVNT 290

Qy     401 PKPFTTEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
               |   ||| |  |  ::| :: ||      |:  |  :  |   :       :  ||
Db     291 QRVPCSNPRWNEWLLYDMFIPDLPRAARVCLSI-C----SVKGRKGA------KEEHCP 338

Qy     461 LYYVNLLIDHRPLLRHGEYVLHMWQLSGKGEDQ----GSFNADKLTSATNPDKENSMSI 516
               |   :||  |||| ||  ||  |  |  ||        :  | :|  :|:| |||:
Db     339 LAWGNINLFDYTDTLVSGKVALNLMPVPHGLEDLLNPIG------VSGSNPNKB-TPCL 390

Qy     517 SILLDNYCHPIALPKHRPTPDPEGDRVRAEM---------PNQLR----KQLEA 557
                :|| | :  ||| :       ||  ||:           :|:|       : :
Db     391 ELEFDCFSSPVKPPDMTAIEDHANKVLEREGYNYSHSGLSNRIVRENEVRENDKEQLRA 450

Qy     558 IIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVW 617
               :: :   :|  :: :|:|| : :| :|||  |:| :|||: :  |: |  |
Db     451 ISNRDPlSEITEQEKEFLWSHRLYCRNIPEVLSKLLLSVKWNCRDDVSQMYCLLKE---W 507

Qy     618 DQSALDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYILLQLVQAVKPEYHDSA 676
               :  ::  | :|  | ::|:|  ||  | ||:    | ||::||| :| |||||||||||
Db     508 --PAIRPEQAMELLDFNYPDRIVRSFAVSCLEKYLTDDKLSQFLIQLVQVMKYEQYLDNH 565

Qy     677 LARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQV 736
               |  |||| ::||||:||| |  : |||  |||  |: :  ||  | |::   |:  : :|
Db     566 LVRFLLKRALVNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LSKQV 623

Qy     737 QVIDMLQKVTIDIKSLsAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKA 793
                  :|||||: :::  |:|:|||| :::|:  |::||:|    |:|  :||:|: ||:|
Db     624 EAMEKLINLT-DI--LKQEKKDETQKV--QMKFLFEQMKRPDFMDALQGFTSPLNPAHQL 678

Qy     794 GALVIEKCKVMASKKKPLWLEFKCADPTA----LSNETIGIIFKHGDDLRQDMLIIQILR 849
               | ::|:  |:  :: |||  |  ||         ::|| | |:|||:|||||:|: ||:|
Db     679 GNLRLECRIMSSAKRPLWILSWENPDIMSEMLFLNNE---IIFKHGDDLRQDMLTIQIIR 735

Qy     850 IMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVL 907
               |||:||| ||||:|| ||| |: ||:|| |: |:  |::|::|:|  ||   |:||:|
Db     736 IMENIWQNQGLDLRMLPYGCLSIGDCVGLIVVRCSHTIMQI-QCKGGLKGALQFNSHTL 794

Qy     908 SHWLKEKCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFG 966
               | ||:|:|||:|::  : :|||SCAGYCVATF:LGIGDR:N|NIMV|::| LFHIDFG
Db     795 HQWLKDKNK-GETYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDSGQLFHIDFG 852

RESULT 14
Q61182
ID   Q61182          PRELIMINARY;      PRT;   1658 AA.
AC   Q61182;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide 3-kinase.
GN   PIK3C2A OR CPK-M.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb c;
RX   MEDLINE=96278830; PubMed=8662856;
RA   Molz L., Chen Y.W., Hirano M., Williams L.T.;
RT   "Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
RT   domain.";
RL   J. Biol. Chem. 271:13892-13899(1996).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; U52193; AAC52604.1; -.
DR   HSSP; P21707; 1BYN.
DR   MGD; MGI:1203729; Pik3c2a.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
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Db   867  LWENRYYCLKHPNCLPKILASAPNWKWAN---LAKTYSLLHQ---W--PPLCPLAALELL  918
          :|| ::  | |   |  :  : | :| ::          :           :  :  :
Qy   632  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARPLLKRGLRNKRI  691

Db   919  DAKFADQGVRSLAVSWMEAISDDELADLLPQFVQALKYEIYLNSSLVRFLLSRALGNIQI  978
          | :   : |  :  : : |::    | :  |:  :| |:| ||:|| | ||| | |||
Qy   692  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKS  751

Db   979  AHSIYWLLKDAL-HDTHFGSRYEHVLGALLSVGGKGLREELSKQMKLVQLLGGVAEKVRQ  1037
          | : :::  :   :|:  | | ::| |  :    || ::| |:| |: | |||  :
Qy   752  LSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPL  811

Db  1038  ASGS----TRQVV-LQKSMERVQSFFLRNKCRLPLKPSLVAKELNIKSCSFFSSNAMPL  1091
          :|       |:    |: :||| |:| |||  ||| |:| | || || |||: |: ||
Qy   812  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETESLDLCLLPYGCIS  871

Db  1092  KVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKIWLKEGLDLRMVIFRCLS  1148
          : | :  |    | :| ::|| |  ||||||| :| |:|:|||| :| |||  :|| ||
Qy   872  TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYS  931

Db  1149  TGRDRGMVELVPASDTLRKIQVE-YGVTGSFKDKPLAEWLRKYNPSEEYEKASENFIYS  1207
          :| | || |:  |:||||:|| |  |:||||||:| | || || || :|||| |||||
Qy   932  CAGYCVATPVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDF  991

Db  1208  CAGCCVATVVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRDRAPPVLTSDM  1267
          |   ::||  |:| ::  |   :: || :  :|  ::|:     | | |:| |||:||
Qy   992  LFVMGTSGKKTSLHFQKPQDVCVKAYLALRHHTNLLIILFSMWLMTGMPQLTSKEDIEYI  1051

Db  1268  AYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPELTSIQDLKYV  1326
           || | ||  | | | | |: :|||| |: |||||| ||| ::||:|||:|||||:||
Qy  1052  RDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQPNWFLH  1089

Db  1327  RDALQPQTTDAEATIFFTLRLIESSLGSIAT-KPNFFIH  1363
          |||  |  |||| :|||||: ||||||||:|  |||||:
```

RESULT 15
O00443

ID	O00443;	PRELIMINARY; PRT; 1686 AA.
AC	O00443;	
DT	01-JUL-1997 (TrEMBLrel. 04, Created)	
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Phosphoinositide 3-kinase.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=97479209; PubMed=9337861;	
RA	Domin J., Pages F., Volinia S., Rittenhouse S.E., Zvelebil M.J.,	
RA	Stein R.C., Waterfield M.D.;	
RT	"Cloning of a human phosphoinositide 3-kinase with a C2 domain which	
RT	displays reduced sensitivity to the inhibitor wortmannin.";	
RL	Biochem. J. 326:139-147(1997).	
CC	-!- SIMILARITY: CONTAINS 1 C2 DOMAIN.	
DR	EMBL; Y13367; CAA73797.1; -.	
DR	HSSP; P21707; 1BYN.	
DR	Genew; HGNC:8971; PIK3C2A.	
DR	InterPro; IPR000008; C2.	
DR	InterPro; IPR001263; PI3Ka.	
DR	InterPro; IPR002420; PI3K_C2.	
DR	InterPro; IPR000341; PI3K_ras_bind.	
DR	InterPro; IPR000403; PI3_PI4_Kinase.	
DR	InterPro; IPR001683; PX.	
DR	Pfam; PF00168; C2; 1.	
DR	Pfam; PF00613; PI3Ka; 1.	
DR	Pfam; PF00792; PI3K_C2; 1.	
DR	Pfam; PF00794; PI3K_rbd; 1.	
DR	Pfam; PF00454; PI3_PI4_kinase; 1.	
DR	Pfam; PF00787; PX; 1.	
DR	SMART; SM00239; C2; 1.	
DR	SMART; SM00145; PI3Ka; 1.

Continuation of annotation:

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DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_Kinase.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00312; PX; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   PROSITE; PS50195; PX; 1.
KW   Kinase.
SQ   SEQUENCE  1658 AA;  187439 MW;  BBCC8E581DB20F20 CRC64;

Query Match             18.6%;  Score 1076.5;  DB 11;  Length 1658;
Best Local Similarity   28.0%;
Matches  330;  Conservative 198;  Mismatches 381;  Indels 269;  Gaps  39;
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Pred. No. 3.6e-74;

Qy   108  EIYDKTQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLN--ALIGYDVTDV  165
          :|  :|| |: :|  :   : |  ||  :  :            |:|    ||:|     :
Db   259  QISPKSEDINKPD----W--LDLDPWDAVLLEERSPS---CHLERKVNGKSLSGATVTRS  309

Qy   166  SNVHDDELEFTRRRLVTPRMAEVAGRDP------------------------K  194
          ::  :  |:        |:  |:  |  :                          :
Db   310  QSLIIRTAQFTKAQ------GQVSQKDPNGTSSLPTGSSLLQEFVQNDEVAAFCQSIMK  363

Qy   195  LYAMHPWVTSKPLPEYLLKKIT---NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFPT-  250
          | :  |:   ||| | |||:||      ||::|  ::  :   ::|  ::|  | |  |
Db   364  LKTKFPYTDHCTNPGYLLSPVTVQRNMC------GENASVKVSI-EIEGLQLPVTFTC  414

Qy   251  -----KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNGE  301
                | |:| ||  :|| : |||   |:|:|||::| |     :| :  :  | |  :|
Db   415  DVSSTVEIIMQALCWVHDDLNQVDVGSYILKVCGQEEVLQNNHCLGSHEHIQNCRKWDT  474

Qy   302  EIHLVLDT----------PPDALDEVRKE------EWPLVDDCTG------VTGYHEQL  339
          ||:  |             | | ::  ::|       | ||| |         || |::|
Db   475  EIKLQLLTLSAMCQNLARTAEDDEAPVDLNKYLYQIEKPYKEVWTRHPVEELLDSYHYQV  534

Qy   340  TI---HGKDHESVFTVSLWDCCDRKFPVKIRGIDIPV-----------LPR--TADLT-  380
          |:    ::  : |  |: |   ::| | :  | | :            |     |||
Db   535  ELALQTENQHRAVDQVI--KAVRKICSALDGVETPSVTEAVKKLKRAVNLPRNKSADVTS  592

Qy   381  ------------VFVEANIQYGGQVL----------CQRRT------  399
                       :  ::::|  |:            | :|
Db   593  LSGSDTRKQNSTKGSLNPENPVQVSMDHLTTAIYDLLRLHANSSRCSTGCPRGSRNIKEAW  652

Qy   400  ------------------SPKPFTEEVL  409
                             |  |  | |:
Db   653  TATEQLQFTVYAAHGISSNWVSNYEKYYLICSLSHNGKDLFKFPIQSKKVGTYKNFFYLIK  712

Qy   410  WNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMFSPESKGKAQLLYYVNLL  467
          |: |:  :||| :| : ||| | :|   |  | |||: : |   ||::|| | | | ||
Db   713  WDELIIFPIQISQLPLESVLHLTLFGVLNQSSGSSPDSNKQRKGPEALGK------VSLT  766

Qy   468  LIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPI  527
          |:| :|||   |  | :|  |: :        :| |::: | ||:||: || | |
Db   767  LFDFKRFLITCGTKLLYLWTSSHTNSIPGAI------PKKSYVMERIVLQVDF----  812

Qy   528  ALPKIRPTP------DPEGDR--VRAE---MENQLRKQLEAIIATDPLNPLTAEDKEL  574
          | |:  | |      :| |:    |:|    |::|| || : |:| |:  :|||||::
Db   813  ------PSPAFDIIYTSPQIDRNIIQQDKLETLESDIKGKLLDIIHRDSSFGLSKEDKVF  866

Qy   575  LWHFRYESLKDPKAYPKLFSSV---KWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL  631
          |  | ||| |||  | ||| |     ||| |::|  |:||||||| ||| | ||| ||||
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DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00312; PX; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   PROSITE; PS50195; PX; 1.
KW   Kinase.
SQ   SEQUENCE  1686 AA;  190736 MW;  E9311C803025C96F CRC64;

Query Match          18.5%;  Score 1074;  DB 4;  Length 1686;
Best Local Similarity   28.9%;  Pred. No. 5.8e-74;
Matches 309;  Conservative 178;  Mismatches 343;  Indels 238;  Gaps 32;


Qy   194 KLYAMHPWVTSKPLPEYLLKKIT---NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT  250
             || : |||:||           ||:| |||||:  |  ::||: :|
Db   390 KLKTKFPYTNHRTNPGYLLSPVTAQRNIC--------GENASVKVSI-DIEGFQLPVTFT  440

Qy   251 ------KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNG   300
               :|:   :|: ||||:|      ||:|||:    :    :|
Db   441 CDVSSTVEIIIMQALCWVHDDLNQVDVGSYVLKVCGQEVLQNNHCLGSHEHIQNCRKWD  500

Qy   301 EEIHLVL-------------------DTPPDPALDEVRKGEWPLVDDCTG---------VT  333
             :|: :                       :|::|  :|
Db   501 TEIRLQLLTPSAMCQNLARTAEDDETPVD----LNKHLYQIEKPCKEAMTRHPVEELID  555

Qy   334 GYHEQ----LTIHGKDH---------------ESVFTVSLWDCDRKFRVKIRGIDIPVL  373
            |:|:|    |:  |                  |::|:  :|
Db   556 SYHNQVELALQIENQHRAVDQVIKAVRKICSALDGVETLAITESVKKLK---RAVNLP-R  611

Qy   374 PRTADLTVFV-----------------EANIQYGGQVLCQRRT------------SP-----  401
            :|:|:|                     ||||        |||
Db   612 SKTADVTSLFGGEDTSRSSTRGSLNPENPVQVSINQLTAAIYDLLRLHANSGRSPTDCAQ  671

Qy   402 ------------------------------------------------------------  401
Db   672 SSKSVKEAWTTEQLQFTIFAAHGISSNMVSNYEKYYLICSLSHNGKDLFKPIQSKKVGT  731

Qy   402 -KPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKA  458
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Db   732 YKNFYLIKWDELIIFPIQISQLFLESVLHLTLFGILNQSSGSSPDSNKQRKGPEALGK-  790

Qy   459 QLLYVNLLLIDHRFLLRGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISI  518
             ::   |||:||                          ::  :|:
Db   791 ----VSLPLCDFRRFLTCGTKLLYIWTSS-----------------HTNSVPGTV  824

Qy   519 LDDNY-CHPIALPKHRPTP----------DPEGDRVRAE------MENQLRKQLEAIIATDPL  564
             :    | : :|||   |          |  |:|:        |:||:|::   :  |
Db   825 TKKGVMERIVLQVDFPSPAFDIYTTPQVDRSIIQQHNLETLENDIKGKLLDILHKDSS  884

Qy   565 NPLTAEDKELLWHFRYESLKDPKAYPKLFSSV---KWGGQEIVAKTYQLLAKREVWDQSA  621
             :| :|||| ||: ||: :|          ||   :|:|:|  :||
Db   885 LGLSKEDKAFLWEKRYYCFXHPNCLPXIILASAPNWKWGN---LAKTYSLLHQ---W--PA  936

Qy   622 LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARPL  681
             | |: :||| ::   :| : :||| |:  :|   : ||||::|: :|:
Db   937 LYPLIALELLDSKPADQEVRSLAVTWIEAISDDELTDLLPQFVQALKYEIYLNSSLVQFL  996

Qy   682 LKRGLRNKRIGHFLPWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM  741
             |: |||:: |:: |:|  :| :|||  |  :   |::|:||   :|:|||  :|::|
Db   997 LSRALGNIQIAHNLYWLLKDAL-HDVQFSTRYEHVLGALLSVGGKRLREELLKQTKLVQL  1055

Qy   742 LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKC  801
             |::  :|   :|:     ::  ||:: :|       |:|:  : |::  :|:: :: :|
Db  1056 LGGVAEKVRQASGS---ARQVV-LQRSMERVQSFFQNKCRLPLKPSIVAKEINIKSC  1109

Qy   802 KVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETESLD  861
             :| :|: |:|      :|:|   |::    ||| ||| ::::| ::| |::
Db  1110 SFFSSNAVPLKVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKIWLKEGLD  1166

Qy   862 LCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKF  921
             |::|  :|:|||     ||: || : ::|:|||:  ||: :||   |:  :: | ||:
Db  1167 LRMVIFKCLSTGRDRGMVELVPASDTLRKIQVB-YGVTGSFKDKPLAEWLRKYNPSEEEY  1225

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             :|:|:|||||||     |||||:||||||||:: || :|||||||:  |: :|:
Db  1226 EKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRD  1285

Qy   982 RVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLALRHHTNLLILFSMMLMTGMPQ  1041
             | ||: :|:||::|:::|:|   :|:|: || |:|  |  ::|  |:: :: :|  |
Db  1286 RAPFVLTSDMAYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPE  1344

Qy  1042 LTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH  1089
             ||| :: : ||||         |:|:||::   ::|||  ||  |::|
Db  1345 LTSIQDLKYVRDALQPQTTDAEATIFFTRLIESSLGSIAT-KFNFFIH  1391


Search completed: February 15, 2004, 02:06:56
Job time : 104 secs
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OM protein - nucleic search, using frame_plus_p2n model

```
                  GenCore version 5.1.6
        Copyright  (c) 1993 - 2004  Compugen Ltd.

Run on:      February 15, 2004, 02:10:12 ; Search time 5171 Seconds
                         (without alignments)
                         5179.565 Million cell updates/sec

Title:            US-09-974-573-1
Perfect score:    5790
Sequence:         1 MELENYEQPVVLREDNRRRR.........QFRWFLHLVLGIKQGEKHSA 1102

Scoring table:    BLOSUM62
                  Xgapop  10.0 , Xgapext   0.5
                  Ygapop  10.0 , Ygapext   0.5
                  Fgapop   6.0 , Fgapext   7.0
                  Delop    6.0 , Delext    7.0

Searched:         22781392 seqs, 1215223056 residues

Total number of hits satisfying chosen parameters:        45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlh
 -Q=/cgn2_1/USPTO.spool/US09974573/runat_11022004_180014_18105/app_query.fasta_1.1287
 -DB=EST -QFMT=fasta -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=30 -TIMEOUT=7
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        EST:*
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       4:  em_estmu.:*
       5:  em_estov.:*
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      12:  gb_est3.:*
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      16:  em_eston:*
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      25:  em_gss_rod.:*
      26:  em_gss_phg.:*
      27:  em_gss_vrl.:*
      28:  gb_gss1:*
      29:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID		Description
1	5484	94.7	4805	11	AK040543	AK040543	Mus muscu
2	1429	24.7	3866	11	AK051885	AK051885	Mus muscu
3	1363	23.5	4731	11	AK090116	AK090116	Mus muscu
4	1361	23.5	880	14	CD171634	CD171634	AGENCOURT
5	1347.5	23.3	4996	11	AK081350	AK081350	Mus muscu
6	1339	23.1	4852	11	AK040867	AK040867	Mus muscu
7	1335	23.1	1937	11	AK077772	AK077772	Mus muscu
8	1286.5	22.2	915	10	BB619812	BB619812	BB619812
9	1268.5	21.9	1127	10	BG389556	BG389556	602414255
10	1244	21.5	861	13	BU517397	BU517397	AGENCOURT
11	1181.5	20.4	1043	13	BQ072706	BQ072706	AGENCOURT
12	1170	20.2	976	14	CA966024	CA966024	CcLL03a12
13	1163.5	20.1	761	10	BG615507	BG615507	602642812
14	1106	19.1	896	14	CA471197	CA471197	AGENCOURT
15	1036.5	17.9	852	13	BQ232683	BQ232683	AGENCOURT
16	1032	17.8	649	9	AJ450490	AJ450490	AGENCOURT
17	1029	17.8	1170	12	BM920113	BM920113	AGENCOURT
18	977.5	16.9	695	14	CA376640	CA376640	655052 NC
19	953	16.5	542	9	AW786623	AW786623	119902 MA
20	951	16.4	581	14	CA579737	CA579737	KO741F09-
21	951	16.4	583	14	CA577647	CA577647	KO712D03-
22	928	16.0	558	12	BI775259	BI775259	467670 MA
23 c	921	15.9	665	12	BM935801	BM935801	UI-M-BH3-
24	919	15.9	575	2	HSM062224	Bx504620	Homo sapi
25	917.5	15.8	806	13	BU598381	BU598381	AGENCOURT
26	889	15.4	547	10	BG019410	BG019410	dab08e12.
27 c	886	15.3	769	29	BX185016	BX185016	Danio rer
28	851	14.7	577	12	BM878584	BM878584	if42b10.Y
29	820.5	14.2	1627	11	AK003230	AK003230	Mus muscu
30	816	14.1	664	10	BB613870	BB613870	BB613870
31	814	14.1	509	12	BI326875	BI326875	AR07H08i
32	782	13.5	499	9	AW761865	AW761865	uq26f05.Y
33	771	13.3	576	9	AW491415	AW491415	UI-M-BH3-
34	743.5	12.8	759	12	BI459766	BI459766	603200816
35	738	12.7	861	14	CA472545	CA472545	AGENCOURT
36	729	12.6	617	14	CA352614	CA352614	623926 NC
37	721.5	12.5	1069	12	BM557370	BM557370	AGENCOURT
38	719.5	12.4	661	13	BW037945	BW037945	BW037945
39	719	12.4	630	14	CA346520	CA346520	677427 NC
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44	684.5	11.8	3211	11	BC027029	BC027029	Mus muscu
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ALIGNMENTS

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RESULT 1
AK040543
LOCUS       AK040543      4805 bp    mRNA    linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
            library, clone:A430105015 product:phosphoinositide-3-kinase,
            catalytic, gamma polypeptide, full insert sequence.
ACCESSION   AK040543
VERSION     AK040543.1  GI:26087918
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   10349636
PUBMED   99279253
REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M. Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE   4
AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
             Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
             Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
             Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
             Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
             Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
             Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J.,
             Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
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             Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
             Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
             Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
             Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
             Ring,B., Ringwald,M., Rodriguez,J., Sakamoto,N., Sasaki,H.,
             Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
             Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
             Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
             and Hayashizaki,Y.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409 (6821), 685-690 (2001)
MEDLINE   21085660
PUBMED   11217851
REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4805)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,T.,
             Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,S., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,Y., Sakazume,N.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome

             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
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     misc_feature   106..3415
                     /note="Phosphoinositide-3-kinase, catalytic, gamma
                     polypeptide (MGD|MGI:1353576, GB|NM_020272, evidence:
                     BLASTN, 99%, match=3776)
                     putative"
BASE COUNT   1261 a   1215 c   1149 g   1180 t
ORIGIN

Alignment Scores:
Pred. No.:   Length: 4805
Score: 0   Matches: 1038
Percent Similarity: 5484.00   Conservative: 31
Best Local Similarity: 96.92%   Mismatches: 33
Query Match: 94.11%   Indels: 1
DB: 94.72%   Gaps: 0
                              11

US-09-974-573-1 (1-1102) x AK040543 (1-4805)

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Db   166 CGGAGGATGAAGCCACGGCAGCGCAGCGGCAGGCGGCCGTGTCTTCCATGGAGCTCATCCCCATT 225

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrHisAlaLeuLeuHis 60
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Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
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Qy   81 ThrSer-ValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuTy 100
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Db   346 ACCAGCGTGGGTCGCGGAGTTCTACCACCGATTGGGCCGGACCAATTCCTCCTGCTCTA 405

Qy   100 rGlnLysLysGlyGlnTrpTyrGlnIleTyrAspTyrTyrGlnIleValGlnThrLeuAs 120
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Db   466 CTGCCTGCATTACTGGAAGTTGATGCACAAGACCCTGGCCAGATCCACGTGGTACAGCG 525

Qy   140 gHisAlaProSerGluGluGlnThrLeuAlaPheGlnArgGlnAsnAlaLeuIleGlyTy 160
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Db   526 ACACGTACCTTCTGAGGAGCAGACCTTGGCTTTCCAGAAGCAGCTCACCTCCCTGATTGGCTA 585

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Qy    540 yAspArgValArgAlaGlyMetProAsnGlnLeuArgLysGlnLeuAlaIleIleAl 560
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Qy    620 rAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVa 640
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Qy    640 lArgAlaIleAlaValGlnLysLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLe 660
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Qy    660 uLeuGlnLeuValGlnAlaValGlnAlaLysTrpPheGluProTyrHisAspSerAlaLeuAlaArgPh 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 TCTCCAGCTGGTACAGGCTGTGAAATTGAACCGTACCACAGACAGTGCGCTGGCCAGATT 2145

Qy    680 eLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuAr 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 CCTGCTGAAGCGTGGCTTGCGGAACAAAAGAATCGGTCACTTCTTGTTCTGGTTCCTGCG 2205

Qy    700 gSerGlulleAlaGlnSerArgHisTyrGlnArgPheAlaValLeuGluLeuAlaTy 720
              ||||||||||||||||||||||||||||||||||||||||||||||
Db   2206 AAGTGAGATCGCACAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATCCTGGAGCGTA 2265

Qy    720 rLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAs 740
              ||||||||||||||||||||||||||||||||||||||||||||::::
Db   2266 CCTGCGAGGCTGTGGCACAGCCATGTTGCAGGACTTCACACAGCAGGTCCAGTGATTGA 2325

Qy    740 pMetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSe 760
              :||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 GATGTTACAGAAAGTCACCATTGATATTAAATCGCTCTCGGCAGAGAAGTATGACGTCAG 2385

Qy    760 rSerGlnValIleSerGlnLysLeuGlnLysGlnAsnLeuAsnLeuPr 780
              ||||||||||||||||||||||||||||||||||||||||
Db   2386 TTCCCAAGTTATTTCACAGCTTAAGCAAAAGCTTGAAAGCCTTCAGAACTCCAATCTCCC 2445

Qy    780 oGlnSerPheArgValProTyrLeuTrpLeuGluPheLysProGlyLeuLysAlaLeuValIleGluLuY 800
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 CGGAAAGCTTTAGAGTTCCCTATGCTTCCTATGATCTCTTAAACTATGTTCGTGCTGCGA 2505

Qy    800 sCysLysValMetAlaSerLysLysProLeuPheLysLysGlyAlaAspPr 820
              |:::||||||||||||||||||||||||||||||||||||||||||||
Db   2506 ATGCAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTAAGTGTGCTGATCCC 2565

Qy    820 oThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysLysGlyAspArgGl 840
              ||||||||||||||||||||||||||||||::||||||||||||||||||||||
Db   2566 CACAGTCCTATCCAACGAAACCATTGGAATCATCTTTAAACATGGTGATGATCTGCGCCA 2625

Qy    840 nAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLe 860
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 AGACAATGTTGATCTTGCAGATTCTACGCGATCCATTGGGGACTGAATCTCT 2685

Qy    860 uAspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyTyrAspLysMetIleGl 880
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 GGACCTGTGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGATCGA 2745

Qy    880 ulleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGl 900
```

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Qy    160 rAspValThrSerAlaArgValHisAspAspArgLeuGluPheThrArgArgGle 180
              ||||||||||||||:::||||||||||||||||||||||||||||||||
Db    586 TGACGTCACTGCACATCAGCAATGTCCACGATGATGATGAGAGTTCACTCGCCGCCGTCT 645

Qy    180 uValThrProArgMetAlaGlyValAlaGlyTyrArgAspProLysLeuTyrAlaMetHisPr 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 GGTTACGCCCCGCATGGCTGGCCGGGATGCCAAACTCTATGCTATGCACCC 705

Qy    200 oTrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVa 220
              ||||||||||||||||||||||||||||||||::::||||||||||||||||
Db    706 TTGGGTAACGTCCAAACCTCTCCCAGACTACCTGTCAAAAAGATTGCCAACAACTGCAT 765

Qy    220 lPheIleValIleHisArgSerThrArgGlnThrIleLysValSerAlaAspAspTh 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 CTTCATCGTCATCCACCGCGGTACCCACCAGCCAAACCATCAAGGTCTCCGCAGATGATAC 825

Qy    240 rProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysHisLysSerLeuMetAs 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 TCCTGGTACCATCCTTCAGAGCTTCTTCACCAAGATGGCCAAGCATAAGAGTCCCTAATGAA 885

Qy    260 pIleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTy 280
              ||||||||||||||||||||||||::||||||||||||||||||||||||||
Db    886 TATCTCAGAAAGTCAAAGTGCAGGATTTTGTATTGCGGGTTTGTGGGCCGGATGAGTA 945

Qy    280 rLeuValGlyThrProIleLysAsnPheGlnIleTrpValArgGlnCysLeuUsyAsnGl 300
              ||||||||||||||||||||||||||||||||||||||||||||||
Db    946 CCTGGTGGGTGAAACACCCCTCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGG 1005

Qy    300 yGluGlulleHisLeuValLeuAspHisProLeuValAlaAspAspLeuHisGlyGlnLeuTh 320
              |:::|||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 AGATGAAATACACCTCGGTGCTGGATGACACTGGAGTGACTGAGGTGAGGA 1065

Qy    320 sGluGluTrpProLeuValAspAspCysThrrGlyTyrValThrGlyTyrHisGlnLeuTh 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 GGAAGAATGGCCGCTGGTGGATGACACTGGAGTGCACCGGCTACCACAGCAGCTGAC 1125

Qy    340 rIleHisGlyLysAspHisGluSerValPheThrThrValSerLeuTrpAspCysAspArgGly 360
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 CATCCATGGAAAGGACCACGAGAGTGTTTTCACCACAGTGTCTTTGTGGGACTGCGACCGAAA 1185

Qy    360 sPheArgValLysGlyArgGlyIleGluAspIleProValLeuProArgThrAlaAspLeuTh 380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 GTTCAGGGTCAAGATCAGAGGCATTGAATCCCGTGCCTCGCCTGTCCTCGGAACACCGACCTCAC 1245

Qy    380 rValPheValGlnAlaAsnIleGlnTyrGlyGlnLeuCysGlnInArgGlnThrSe 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TGTGTTTGTGCAGGCAAACATCCAGTACGGGGCAACAAGTCCTCTGCCAAAGGAGAACCAG 1305

Qy    400 rProLysProPheThrGluValTrpAsnValTrpLeuGluPheSerIleLysyIl 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 CCCTAAGCCCTTTGCCAAGAGAGAGTACTCTGGAATGTGTGGCTGGAGTTTGGCATCAAAAT 1365

Qy    420 eLysAspLeuProLysGlyLeuAlaLeuAsnLeuGlnIleTyrCysGlyLysValAlaProAl 440
              |||||||||||||||||||||||||||||||||||||||||||||||::::
Db   1366 CAAAGACTTGCCCAAAGGGGCTCTATTGAACCTGCAGATCTACTGCTGTAAAAGCCCCATC 1425

Qy    440 aLeuSerGlyLysThrSerArgAlaGluMetProSerGluSerProLysGlyLysAlaGlnLe 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 ACTGTCCAGCAAGGGCTTCTGCAGACTCCAGGGTCCAAGGGCAAAGCCCAGCT 1485

Qy    460 uLeuTyrTyrValAsnLeuLeuLeuIleAspLeuAsnArgArgPheLysProArgHisGlyGluTy 480
              ||||||||||||||||||||||||||||::|||||||||||||||||||||||||||
Db   1486 TCTCTATTACGTGAACTTGCTGTTAATAGATCCAGATATCTCCAGAGGCTTCAATGCTAA 1545

Qy    480 rValLeuHisMetTrpGlnLeuSerGlyLysGluAspGlnGlyGlnSerPheAsnAlaAs 500
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 TGTGCTCCACATGTGGCAGATATCTCGGCAAGAGGACCAGGGCAGGGGCAGTCAATGCTGA 1605

Qy    500 pLysLeuThrSerAlaThrAsnProAspLysLysGluAsnSerMetSerIleIleLeuLeue 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 CAAGCTTGCACTGCTACTCCTGACAACAATCCTGACAAGAAGGAGAACTCATTCCATCCTGCT 1665
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Db    2746  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
            GATTGTAAAGGATGCCCAACGATCGCTCAAATTCAGCAAGCACAGTGGGTAACACGGG  2805

Qy     900  yAlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluLysLy  920
            |||||||||||||||:::|||||||||||||||||||||||||||||||:||||||
Db    2806  GGCATTCAAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATGTCCATTGAAGAAAA  2865

Qy     920  sPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPh  940
            ||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db    2866  GTTTCAGGCGCCGAGTGGAAAGGTTTGTTTACTCCTGTGCAGGCTACTGTGCCACATT  2925

Qy     940  eValLeuGlyIleGlyTyrAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLe  960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2926  TGTTCTTGGATCGGTGACAGGCACAACGACACATTATGATCTCAGACAGGAAACCT  2985

Qy     960  uPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLy  980
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2986  ATTTCATATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCAATAA  3045

Qy     980  sGluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLy  1000
            ||||||||||||||:|||||||||||||||||:::||||||||||||||||||||
Db    3046  AGAGAGAGTGCCCCTTCGTCCTAACCCCGACTTCTTGTTTGTGATGGGATCTTCTGGAAA  3105

Qy    1000  sLysThrSerLeuHisPheGlnLysAspValCysValLysValAlaTyrLeuAlaLe  1020
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3106  AAAGACAAGTCCACACTTCCAGAAATTCCAGAGTCTGTGTTAGAGCTTACCTAGCTCT  3165

Qy    1020  uArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPr  1040
            |||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db    3166  TCGGCCATCACCAACAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGGAATGCC  3225

Qy    1040  oGlnLeuThrSerLysGluAspIleTyrIleArgArgAspAlaLeuThrValGlyLysSe  1060
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3226  CCAGCTGACAAGCAAAGAGGACAATTGAATATACCGGGATGCCCTCACCGTGGGAAAAAG  3285

Qy    1060  rGluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTh  1080
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3286  CGAGGAGGACGCCTAAGAAATATTTCCTTGATCAGATCGAAGTCTGCAGAGACAAAGGATG  3345

Qy    1080  pThrValGlnPheAsnTrpPheLeuValLeuGlyHisGluLeuGlyIleLysGlyLysHi  1100
            ||||||||:||||||||||||||||||||||||||||||||||||||||
Db    3346  GACTGTGCAGTTTAACTGGTTCCTACATCTTGTTCTTGGCATCAACAAGGAGAAAGCA  3405

Qy    1100  sSerAla  1102
            |||||||
Db    3406  CTCCGCT  3412
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RESULT 2
AK051885
LOCUS　　　　AK051885　　　　3866 bp　　mRNA　　linear　HTC 05-DEC-2002
DEFINITION　Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
　　　　　　　enriched library, clone:D23001E05 product:phosphatidylinositol
　　　　　　　3-kinase, catalytic, alpha polypeptide, full insert sequence.
ACCESSION　　AK051885
VERSION　　　AK051885.1　GI:26094824
KEYWORDS　　HTC; CAP trapper.
SOURCE　　　Mus musculus (house mouse)
ORGANISM　　Mus musculus
　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE　　1
AUTHORS　　Carninci,P. and Hayashizaki,Y.
TITLE　　　High-efficiency full-length cDNA cloning
JOURNAL　　Meth. Enzymol. 303, 19-44 (1999)
MEDLINE　　99279253
PUBMED　　　10349636
REFERENCE　　2
AUTHORS　　Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
　　　　　　Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE　　　Normalization and subtraction of cap-trapper-selected cDNAs to
　　　　　　prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL　　Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE　　20499374
PUBMED　　　11042159
REFERENCE　　3
AUTHORS　　Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
　　　　　　Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
　　　　　　Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
　　　　　　Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
　　　　　　Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
　　　　　　Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
　　　　　　Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE　　　RIKEN integrated sequence analysis (RISA) system--384-format
　　　　　　sequencing pipeline with 384 multicapillary sequencer
JOURNAL　　Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE　　20530913
PUBMED　　　11076861
REFERENCE　　4
AUTHORS　　Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
　　　　　　Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
　　　　　　Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
　　　　　　Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
　　　　　　Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
　　　　　　Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
　　　　　　Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
　　　　　　Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
　　　　　　Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
　　　　　　Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
　　　　　　Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
　　　　　　Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
　　　　　　Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
　　　　　　Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
　　　　　　Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
　　　　　　Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
　　　　　　Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
　　　　　　Wynshaw-Boris,A., Yoshida,N., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
　　　　　　and Hayashizaki,Y.
TITLE　　　Functional annotation of a full-length mouse cDNA collection
JOURNAL　　Nature 409 (6821), 685-690 (2001)
MEDLINE　　21085660
PUBMED　　　11217851
REFERENCE　　5
AUTHORS　　The FANTOM Consortium and the RIKEN Genome Exploration Research
　　　　　　Group Phase I & II Team.
TITLE　　　Analysis of the mouse transcriptome based on functional annotation
　　　　　　of 60,770 full-length cDNAs
JOURNAL　　Nature 420, 563-573 (2002)
REFERENCE　　6　(bases 1 to 3866)
AUTHORS　　Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
　　　　　　Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
　　　　　　Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
　　　　　　Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J.,
　　　　　　Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
　　　　　　Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
　　　　　　Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
　　　　　　Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
　　　　　　Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
　　　　　　Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
　　　　　　Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
　　　　　　Muramatsu,M. and Hayashizaki,Y.
TITLE　　　Direct Submission
JOURNAL　　Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
　　　　　　Physical and Chemical Research (RIKEN), Laboratory for Genome
　　　　　　Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
　　　　　　RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
　　　　　　Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
　　　　　　URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
　　　　　　Fax.81-45-503-9216)
COMMENT　　cDNA library was prepared and sequenced in Mouse Genome
　　　　　　Encyclopedia Project of Genome Exploration Research Group in Riken
　　　　　　Genomic Sciences Center and Genome Science Laboratory in RIKEN.
　　　　　　Division of Experimental Animal Research in Riken contributed to
　　　　　　prepare mouse tissues.
　　　　　　Please visit our web site for further details.
　　　　　　URL:http://genome.gsc.riken.go.jp/
　　　　　　URL:http://fantom.gsc.riken.go.jp/.

```
FEATURES          Location/Qualifiers
source            1..3866
                  /organism="Mus musculus"
                  /mol_type="mRNA"
                  /strain="C57BL/6J"
                  /db_xref="PANTOM_DB:D230015E05"
                  /db_xref="taxon:10090"
                  /clone="D230015E05"
                  /tissue_type="eyeball"
                  /clone_lib="RIKEN full-length enriched mouse cDNA library"
                  /dev_stage="12 days embryo"
misc_feature      1..3866
                  /note="phosphatidylinositol 3-kinase, catalytic, alpha
                  polypeptide (MGD|MGI:1206581, GB|NM_008839, evidence:
                  BLASTN, 99%, match=2855)"
BASE COUNT        1149 a    786 c    878 g    1053 t
ORIGIN

Alignment Scores:
Pred. No.:              3.63e-154         Length:          3866
Score:                  1429.00           Matches:         356
Percent Similarity:     53.19%            Conservative:    177
Best Local Similarity:  35.53%            Mismatches:      343
Query Match:            24.68%            Indels:          126
DB:                     11                Gaps:            34

US-09-974-573-1 (1-1102) x AK051885 (1-3866)
```

```
Qy  1050 TyrIleArgAspAlaLeuThrHrValGlyLysSerGluGluAspAlaLysLysTyrPheLeu 1069
              ||||||        ||||    ::::|||||       :::|||    ||:||
Db  2749 TATATCCGAAAGACTCTAGCCTTGACAAAATCAAGAGCTTGGAATATTTCACA 2808

Qy  1070 AspGlnIleGluValCysArgAspLysGlyTrpThrValGlnPheAsnTrpPheLeuHis 1089
              ||:|||         :::|||          ::: |||    :::|||
Db  2809 AAGCAAATGAATGATGCACATCATGGTGATGGACGACAAAAATGGATTGGATCTTCCAC 2868

Qy  1090 LeuVal 1091
              :::
Db  2869 ACCATC 2874


RESULT 3
ACCESSION   AK090116
LOCUS       AK090116         4731 bp    mRNA    linear   HTC 10-APR-2003
DEFINITION  Mus musculus embryo RCB-0549 Cle-H3 cDNA, RIKEN full-length
            enriched library, clone:G430147P21 product:PHOSPHATIDYLINOSITOL
            3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM (PTDINS-3-KINASE
            P110 SUBUNIT BETA) (PI3-KINASE P110 (EC 2.7.1.137) (PI3K) (PI3KBETA) homolog
            [Rattus norvegicus], full insert sequence.
ACCESSION   AK090116
VERSION     AK090116.1  GI:26354950
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,T., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4731)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,M., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
          Physical and Chemical Research (RIKEN), Laboratory for Genome
          Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
          RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
          Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
          Fax:81-45-503-9216)

COMMENT   cDNA library was prepared and sequenced in Mouse Genome
          Encyclopedia Project of Genome Exploration Research Group in Riken
          Genomic Sciences Center and Genome Science Laboratory in RIKEN.
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues.
          Please visit our web site for further details.
          URL:http://genome.gsc.riken.go.jp/
          URL:http://fanton.gsc.riken.go.jp/.

FEATURES   Location/Qualifiers
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Score: 1363.00   Matches: 357
Percent Similarity: 50.09%   Conservative: 195

Best Local Similarity: 32.40%   Mismatches: 400
Query Match: 23.54%   Indels: 150
DB: 11   Gaps: 35

US-09-974-573-1 (1-1102) x AK090116 (1-4731)

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Db 280 GCATCCGATGGCGCCATATCCGTCGATTTCCTTCTGCGCCACCGGGATTATATCCAGTG 339

Qy   93 ------ProAspHisPheLeuLeuTyrGlnLysLysGlyGlnTrpTyrGluIle------- 109
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VERSION   CD171634.1 GI:30852375
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SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 880)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM445 row: i column: 22
            High quality sequence start: 20
            High quality sequence stop: 719.
FEATURES   Location/Qualifiers
     source   1..880
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30378933"
                     /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_180"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon cloning
). Average insert size 1.68 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
BASE COUNT   229 a   254 c   224 g   173 t
ORIGIN

Alignment Scores:
Pred. No.:   2.5e-147   Length: 880
Score: 1361.00   Matches: 267
Percent Similarity: 94.81%   Conservative: 7
Best Local Similarity: 92.39%   Mismatches: 11
Query Match: 23.51%   Indels: 5
DB: 14   Gaps: 0

US-09-974-573-1 (1-1102) x CD171634 (1-880)
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Qy  293  ValArgGlnCysLeuLysAsnGlyGluGluIleHisLeuValLeuAspThrProProAsp  312
Db   21  CTCCGGATCTGCCTCAAGAACGGAGAAGATATTCC-GTGGTACTGGACACGCCTCCAGAC  79
Qy  313  ProAlaLeuAspGluValArgLysGluTrpProLeuValAspAspCysThrGlyVal  332
Db   80  CCGGCCCTAGACGAGGTGAGGAAGGAAGAGTGGCCCGCTGGTGACGACTGCACGGGAGTC  139
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Qy  333  ThrGlyTyrHisGluGlnLeuThrIleHisGlyLysAspHisGluSerValPheThrVal  352
Db  140  ACCGGCTACCATGAGAGCTTACCATCCACGGCAACGAAGGAGAGTGTTCACCGTG  199

Qy  353  SerLeuTrpAspCysAspArgValArgPheArgValLysIleArgGlyTyrIleProVal  372
Db  200  TCCCTGTGGGACTGCGACCGCAAGTTCAGGGTCAAGATACAGATTGATATCCCGTC  259

Qy  373  LeuProArgThrAlaAspLeuPheValGluValGlnAsnIleGlnTyrGlyGlnGln  392
Db  260  CTGCCTCCGAACACCGACCTCCACAGTTTTGTGAGAGGCAAACATCCAGCATGGGCAACAA  319

Qy  393  ValLeuCysGlnArgArgThrSerProLysProPheThrGluGlnValLeuTrpAsnVal  412
Db  320  GTCCTTTGCCAAAGGAGAACCAGGCCCAAACCCTTCACAGAGGAGGTGTTGGAATGTG  379

Qy  413  TrpLeuGluPheSerIleLysIleLysAspLeuProLysGlyAlaLeuLeuAsnLeuGln  432
Db  380  TGGCTTGAGTTCAGTATCAAAATCAAAGACTTGCCCAAAGGGGCTCACTGAACCTCCAG  439

Qy  433  IleTyrCysGlyLysLysAlaProAlaLeuSerGlyLysThrSerAlaGluMetProSerPro  452
Db  440  ATCTACTGCGGTAAAGCTCCAGCACTGTACAGCAAGGCCTGCAGAGTCCCCAGTTCT  499

Qy  453  GluSerLysGlyLysAlaGlnLeuLeuTyrTyrValAsnLeuLeuLeuIleAspAspHisArg  472
Db  500  GAGTCCAAGGGCAAAGTTCAGCTTCTCTATTATGTGAACCTGCTGCTGATAGACCACCGT  559

Qy  473  PheLeuLeuArgHisGlyHisGluTyrValLeuHisMetTrpGlnLeuSerGlyGlyGlu  492
Db  560  TTCCTCCTGCGCCGTGGAGAATACGTCCTCCACATGTGGCAGATATCTGGGAGGGAGGAA  619

Qy  493  AspGlnGlySerPheAsnAlaAspLysLeuThrSerAlaThrAsnProAspLysGluAsn  512
Db  620  GACCAAGGAAGTTCAATGCTGACAAACTCACGTCTGACAACTAACCCAGACAAGGAGAAC  679

Qy  513  SerMetSerIleSerIleLeuLeuAspAsnTyrCysHisProIleAlaAlaLeuProLysHis  532
Db  680  TCAATGTCCATCTCCATTCTTCTGGACAATTACTGCCACCCCGATAGCCCTGCCTAAGCAT  739

Qy  533  ArgProThrProAspPro-GluGlyAspArgValArgAlaArgAlaGluMetProAsnGlnLeuAr  552
Db  740  CAGCCCACCCCTGACCCGGAGGGAGACCGGGTTCAGCAGAAATGCCAACCAGCTTCG  799

Qy  552  glyLysGlnLeuGluAlaIleIleAlaThrAspProLeu-AsnProLeuThrAlaGlu-Asp  571
Db  800  CAAGCAATTGGAGGCGATCATAGCCACTGATCCACTTTAACCCTCTCACAGCAGAAGGAC  859

Qy  572  -LysGluLeuLeuTrpHis  577
Db  860  CAAAGATTTGCTCTGGCAT  878
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RESULT 5
AK081350
LOCUS   AK081350   4996 bp   mRNA   linear   HTC 05-DEC-2002
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
            library, clone:C130009D19 product:PHOSPHATIDYLINOSITOL 3-KINASE
            CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110
            SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) (PI3KBETA) homolog
            [Rattus norvegicus], full insert sequence.
ACCESSION   AK081350
VERSION   AK081350.1 GI:26099860
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636

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REFERENCE   2
AUTHORS     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,M., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409 (6821), 685-690 (2001)
MEDLINE     21085660
PUBMED      11217851
REFERENCE   5
AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
REFERENCE   6   (bases 1 to 4996)
AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kanagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp;
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
```

```
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1..4996
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                     BETA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT BETA)
                     (PTDINS-3-KINASE P110) (PI3K) (PI3KBETA) homolog [Rattus
                     norvegicus] (SWISSPROT|Q92IL0, evidence: FASTY, 98.1%ID,
                     108length, match=3210)
                     putative"
     polyA_signal    4975..4980
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     polyA_site      4996
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BASE COUNT     1326 a     1113 c     1222 g     1335 t
ORIGIN
Alignment Scores:
Pred. No.:                    4996
Score:                        1.81e-144
Percent Similarity:           1347.50
Best Local Similarity:        50.27%
Query Match:                  32.61%
DB:                           23.27%
                              11

Length:               4996
Matches:              360
Conservative:         195
Mismatches:           395
Indels:               155
Gaps:                 37

US-09-974-573-1 (1-1102) x AK081350 (1-4996)

Qy       78 AlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGly------------------------ 92
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Db      598 GCATCCGATGGGCCCATATCCGTCGATTTCCTTCTGCCCACCGGGATTATATCCAGTTG 657

Qy       93 ------ProAspHisPheLeuLeuLeuTyrGlnIleLysGlyGlnTrpTyrGluIle--- 109
            ||:
Db      658 GAAGTACCTCGGGAGCTACCATTTCTTATATTAAACACGATGTTATGGAAGCAAGTTCAC 717

Qy      110 ---TyrAspLysTyrGlnValValGlnThrLeuAsp------------------CysLeuArg 123
            ||| :::       |||  :::::::|||                      ||:
Db      718 AACTACCCGATGTTAACCTCCTATGGACATTGACTCGTATATATGTTTGCATGTGTGAAT 777

Qy      124 TyrTrpLysValLeuHisArgSerProGlyGln------------------------- 134
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Db      778 CAAACTGCTGTATATGGAGGACTGGAAGACCGAAACACGAAGAGACTTTGTGATGTCAGACCT 837

Qy      135 -------------IleHisValGlnArgHisAlaProSerGluGlnThrLeuAlaPhe 150
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Db      838 TTTCTCCAGTTCTCAAACTAGTGACTAGAAGCTGTGACCCCGCAGAAAAATTG----- 891

Qy      151 GlnArgGlnLeuAsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAsp 170
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Db      892 GACTCAAAAATTGGGGTCTTATAGGAAAAGGTCTTCATGAGTTTGATGCCTTGAAGGAT 951

Qy      171 AspGluLeu------GluPheThrArg------ArgArgLeuValThrProArgMetAlaGlu 187
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Db      952 CCCGAAGTGAATGAATTTAGAAGAAAATCGCAAATTCAGTGAGGCCAGATTCAGTCT 1011

Qy      188 ValAlaGlyArgAspProLysLeuTyrAlaMetHisProTrpValThrSerLysProLeu 207
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Db     1012 CTGGTAGGG------------------TTGTCTTGGATCGGACTGGCTAAAGACACGTATCCG 1056
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527 Qy  IleAlaLeuProLysHisArgProThrProAspProGluGlyAspArgValArgAlaGlu  546
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2032 Db  TGTTATTATCCCCCCTCGATAAGATCATTGAGAAGGCAGCTGAGCTTGCCAGCGGAGAC 2091

547 Qy  MetProAsnGlnLeuGln-----------------LysGlnLeuGluAlaIleIleIleAla  560
              |||                                    ||:|||||  | ||:|:
2092 Db  AGTGCTAATGT-AGTCGTGGTGGAAAAAATTTCTGTCGTGCTGAAAGAAATCTTCGAC 2150

561 Qy  ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyr  580
              ||| :::                             | ::   |||:|| :::::::
2151 Db  AGGGACCCCCTGTCTCAGCTGTGTGAGAACGAAATGGACCTTATTTCGACTCTACGGCAA 2210

581 Qy  GluSerLeuLysAsp---ProLysLeuPheSerSerValLysTrpGly  599
             ::::::      :::                  |||||||||:|||:
2211 Db  GACTGCCGGAAGATGAAGCTAGCCCCTGTGCCTGTCAATCACTTCTGTCAATCAAGTGGAAT 2270

600 Qy  GlnGlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGln  619
                ||||||||   |||    :::                               :::
2271 Db  CAGCTCAGGCGCTCCTGCAGATATGGCCCAAA 2321

620 Qy  SerAlaLeuAspValGlyLeuThrMetGlnLeuLeuLeuAspCysAsnPheSerGluAsn  639
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2322 Db  CTGCCCCCCAGGGAGCCCTGGAACTCCTGGATTTCAACTATCCAGACCAGTAT 2375

640 Qy  ValArgAlaIleAlaValGlnLysLeuGluSerLeuLeuAspAspAspValLeuHisTyr  659
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2376 Db  GTCCGGAAATACGCTGTAGGCTGGCCTTCGACCAGATGAGTGATGAAGAACTTCTCAGTAT 2435

660 Qy  LeuLeuGlnLeuValGlnAlaValPheLysPheTyrHisAspSerAlaLeuAlaArg  679
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2436 Db  CTTTTACAATTGGTGCAAGTTTGAAATATGAGCCTTTCTGGATTGTGCCCTCCAGA 2495

680 Qy  PheLeuLeuLysGlyLeuArgAsnLysGlyHisPheLeuGluPheTrpPheLeu  699
             ||| |||                  |:: | ::::::::::|||:|||||||:|
2496 Db  TTCCTATTAGAAGAGCACTTGATAATCGGAGGAGTTTCTGTTTTTGGCATCTT 2555

700 Qy  ArgSerGluLeuAlaGlnSerArgHisTyrGlnInArgPheAlaValLeuLeuGluAla  719
             |||:||        |||                    ||| |:|| || |||||||||
2556 Db  AGGTCAGAGGTG---CACACTCCTGCTGTGTCCGTACAGTTGGTGTCATCCTGGAAGCA 2612

720 Qy  TyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValIleGlnValIle  739
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2613 Db  TACTGTGCGAGGA---AGCGTGGGGCACATGAAAGTGCTTTCCAAACAGGTGGAAGCACTC 2669

740 Qy  AspMetLeuGlnLysValThrIleAspIleLys---------SerLeuSerAlaGlu  755
             ::: ::: :::      ||||                           |||||||
2670 Db  AATAAGTTAAAAACTTTAAATAGCTTAATCAAACTGAATGGTGAAGCTGAGCAGAGCT 2729

756 Qy  LysTyrAspValSerSerGlnValIle----------SerGlnLeuLysGlnLeuGlu  772
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2730 Db  AAGGGAAAGGAGGGCCATGCAACGTGCCTGAAACAGAGTGCTTACCGGGGGGCCGTCTCT 2789

773 Qy  AsnLeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLys  792
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2790 Db  GACCTGCAGTCG-----------------------CCGCTGAACCCCTGCTGCTCATC 2822

793 Qy  AlaGlyValAlaLeuValIleGluCysLysLysValMetAlaSerLysLysProLeuTrp  812
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2823 Db  CTCTCAGAGCTTCCTATGTTGAAAAGTGCAAATACATGGACTCCAAGATGAAGCCCGTGG 2882

813 Qy  LeuGluPheLysCysAlaAspProThrAlaLeuSerAsnGluThrIleGlyIleIlePhe  832
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2883 Db  CTCGGTCTAC--------AGCAGCAGCCTTTGGAGAGGACTCGGTTGGAGTGGATCTTT 2933

833 Qy  LysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGlu  852
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2934 Db  AAAAATGGTGACGATTTGCGCCAGACCATGCTGATACTGCAGATTTTGCGCATGGAT 2993

853 Qy  SerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThr  872
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2994 Db  CTGCTTTGGGAAACAGAGAGTCTGGACCTGTGCCTCCCATGGGCTGTCTTAGCACAACA 3053

873 Qy  GlyAspLysIleGlyMetIleGluIleValLysAspAlaThrThrIleAlaLysIleGln  892
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PUBMED　　11042159

REFERENCE　3

AUTHORS　Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
　　　　　Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
　　　　　Sumi,N., Ishii,Y., Nakamura,S., Hazama,S., Nishine,T., Harada,A.,
　　　　　Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
　　　　　Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
　　　　　Yoneda,Y., Ishikawa,T., Ozawa,A., Tanaka,T., Matsuura,S., Kawai,J.,
　　　　　Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE　RIKEN integrated sequence analysis (RISA) system--384-format
　　　　sequencing pipeline with 384 multicapillary sequencer

JOURNAL　Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE　20530913

PUBMED　11076861

REFERENCE　4

AUTHORS　Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
　　　　　Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
　　　　　Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
　　　　　Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
　　　　　Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
　　　　　Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
　　　　　Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
　　　　　Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
　　　　　Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
　　　　　Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
　　　　　Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
　　　　　Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
　　　　　Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
　　　　　Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
　　　　　Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
　　　　　Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
　　　　　Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
　　　　　Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
　　　　　and Hayashizaki,Y.

TITLE　Functional annotation of a full-length mouse cDNA collection

JOURNAL　Nature 409 (6821), 685-690 (2001)

MEDLINE　21085660

PUBMED　11217851

REFERENCE　5

AUTHORS　The FANTOM Consortium and the RIKEN Genome Exploration Research
　　　　　Group Phase I & II Team.

TITLE　Analysis of the mouse transcriptome based on functional annotation
　　　　of 60,770 full-length cDNAs

JOURNAL　Nature 420, 563-573 (2002)

REFERENCE　6　(bases 1 to 4852)

AUTHORS　Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
　　　　　Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
　　　　　Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
　　　　　Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
　　　　　Katoh,H., Kawaji,C., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
　　　　　Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
　　　　　Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
　　　　　Okazaki,Y., Sasaki,D., Shibata,K., Sakai,C., Sakai,K., Sakazume,N.,
　　　　　Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
　　　　　Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
　　　　　Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
　　　　　Muramatsu,M. and Hayashizaki,Y.

TITLE　Direct Submission

JOURNAL　Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
　　　　　Physical and Chemical Research (RIKEN), Laboratory for Genome
　　　　　Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
　　　　　RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
　　　　　Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
　　　　　URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
　　　　　Fax:81-45-503-9216)

COMMENT　cDNA library was prepared and sequenced in Mouse Genome
　　　　　Encyclopedia Project of Genome Exploration Research Group in Riken
　　　　　Genomic Sciences Center and Genome Science Laboratory in RIKEN.
　　　　　Division of Experimental Animal Research in Riken contributed to
　　　　　prepare mouse tissues.
　　　　　Please visit our web site for further details.
　　　　　URL:http://genome.gsc.riken.go.jp/
　　　　　URL:http://fantom.gsc.riken.go.jp/.

Db　　3054　GGAGATCGCTCTGCCTCATTGAGGTTGTGAGCACCTGAGCAATCGCTGACATTCAG　3113
　　　　　　　||||||::.　|||||::||||||:.||　　　:::　　　|||||||　||||||
Qy　　893　------GlnSerThrValGlyAsnThrGlyAlaPheLysAspGluValLeuSerHisTrp　910

Db　3114　CTGAACAGTAGTAACGTGGCTGCCACGGCAGCCTTCAACAAAGACGGCGTCCTGAACTGG　3173
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Qy　911　LeuLysGluLysCysProIleGluGlyLuLysPheGlnAlaAlaValGluArgPheValTyr　930

Db　3174　CTCAAGGAGTACAACTCTGGGATGAC---CTGGACCGAGCGATTGAGGAGTTTACCTTG　3230
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Qy　931　SerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAsp　950

Db　3231　TCCTGTGCTGGCTACTGTGTAGCCTCTTATGTCCTCGGCATTGGTGACACAGGTGAC　3290
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Qy　951　AsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGly　970

Db　3291　AACATCATGTGAAGAAAACCGGCAGCTCTTCCACATAGATTTTGGGCATATTCTTGGA　3350
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Qy　971　AsnTyrLysSerPheLeuGlyIleLeuAsnLysGluArgValProPheValLeuThrProAsp　990

Db　3351　AATTTCAAATCTAAATTTGCATTAAAAAGGGAGGGAGTTACCTTTATTCTTACTTATGAC　3410
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Qy　991　PheLeuPheValMetGlyThrSerGlyAlaGlyLysThrSerLeuHis------PheGlnLeuTyr　1008

Db　3411　TTCATTCATGTCATT------CAAGCAAGGAAAAACGGGAAACACTGAAAAATTTGGCAG　3464
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Qy　1008　sPheGlnAspValCysValLysValAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIl　1028

Db　3465　ATTCCGCCAGTGCGTGAAGATGCGTATCGATTTACGGCGGCATGGGAATCTCTTCAT　3524
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Qy　1028　eIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluAspIl　1048

Db　3525　CACCCTGTTTGCCCTGATGTTGACTGCGCAGGGCGTGCCTGAGCTCCACATCCGGTCAAAGATAT　3584
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Qy　1048　eGluTyrIleArgAspAlaLeuThrValGlyTyrLysSerGluAlaThrValGlyLysTyrPh　1068

Db　3585　ACAGTATCTTAAGGACTCCGCTTGCCTTAGGGAAGGAGGAGGAAGCACTGAAGCAGTT　3644
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Qy　1068　eLeuAspGlnIleGluValCysArgAspLysGlyTrpThrValGlnPheAsnTrpPheLe　1088

Db　3645　CAAGCAGAAGTTTGACGAGCCCCTCAGGGAAAGCTGGACTACTAAAGTGAACTGGATGGC　3704
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Qy　1088　uHisLeuVal　1091

Db　3705　TCACACAGTA　3714
　　　　　　||||||||||

RESULT 6

AK040867

LOCUS　AK040867　　4852 bp　　mRNA　　linear　　HTC 05-DEC-2002

DEFINITION　Mus musculus adult male aorta and vein cDNA, RIKEN full-length
　　　　　enriched library, clone:A530031P09 product:phosphatidylinositol
　　　　　3-kinase catalytic delta polypeptide, full insert sequence.

ACCESSION　AK040867

VERSION　AK040867.1　GI:26334014

KEYWORDS　HTC; CAP trapper.

SOURCE　Mus musculus (house mouse)

ORGANISM　Mus musculus
　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE　1

AUTHORS　Carninci,P. and Hayashizaki,Y.

TITLE　High-efficiency full-length cDNA cloning

JOURNAL　Meth. Enzymol. 303, 19-44 (1999)

MEDLINE　99279253

PUBMED　10349636

REFERENCE　2

AUTHORS　Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
　　　　　Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE　Normalization and subtraction of cap-trapper-selected cDNAs to
　　　　prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL　Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE　20499374

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FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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                     AREGDRVKKLINSQISLLIGKGLHEFDSLRDPEVNDPRTKMRQFCEEAAHRQQLGWV
                     EWLQYSFPMQLEPSARGWRAGLLRVSNRALLVNVKFEGSESFTFQVSTKDMPLALMA
                     CALRKKATVFRQPLVEQPEEYALQVNGRHEYLYGNYPLCHPQYICSCLHSGLTPHLTM
                     VHSSSILAMRDEQSNPAPQVQVKPRAKPPIPAKKPSSVSLWSLEQPFSIELIEGRKVN
                     ADERMKLVVQAGLFHGNEMLCKTVSSSEVNVCSEPWKQRLEFDISVCDLPRMARLCF
                     ALYAVVEKAKKARSTKKKSKKADCPIAWANLMLFDYKDQLKTGERCLYMWPSVPDEKG
                     ELLNPAGTVRGNPNTESAAALVIYLPEVAPHPVYPPALEKILELGRHGERGRITEEEQ
                     LQLREIERRGSGELYEHEKDLVWKRHEVQEHPEALARLLLVTKWNKHEDVAQLSQ
                     MLYLLCSWPELPVLSALELDFSPDCYVGSSFAIKSLRKLTDDELFQYLLQLVQVLKY
                     ESYLDCELITKFLGRALANRKIGHFLFWHLRSEMVPSVALRFGLIMEAYCRGSTHHM
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                     LMDVLMKQEGLDLRMTPYGCLPTGDRTGLIEVVLHSDTIANIQLNKSNMAATAAFNKD
                     ALLNWLKSKNPGEALDRAIEEFTLSCAGYCVATYVLGIGDRHSDNIMIRSGQLPHID
                     FGHFLGNFKTKFGIRNRERVPFILTVDFVHVIQQGKTNNSEKFERPRGYCBRAYTILRR
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     polyA_site      4852
                     /note="putative"
BASE COUNT      1086 a   1391 c   1364 g   1011 t
ORIGIN

Alignment Scores:
Pred. No.:                        Length:          4852
Score:            1.69e-143       Matches:         1339.00
Percent Similarity:  50.45%       Conservative:    353
Best Local Similarity: 31.92%     Mismatches:      205
Query Match:      23.13%          Indels:          412
Db:                               Gaps:            136
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US-09-974-573-1 (1-1102) x AK040867 (1-4852)

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Qy    38  IleProIleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAla   57
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Db   298  GTGGTTGTTGACTTCTTGCCCACAGGG---------------------------GTC   330

Qy    58  LeuLeuHis------ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnLnValTrp   75
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Db   331  TACTTGAACTTCCCCGTGTCCCGCAATGCCAACCTCAGCACCATCAAGCAGGTGCTGTGG   390

Qy    76  LeuArgAlaLeuGlnThrSerValSerAlaAspPheTyrHisGlyLeuGly--ProAsp   94
          |||||      :::            ||:||:
Db   391  CACCGTGCACAGTATGAGCCACTC--------TTCCACACATGCCAGTGACCCCGAG   438

Qy    95  HisPheLeuLeu--LeuTyrGlnLnLysGlyGlnTrpTyrGluIleTyrArgAspLysTyr  113
          ||||||::      :::||                :|::|
Db   439  GCCTATGTGTCACCTGTGTGGAACCAGACGGCCGAGCAGGAGTTGGAGGATGAGCAG   498

Qy   114  GlnValValGlnThrLeuAspCysLeuArgThrTyrTrpLysValLeuHisArgSerProGly  133
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Db
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Qy  808 LysLysProLeuTrpGluPheLysCysAlaAspProThrAlaLeuSerAsnMetGluThr 827
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Db 2515 ATGAAGCCCCTGTGGACATCATGTACAGCAGCGAGGAGGCGGCCAGTGCTGGCCAAC 2568

Qy  828 IleGlyIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuValLeuGlnIle 847
        |||||  ||||                     |||||
Db 2569 GTGGGCATCATCTTTAAGAACGGGGATGACCTCCGGCAGGACATGCTGACTCTGCAGATG 2628

Qy  848 LeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyr 867
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Db 2629 ATCCAGCTCATGGAGTCCTGTGGAAGCAGGAGCAGGAGGCCTGAGACCTGAGGATGACGCCCTAC 2688

Qy  868 GlyCysIleSerThrGlyAspLysIleGlyMetIleGluValLeuLysAspAlaThrThr 887
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Db 2689 GGCTGCCTCCCCACCGGGACCGCACAGGTCTCATCGGAGGTGGTCCTCCACTCGGACACC 2748

Qy  888 IleAlaLysIleGln-----GlnSerThrValGlyAsnThrGlyAlaPheLysAspGlu 905
        ||||                       :::||||
Db 2749 ATCGCCAAGATCCAGCTGACAGAACAAAGCAACATGGGCGGCCACAGCTGCCTTCAACAAGGAC 2808

Qy  906 ValLeuSerHisTrpLeuLysCysProIleGluGlnLysCysPheGlnLysAlaAlaVal 925
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Db 2809 GCCCTGCTCACCTGCTCAAGTCCCAAGAACCCT---GGGGAGGAGGCCCTGGATCGGGCCATT 2865

Qy  926 GluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIleGly 945
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Db 2866 GAGGAATTCACCCCTCCTGTGCTACTGTGTGGCCACATATGTTCTGGGCATCGGT 2925

Qy  946 AspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAspPhe 965
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Qy  966 GlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgValProPhe 985
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Db 2986 GGCCACTTCTTGGGGAACTTCAAGACAAGTTGGAATCAACCGGAGCCGGTCCCCTTC 3045

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Qy 1006 PheGlnLysPheGlnAspProQysValLysTyrLeuAlaLeuArgHisHisThrAsn 1025
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Db 3106 TTTGAAAGGTTCCGGCGCCATATCTGAAGAGCCATACCATCCTGCGGCGCCACGGGCTG 3165

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Db 3166 CTTTTCCTCCATCTCTTCGCCTGAGCTTCGGGGGCCGCCAGGTCTCGCCTGAGCTTAGCTGTCTCC 3225

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Qy 1066 LysTyrPheLeuAspGlnIleGluValCysArgAspPheLysGlyTrpThrValGlnPheAsn 1085
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Db 3286 AAGCACTTCCGGGTGAAGTTCAACGAGAGCTCTCCGGAGAAAACCAAAGTCAAC 3345

Qy 1086 TrpPheLeuHisVal 1091
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RESULT 7

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Db 1459 ACAAGAG--------AAGTCTAAGAAGGCGGACTGCCCATCGCTGGGCCAAC 1506

Qy  466 LeuLeuLeuIleLeuArgHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMetTrp 485
Db 1507 CTCATGCTATTCGACTACAAAGATCAGCTCAAGACGGGGGAGGCGCTGCTTCTACACGTGG 1566

Qy  486 GlnLeuSerGlyLysGlyGlnGlySerPheAsnAlaAspLysLeuThrSerAla 505
Db 1567 ------CCCTCTGTCCCAGATGAGAAGGGAGACTGCTGAATCCTGCGGGTACAGTGCGC 1620

Qy  506 ThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuArgAspAsnTyrCys--- 524
Db 1621 GGGAACCCCAACACGGAGAGTGCCGTCCCCTGGTCATCTACTCGCTGAGGTGGCCCCCC 1680

Qy  525 HisProIleAlaLeuPro----------LysHisArgProThr 535
Db 1681 CACCCTGGTACTTCCCCGCTCTGGAAGATCCTGAGCTGGGGCGTCAC---------- 1731

Qy  536 ProAspProGluGlyAspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeu 555
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Qy  556 GluAlaIleIleAlaThrAspAsnProLeuThrArgLeuGluAspLysGluLeuLeu 575
Db 1774 CGGGAGGATCCTGGAACGGCGGGGATCCGGGGAACTGTACGAACATGAGAAGGAACCTGGTG 1833

Qy  576 TrpHisPheArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLysProLeuPheSer 594
Db 1834 TGGAAGATGCGCCACGAGCATTCCCAGAGGCGCTGGGGCCGCTGGGTCCCGCCTGCTGCTG 1893

Qy  595 SerValLysTrpGlyGlnGlnIleValAlaLysThrTyrGlnLeuLeuLeuAlaLysLysArg 614
Db 1894 GTCACCAAGTGGAATAAACAGGAGATGTGGCCCAGCTGTCCCAGCGATGCTCATTTGCTG 1953

Qy  615 GluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsn 634
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Qy  635 PheSerAspArgAsnValArgAlaIleLeuAlaValGlnLysLeuGluSerLeuGluAspAsp 654
Db 2008 TTTCCCGACTCACGTGGCTCCTCCGCCATCAAGTCCCTTCGGAAGCTGGAGCTGACGACGAT 2067

Qy  655 AspValLeuHisThrTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHisAsp 674
Db 2068 GAGCTCTTCCAGTACCTTCTGCAGCGCTGGTGCAAGTGCTCAAATATGAGTCCTACCTGGAC 2127

Qy  675 SerAlaLeuAlaArgPheLeuLeuLysArgGlyValArgAsnLysArgIleGlyHisPhe 694
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Qy  695 LeuPheTrpPheLeuValMetAlaSerGluIleAlaGlnSerArgHisTyrGlnGln---------- 711
Db 2188 CTGTTCTGGTTCCTGGTCATGGCCTCTGAGATG------CACGTACCATCAGTGGCTCTG 2235

Qy  712 ArgPheAlaValIleGluAlaThrArgLeuArgGlyCysGlyThrAlaMetLeuHisAsp 731
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Qy  732 PheThrGlnValGlnGlnHisValIleIleAspAspMetLeuGlnLysValThr------IleAspIle 749
Db 2293 CTGATGAAGCAGGGGGAGCCACTGACAAGCTTAAGGCACTGAATGACTTTGTGAAGGTG 2352

Qy  750 LysSerLeuSerAlaGluLysLysTyrAspValSerSerGlnValIleSerGlnLysLysGln 769
Db 2353 AGTTCCCGAGAAGACCACCAGTCCCAAACCAAGGAGATGATGCATAATGCATGCGCCAG 2412

Qy  770 Lys-----LeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyr 787
Db 2413 GAGACCTACACAGGAGGGCCCTGTCCCACTG------CAGTCTCCACTC 2454

Qy  788 AspProGlyLeuLysAspGlyAlaGlyIleAlaLeuValIleGluLysLysCysLysValMetAlaSerLys 807
Db 2455 GACCCCAGCAGCACCCTGCTGAGGAGAAGTCTCGTGTGAGCAGTGACCAGCACCTTCACTCCCAA 2514
```

```
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10049636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M. Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga.N.,
            Carninci,P., de Bonaldo,M.F., Brownstein.M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,J., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6   (bases 1 to 1937)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,H., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamanmura,T., Yamanaka,I., Yasunishi,A.,
            Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1..1937
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:5830428L06"
                     /db_xref="MGI:1909481"
                     /db_xref="taxon:10090"
                     /clone="5830428L06"
                     /sex="male"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             <1..785
                     /note="unnamed protein product; phosphoinositide-3-kinase,
                     catalytic gamma polypeptide [MGD|MGI:1153576,
                     GB|NM_020272, evidence: BLASTN, 99%, match=3776)
                     putative"
                     /codon_start=3
                     /protein_id="BAC37000.1"
                     /db_xref="GI:26346703"
                     /db_xref="MGI:1923289"
                     /translation="LIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDAT
                     TIAQIQQSTVGNTGAFKDEVLNHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGI
                     GDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGSSGKKT
                     SPHFQKFQDVVRAYLALRHHTNLLLILFSMMLMTCMPQLTSKEDIEYIRDALTVGKS
                     EEDAKKYFLDQIEVCRDKGWTVQFNWFLHLVLGIKQGEKHSA"
BASE COUNT      546 a    423 c    407 g    561 t
ORIGIN

Alignment Scores:
Pred. No.:                             Length:         1937
Score:                1.05e-143        Matches:        254
Percent Similarity:   1335.00          Conservative:   4
Best Local Similarity: 99.23%          Mismatches:     2
Query Match:          97.69%           Indels:         0
DB:                   23.06%           Gaps:           0
                      11

US-09-974-573-1 (1-1102)  x  AK077772 (1-1937)

Qy   843 LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeu 862
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Db     3 TTGATCTTGCAGAATTCTACGCATCATGGAGTCCATTTGGGAGACTGAATCTCTGGACCTG 62

Qy   863 CysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGluIleVal 882
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63 TGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGATCGAGATTGTA 122

Qy   883 LysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGlyAlaPhe 902
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 AAGGATGCCACAACGATCGCTAAAATTCAGCAAAGCACCAGTGGGTAACACGGGGCATTC 182

Qy   903 LysAspGluValLeuAsnHisTrpLeuLysGluLysCysProIleGluGluLysPheGln 922
         ||||||||||||||||||||||||||||||||||::|||::|||||||||||||||||||
Db   183 AAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATGTCCTATTGAAGAAAAGTTTCAG 242

Qy   923 AlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeu 942
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Db   243 GCCGCAGTGGAAAGGTTTGTTTACTCCTGCGCAGGCTACTGTGTGGCCACATTTGTTCTT 302
```

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES   Location/Qualifiers
source   1..915
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="5830428L06"
                /sex="male"
                /tissue_type="thymus"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="RIKEN full-length enriched, adult male thymus"
                /note="Site 1: SalI; Site 2: BamHI; cDNA library was
                prepared and sequenced in Mouse Genome Encyclopedia
                Project of Genome Exploration Research Group in Riken
                Genomic Sciences Center and Genome Science Laboratory in
                RIKEN. Division of Experimental Animal Research in Riken
                contributed to prepare mouse tissues. 1st strand cDNA was
                primed with a primer [5'
                GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTN 3'], cDNA was
                prepared by using trehalose thermo-activated reverse
                transcriptase and subsequently enriched for full-length by
                cap-trapper. cDNA went through one round of normalization
                to Rot = 10.0 and subtraction to Rot = 100.0. Second
                strand cDNA was prepared with the primer adapter of
                sequence (5' GAGAGAGAATTCCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                3']. cDNA was cloned into the XhoI and BamHI sites.
                Vector: a modified pBluescript KS(+) after bulk excision
                from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                BamHI."

BASE COUNT   259 a   206 c   212 g   238 t
ORIGIN

Alignment Scores:
Pred. No.:
Score: 1.36e-138   Length: 915
Percent Similarity: 1286.50   Matches: 248
Best Local Similarity: 98.44%   Conservative: 4
Query Match: 96.88%   Mismatches: 4
DB: 22.22%   Indels: 1
                            10   Gaps: 0

US-09-974-573-1 (1-1102) x BB619812 (1-915)

Qy   843 LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeu 862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3 TTGATCTTGCAGATTCTACGCATCATGGAGTCGAGTCCATTTGGGAGACTGAATCTCTGGACCTG 62

Qy   863 CysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGluVal 882
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Db   63 TGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAATAGGAATGATCGAGATTGTA 122

Qy   883 LysAspAlaThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGlyAlaPhe 902
           ||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db   123 AAGGATGCCACACGATCGCTCAAATTCAGCAAAGCACAGTGGGTAACACCGGGGCCATTC 182

Qy   903 LysAspGluValLeuSerHisTrpLeuLysGluLysProIleGluGluLysPheGln 922
           ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||

Qy   943 GlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHis 962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 GGGATCGGTGACAGGCCACAACGACAACATTATGATCTCAGAGACACAGAAACCTATTTCAT 362

Qy   963 IleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArg 982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 ATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCAATAAAGAGAGA 422

Qy   983 ValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLysLysThr 1002
           |||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db   423 GTGCCCTTCGTCCTAACCCCAGATTCTTGTTTGTGATGGGACTTTCTGGAAAAAAGACA 482

Qy   1003 SerLeuHisPheGlnLysPheGlnAsnAspCysValLysValAlaTyrLeuAlaLeuArgHis 1022
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Db   483 AGTCCACACTTCCAGAAATTCCAGGATGTCTATGTTAGAGCTTACCTAGCTCTTCGCCAT 542

Qy   1023 HisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 CACACCAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGGAATGCCCAGCTG 602

Qy   1043 ThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGlu 1062
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 ACAAGCAAAGAGGACATTGAATATATCCGGGATGCCCTCACCGTGGGAAAAAGCGAGGAG 662

Qy   1063 AspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpThrVal 1082
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   663 GACGCTAAGAAATATTTCTTTGATCAGATCGAAGTCTGCAGAGACAAAGGATGGACTGTG 722

Qy   1083 GlnPheAsnTrpPheLeuHisLeuValLeuGlyTyrIleLysLysGlnGlyGluLysHisSerAla 1102
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Db   723 CAGTTTAACTGGTTCCTACATCTTGTTCTTGGCATCAAACAAGGAGAAAAAGCACTCCGCT 782

RESULT 8
BB619812
LOCUS   BB619812   915 bp   mRNA   linear   EST 26-OCT-2001
DEFINITION   BB619812 RIKEN full-length enriched, adult male thymus Mus musculus
              cDNA clone 5830428L06 5', mRNA sequence.
ACCESSION   BB619812
VERSION   BB619812.1   GI:16459063
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 915)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
              ,Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
              ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
              Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
              ,D., Shibata,K., Shinagawa,A., Shiraki,T., Socabe,Y., Suzuki,H.,
              Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
              Muramatsu,M. and Hayashizaki,Y.
TITLE   RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL   Unpublished
COMMENT   Contact: Yoshihide Hayashizaki
              Laboratory for Genome Exploration Research Group, RIKEN Genomic
              Sciences Center(GSC), Yokohama Institute
              The Institute of Physical and Chemical Research (RIKEN)
              1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
              Tel: 81-45-503-9222
              Fax: 81-45-503-9216
              Email: genome-res@gsc.riken.go.jp
              URL:http://genome.gsc.riken.go.jp/
              Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
              ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
              Normalization and subtraction of cap-trapper-selected cDNAs to
              prepare full-length cDNA libraries for rapid discovery of new
              genes. Genome Res. 10 (10), 1617-1630 (2000)
              wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
              Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
              ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
              Hayashizaki,Y.

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/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed;
Average insert size 2.5 kb. library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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BASE COUNT    381 a    252 c    251 g    243 t
ORIGIN

Alignment Scores:
Pred. No.:                         1127
Score:              2.44e-136
Matches:            1268.50        265
Percent Similarity: 89.14%         Conservative:  14
Best Local Similarity: 84.66%      Mismatches:    28
Query Match:        21.91%         Indels:        6
DB:                 10             Gaps:          1
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US-09-974-573-1 (1-1102) x BG389556 (1-1127)

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Qy   642 AlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeuLe 661
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Db     2 GCCATTGCAGTTCAGAAACTGGAGAGCTTGGAGGACGATGATGTTCTGCATTACCTTCT 61

Qy   661 uGlnLeuValGlnAlaValValValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLe 681
         ||||||||||||||||||||||||||  ||||| :||||||||||||||||||
Db    62 ACAATTGGTCAGGCTGTGAAATTTGAACCATACCATGATAGTGCCCTTGCCAGATTTCT 121

Qy   681 uLeuLysArgGlyValLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArgSe 701
         ||||| ||||  |||||||||  ||||||||||||||||||||||||||||||||||
Db   122 GCTGAAGCGTGGTTTAAGAACAAAAGAATTGGTCACTTTTTGTTTTGGTTCTTGAGAAG 181

Qy   701 rGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyrLe 721
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Db   182 TGAGATAGCCCAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAGCCTATCT 241

Qy   721 uArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValIleAspMe 741
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Db   242 GAGGGGCTGTGTGCACAGCCATGCTGCACGACTTTACCCACAAGTAAATCGAGAT 301

Qy   741 tLeuGlnLysValThrIleAspPheLysSerLeuSerAlaGluLysTyrAspValSerSe 761
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Db   302 GTTACAAAAAGTCACCCTTGATATTAAATCGCTCTCGCTGAAAGTATGACGTCAGTTC 361

Qy   761 rGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuProGl 781
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Db   362 CCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCCGA 421

Qy   781 nSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyValLeuValIleLeuLysCy 801
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Db   422 AAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGGCGCTGGCAATTGAAAAATG 481

Qy   801 sLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspProTh 821
         ||||||||||||||||::|||||||||||||||||||||||||||||||||||
Db   482 TAAAGTAATGGCTCCAAGAAAAACCACTATGGCTGAGTTTAAATGTGCCGATCCTAC 541

Qy   821 rAlaLeuSerAsnGluThrIleGlyIleIleGlyIleIleGlyHisGlyAspAspLysLeuArgGlnAs 841
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Db   542 AGCCCTATCAAATGAACAATTGAATTATCTTTAAACATGGTAGATCTTCGCCAAGA 601

Qy   841 pMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluSer-LeuA 861
         ||||||||||||||||||||||||||||||||||||||||||| ||:
Db   602 CATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATATGGGAGACTGAATCTTTGG 661

Qy   861 sp-LeuCysLeuProTyrGlyCysIleSerThrGlyGlyIle-GlyMetIleGl 880
         ||| |||||||||||||||||||||||||||||||||||| |||||||||
Db   662 ATCTTATGCCTTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATTGGAATGATCGA 721

Qy   880 uIle-ValLysAspAlaThrThrIleAlaLysIleGlnSerThrValGlyAsnThrG 900
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Qy   900 lyAlaPheLysAspGluValSerHisTrpLeuLysGluLysCysProIleGluGluL 920
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(left column, read downward)

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Db   183 AAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATGTCCTATTGAAGAAAAGTTTCAG 242

Qy   923 AlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeu 942
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Db   243 GCCCAGTTGGAAAGTTTGTTTACTCCTGTGCAGGCTACTGCGTGGCCACATTTGTTCTT 302

Qy   943 GlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHis 962
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Db   303 GGGATCGGTGACAGGCACACGACACAATTATGATCTCAGAGACAGGAAACCTATTCAT 362

Qy   963 IleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLysGluArg 982
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Db   363 ATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCATAAAGAGAGA 422

Qy   983 ValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyTyrLysLysThr 1002
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Db   423 GTGCCCTTCGTCCTAACCCCAGACTTCTTGTTTGTGATGGGAACTTCTGGATACAAAAGACA 482

Qy  1003 SerLeuHisPheGlnLysPheGlnAspValCysValLysValAlaTyrLeuAlaLeuArgHis 1022
         ||| |||||||||||||||||||||||:|| :||||||||||||||||||||
Db   483 AGTCCACACTTCCAGAAATTCCAGGATGTCTATGTTAAGGCTTACCTAGCTCTTCGCCAT 542

Qy  1023 HisThrAsnLeuLeuIleIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
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Db   543 CACCACAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGAAATGCCCCAGCTG 602

Qy  1043 ThrSerLysGluGluProIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGlu 1062
         ||||||:||||||||||||||||||||||||||||||||||||||||||||
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Qy  1063 AspAlaLysTyrPheLeuArgProGlnIleLeuGluValCysArgArgAspLysGlyTrpThrVal 1082
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Db   663 GACGCTAAGAAATATTTTCTTGATCAGATCAGAAGTCTGCAGAAGGATGGACTGTG 722

Qy  1083 GlnPheAsnTrpPheLeuHisLeuValLeuGlyTyrLeuGlyIleLeuLysGlnGlyGlu 1098
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Db   723 CAGTCTAACTGGTTCCTACATCTTGTTCTGGCATCAA-CAAGGAGAA 769
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RESULT 9
BG389556
LOCUS       BG389556                    1127 bp    mRNA            linear      EST 12-MAR-2001
DEFINITION  6024142557F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4522932 5',
            mRNA sequence.
ACCESSION   BG389556
VERSION     BG389556.1    GI:13282991
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1127)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10424 row: m  column: 13
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
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Qy    920  ysPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrP    940
                ::|||
Db    842  AGTTCCGGCCAGAGGGGGCACACATTGCAATCCCGGAAGGCAGGGACCAGGCGAGTGCAACC-  900
Qy    940  heValLeuGlyIleGlyAspArgHisAsn  949
                :::|||
Db    901  --GTTGGGTCAGTGAAATGGCGGCACAGC  927
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RESULT 10
BU517397
LOCUS        BU517397        861 bp   mRNA   linear   EST 12-SEP-2002
DEFINITION   AGENCOURT_10162715 NCI_CGAP_Mam2 Mus musculus cDNA clone
             IMAGE:6514979 5', mRNA sequence.
ACCESSION    BU517397
VERSION      BU517397.1  GI:22824923
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 861)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             cDNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM14091 row: c  column: 12
             High quality sequence stop: 682.
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N-3"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6514979"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam2"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT     224 a      249 c      218 g      170 t
ORIGIN
```

```
Alignment Scores:
Pred. No.:                        Length:          861
Score:              1.12e-133     Matches:         237
Percent Similarity:  94.70%       Conservative:     13
Best Local Similarity: 89.77%     Mismatches:       13
Query Match:         21.49%       Indels:            1
DB:                     13        Gaps:              0
```

```
US-09-974-573-1 (1-1102) x BU517397 (1-861)

Qy     1  MetGluLeuGluAsnTyrGlnGlnProValValLeuArgValGluAspAsnArgArgArgArg   20
Db    60  ATGGAGCTGGAGAACTATCAGCAACACCGGGTGGTTCTAAGAGAGGACAACCTCCGCCGGGC   119
Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleLeuIleProIle   40
Db   120  CGGAGGATGAAGCCACGCAGCCAGCAGCCAGCGCTGTCTTCCATGGAGCTCATCCCCATT   179
```

```
Db     41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaAlaLeuLeuHis   60
                |||||||||||||||||||| ||     ::|||||||||||||||||||||||
Db    180  GAGTTCGTACTGCCCACCAGCCAGCGCATCGAACTCCAGAAACAGCGCTGCTGCAT     239
Qy     61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
                |||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db    240  GTGGCTGGCCATGGACAATGGAACAGATGAAAGTCAGTGTGGCTGCGCCACTGGAG     299
Qy     81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyLysProAspHisPheLeuLeuTyr  100
                |||||||||||||:::|||
Db    300  ACCAGTGTGGCTGCGGAGTTCTACCACCGATTGGGCCCGGACCAATTCCTCCTGCTCTAC  359
Qy    101  GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnLysValGlnThrLeuAsp  120
                |||||||||||||||||||:::|||
Db    360  CAGAAGAAAGGACAATGGTATGAGATCTATGACAGTAAGTACCAAGTGTGCAGACCCTAGAC  419
Qy    121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValGlnLysArg  140
                |||||||||||:::|||
Db    420  TGCCTGCATTACTGGAAGTTGATGCACAGAGCCCCTGGCCAGATCCACGTGTACAGGCGGA  479
Qy    141  HisAlaProSerGluGluThrLeuGluPheGlnLeuAsnLeuAsnAlaLeuLeuGlyTyr  160
                |||||||||||:::|||
Db    480  CACGTACCTTCTGGAGGAGACCTTGGCTTTCCAGAGGCAGCTCACCTCCCTGATTGGCTAT  539
Qy    161  AspValThrArgAspValSerAsnValHisAspAspLysSerProGluLeuGluPheArgLeu  180
                |||||||||||:::|||
Db    540  GACGTCACTGACATCAGCAATGTGCACGATGATGAGCAGAGTTCACTCGCCGCCGTCTG  599
Qy    181  ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrArgAlaMetHisPro  200
                |||||||||||:::|||
Db    600  GTTACGCCCCGCATGGCTGAAGTGGCTGGCCGCGGATGCCAAACTCTATGCTATGCACCCT  659
Qy    201  TrpTyrSerLysLeuProGluTyrTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
                |||||||||||:::|||
Db    660  TGGGTAACGTCCAAACTCTCCAGACTACCTGTCAAAAAGATTGCCAACAACTGCATC  719
Qy    221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
                |||||||||||:::|||
Db    720  TTCATCGTCATCCACCGCGTACCACCAGCCAAACCATCAAGGTGTCCGCAGATGATACT  779
Qy    241  ProGlyThrIleLeuGlnSerProPhePheThrLysMetAlaLysLysLysSer-LeuMetAs  260
                |||||||||||:::|||
Db    780  CCTGGTACCATCCTCCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAGTCCCCTAATGAA  839
Qy    260  pIleProGlu 263
                |||
Db    840  TATCTCAGAA  849
```

```
RESULT 11
BQ072706
LOCUS        BQ072706        1043 bp   mRNA   linear   EST 02-APR-2002
DEFINITION   AGENCOURT_6763227 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756177
             5', mRNA sequence.
ACCESSION    BQ072706
VERSION      BQ072706.1  GI:19901752
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 1043)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             cDNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
```

```
Qy  201 TrpValThrSerLysProLeuPro-GluTyrLeuLeuLysIleThrAsnAsnCysVa 220
        |||||||||||||||||  ::|: |||  |||||  ||:|||::::  :||||:::::
Db  684 TGGGTGACGTCCCAGCCCCTCCGGNAGTACCTGTGGAAGAAGATTGCCAACAACTGCAT 743

Qy  220 lPheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspTh 240
        ||:||||||| :|||||::|: |||||||||||  :||||:|| ||||||||||||||
Db  744 CTTCATCGTCATTCACCGAGCNACACCAGCCAGACATTAAGGTCTCACCGACGACAC 803

Qy  240 rProGlyThrIleLeuGlnSerPhe-PheThrLysMetAlaLysLysLysSer-LeuMet 259
        |||||:|||||||||||:  ||||  ||||||:|||||||||||||  ::||  |||||
Db  804 CCCCGGCGGCATCTTGCAGAGCTTCCTTCACCAAGATGCCCCANAAGAAAATCTCCGGATG 863

Qy  260 AspIle--ProGluSerGlnAsnGlu--ArgAspPhe--ValLeuArgValCysGlyA 277
        ||:|||  :|||||||  |||||  |  ||||||||  |||:||||||::||||  ||
Db  864 GATATTCCCCGAAAGCCCAAGCGAAACAGGGATTTTTGTGCCCGCCCGTTCTGGGGG 923

Qy  277 rgAspGluTyrLeu----------ValGlyGluThrPro---IleLysAsnPhe---G 291
        |||||||||||||          |||:|||||||||:|   |||||:|||:|:   |
Db  924 CCCGGGATAAAATAAACCCGGGGGGGGAAAACCCCCCATCCCAAAAAACTTTTCCC 983

Qy  291 lnTrp-Val---ArgGlnCys------LeuLysAsnGlyGluGlu 302
        ||||| |||   |||:||:|||     |||||||||||||||||
Db  984 AGTGGGTGGAAAGGCACTGTCCCCTCCTAAAAAAGGGGGAAAA 1028
```

```
RESULT 12
CA966024
LOCUS        CA966024                  976 bp    mRNA      linear    EST 03-JAN-2003
DEFINITION   CcLL03a12h19f2 Carp liver library 3 Cyprinus carpio cDNA clone
             12h19 5', mRNA sequence.
ACCESSION    CA966024
VERSION      CA966024.1  GI:27492581
KEYWORDS     EST.
SOURCE       Cyprinus carpio (common carp)
  ORGANISM   Cyprinus carpio
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
             ; Cyprinidae; Cyprinus.
REFERENCE    1  (bases 1 to 976)
  AUTHORS    Gracey,A.Y., Fraser,E., Li,W. and Cossins,A.R.
  TITLE      Microarray and EST analysis of the carp (Cyprinus carpio)
             transcriptome during environmental stress
  JOURNAL    Unpublished
COMMENT      Contact: Andrew R. Cossins
             Laboratory for Environmental Gene Regulation
             University of Liverpool
             School of Biological Sciences, The Biosciences Building, Crown
             Street, Liverpool, United Kingdom, L69 7ZB
             Tel: +44(0)151-795-4510
             Fax: +44(0)151-795-4431
             Email: cossins@liv.ac.uk
             Vector has been trimmed from this EST.
             Plate: 12 row: h column: 19
             Seq primer: TriplEx 5' LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3')
             High quality sequence start: 80
             High quality sequence stop: 676.
FEATURES             Location/Qualifiers
     source          1..976
                     /organism="Cyprinus carpio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7962"
                     /clone="12h19"
                     /sex="Male & female"
                     /tissue_type="Liver"
                     /dev_stage="Adult"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="Carp liver library 3"
                     /note="Vector: pTriplEx2; Site_1: Sfil GGCCATTACGGCC;
                     Site 2: Sfil GGCCGCCTCGGCC; Normalized and serially
                     subfacted cDNA library prepared from liver of warm, cold
                     and hypoxia challenged animals"
BASE COUNT      263 a   220 c   243 g   247 t    3 others
ORIGIN
```

```
FEATURES             Location/Qualifiers
     source
                     Plate: LLAM12796  row: f  column: 18
                     High quality sequence stop: 691.
                     Location/Qualifiers
                     1..1043
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5756177"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH MGC Library."
BASE COUNT    244 a   323 c   293 g   180 t    3 others
ORIGIN

Alignment Scores:
Pred. No.:                                   1043
Score:                     3.04e-126         253
Percent Similarity:        1181.50           14
Best Local Similarity:     83.78%            35
Query Match:               79.31%            17
DB:                        20.41%            7
                           13

US-09-974-573-1 (1-1102) x BQ072706 (1-1043)

Qy    1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg 20
        |||||||||||||||||||||||||||||||||||  |||:::||||||||||||||
Db   84 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTAGAGAGGACAACTGCCAAGGGGC 143

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
        ||||||||||||||  :||||:|| |||| ||| ::|||||::||:||||||:|||||:|
Db  144 CGGAGGATGAAGCCCGCAGTGCTGCGGCCAGCGTGTCTCCTGAGCTCATCCCCATC 203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
        ||:|||||||:|||||||  :||||:|| :||||||||:|||||||||||||||||||:|
Db  204 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGAGCCCGAAACGGCGCTGCGACAC 263

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
        |||||||||||||||||||||||||| :|||||||||||  ||:||||||||||:|||||
Db  264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
        ||||| ||| ||||||||:|||||||||  :|||||||| |||  |||||||:|||||||
Db  324 ACCAGCGTGGCGGGACTTCTACCACCGGCTGGGACCGGACCCGATCACTTCCTCCTGCTCTAT 383

Qy  101 GlnLysLysGlyGlnTrpTyrAspSerTyrArgValValGlnThrLeuAsp 120
        |||||  :|||||:|||||||||||| ::|| ||||||:| |:|||||||:
Db  384 CAGAAGAGAGGGGCAGTGGTACGGAGTCTACCACACAGTGGTGCAGACTCTGGAC 443

Qy  121 CysLeuArgTyrTrpLysValSerLeuHisArgSerProGlyGlyGlnIleHisValValGlnArg 140
        |||||:||||:|:|||||||| :||||||||||:|||||:|| :||  ::|||:|||||:|||||
Db  444 TGCCTGCGCTACTGGAAGGCCCACCGGAGCCCAGGATCCACCTGGTGCAGCGG 503

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaLeuLeuGlyTyr 160
        |||||||| :||||:||||:||  ||||||  :|||||||:|||||||||||||||:|||:|
Db  504 CACCCGAGCGGGAAGAGACCAGCCTTCCAGCGGCAGCTCACGCGGCTGATTGGCTAT 563

Qy  161 AspValThrAspValSerAsnValHisAspAspAspGluLeuGluLeuThrThrArgArgLeu 180
        ||:||:|||:||||||||||||||:|||||||||||||:||||:|||:|||||||:|||
Db  564 GACGTCACTGACGTCAGCAACGTGACGACGATAGCTGAGTTCACCGCCGTGGCTTG 623

Qy  181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
        |||||||||||:||||||:||| :|||||||||||||  :||||||:|||||||:|||||
Db  624 GTGACCCCGCGGCATGGCGGAGGTGGCCGGCAGCTCCACGCCGTAGCTTCACACCCCG 683
```

```
Alignment Scores:
Pred. No.:         5.97e-125       Length:              976
Score:             1170.00         Matches:             232
Percent Similarity: 88.97%         Conservative:        26
Best Local Similarity: 80.00%      Mismatches:          32
Query Match:       20.21%          Indels:              2
DB:                                Gaps:                0

US-09-974-573-1 (1-1102) x CA966024 (1-976)
```

```
Qy   792 LysAlaGlyGluValIleGluValCysLysValMetAlaSerLysLysProLeu 811
         :::     ||||||::||:::||::||    |||||||||||||||||||
Db    29 CGTCGAGGGGTCGGAGTGATTGAACAATGCAGATCGCATCCAAAAAGAACCCTTTG 88

Qy   812 TrpLeuGluPheLysCysAlaAspProThrAlaLeuSerAsnGluThrIleGlyIleIle 831
         ||||||||||||     |:::  :||  ||||||||||||||
Db    89 TGGCTGCAGTTCAAACAGCACGGCCGACACCCACAACTTGCCGAGTGACACGATTGGGATCATC 148

Qy   832 PheLysHisGlyAspAspArgIleAspMetLeuIleLeuGlnIleLeuArgIleMet 851
         ||||||     ||||| |||||:|||||:|||||||||||||||||
Db   149 TTTAAAGAGCGGGATGACCTTGCTCAGGACATGCTGATATTACAGATTTTACTGATAATG 208

Qy   852 GluSerIleTrpGluThrGluSerLeuAspLeuCysLeuProTyrGlyCysIleSer 871
         ||||||||||     |||:|||||||||||||||||::|||||||||
Db   209 GAGTCTATCTGGGAACTGGAGTCTTTGGATCTTTCCTTGTTACCATATGGATGTATTTCC 268

Qy   872 ThrGlyAspLysIleGlyMetIleGluIleValLysAspAlaThrArgIleAlaLysIle 891
         |:|||||     ||||||:|||||||     |||||||:|||||||||||||||
Db   269 ACTGGAAATAAAATTGGAATGATTGAAATAGTAGGAGATGCCACTACTATTGCTAAACATT 328

Qy   892 GlnGlnSerThrValGlyAsnThrGlyAlaPheLysAspGluValLeuSerHisTrpLeu 911
         ||     ||||||||||||||     |||||:||||||||||||
Db   329 CAACAAAGTACTGTGGGAACACCGGAGCTTTTAAAGATGAAATCCTCAGTCAGTGGCTT 388

Qy   912 LysGluCysProIleGlnGluLysPheGlnAlaAlaValAlaValGluArgPheValTyrSer 931
         ::|||     |||||:|||||||||:::|||||||||||||||||
Db   389 CGTGAAAAGTGTGAATGAAGGACAAGCACCAGCGGCTGTTGAAGCGTTTGTGTTCTCC 446

Qy   932 CysAlaGlyTyrCysValAlaThrPheValLeuGlyIleTyrIleGlyAspArgHisAsnAspAsn 951
         ||||||||||:||||||||||||||:::||::||||||||||||
Db   449 TGTGGAGGGTATTGTGTGGCAACTTATGTCTCTGGGCATCGTGATCGTCACAATGACAAC 508

Qy   952 IleMetIleSerGluThrGlyLeuAsnLeuPheHisIleIleGlyHisGlyLeuGlyAsn 971
         |||||:::|||::|||||:::|||::||||||||||||||||||
Db   509 ATAATGATTACAGAGACAGGCAACCTATTCCACATTGATTTCGGTCACATACTTGGAAAC 568

Qy   972 TyrLysSerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProAspPhe 991
         |||||||||:::||||||||||:||||||||:::|||||||||||
Db   569 TACAAGAGTTTCATGGGGATCAGCAAGGAGCGAGTTCCTTTTGTGCTGACTCCTGATTTC 628

Qy   992 LeuPheValMetGlyThrSerGlyLysLysThrSerLeuHisPheGlnLysPheGlnIleAsp 1011
         ||||||||||||||||::|||     ::|||||||||:::||||||
Db   629 CTCTATGTGATGAGCACGACGGGCAAAAAAAGCAGCCCCATTTCCTTCAGTTTCAGAAC 688

Qy  1012 ValCysValLysAlaThrTyrLeuAlaLeuArgHisHisThrAsnLeuPheIleIleLeuPhe 1031
         |:||||||||||||||||||||||||     :::||||||||||
Db   689 GTTTGCCTGAAGGCCTCGAAGGCTCTGGCTCTGCGACC-CACACTCAACCTGCTGATCATCCTGTTC 747

Qy  1032 SerMetMetLeuMetThrGlyMetProGlnLeuThrGlySerLysGluThrIleGluGlyLys 1051
         :::|||||||||||||||||||:::|||||||||||||||
Db   748 TCCATGATGCTGATGACCGGGATGCCGCAGCTGACTGGCCAGAAGGAGAATCNAGTACACATA 807

Qy  1052 ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysAlaLysTyrProLeuLeuGln 1071
         ||||||||:::||||||||||||||||:::|||||||||||
Db   808 CGGGAACCGCCTACGTCGGATGCTCGGAGGACAGCAGGCCAACCA-CACTTTTTGGAACAA 866

Qy  1072 IleGluValCysArgAspLysGlyTyrTrpThr 1081
         |||:::||||||||||||||||||||||
Db   867 ATCGAGATCTGCCGGGACAAGGGGTGGGACG 896
```

```
BASE COUNT    239 a    157 c    161 g    203 t

ORIGIN
```

```
Alignment Scores:
Pred. No.:         2.25e-124       Length:              761
Score:             1163.50         Matches:             235
Percent Similarity: 93.00%         Conservative:        4
Best Local Similarity: 91.44%      Mismatches:          12
Query Match:       20.09%          Indels:              6
DB:                                Gaps:                1

US-09-974-573-1 (1-1102) x BG615507 (1-761)
```

```
Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaAlaLeuGlyAlaValIleGluGlyLys 800
         :::     |||||||||||||||||||||||||||||||||||||||
Db     1 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGCGCTGGGAGCGGTGATTGAAGGGAAAA 60

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluTrpLeuGlnSerAlaAspPro 820
         |||||||||||||||||||||||||||||||||||||||||||
Db    61 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 120

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGCCCTATCAAATGAACAATTGAATTATCTTTAAACATGGTGATGATCTGCGCCAA 180

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
         |||||||||||||:||||||||||||||||:::||||||||||||
Db   181 GACATGCTTATTTACAGATTCTACGAATCATCATGGAGTCTATTTGGGAGACTGAATCTTTG 240
```

```
RESULT 13
BG615507
LOCUS       BG615507       761 bp    mRNA    linear    EST 18-APR-2001
```

/note="Organ: kidney; Vector: pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard Univerity). Note: this is a NCI_CGAP Library."

```
BASE COUNT    250 a   210 c   215 g   221 t
ORIGIN

Alignment Scores:
Pred. No.:              1.52e-117          Length:         896
Score:                  1106.00            Matches:        214
Percent Similarity:     82.72%             Conservative:    35
Best Local Similarity:  71.10%             Mismatches:      44
Query Match:            19.10%             Indels:           8
DB:                     14                 Gaps:             1

US-09-974-573-1 (1-1102) x CA471197 (1-896)

Qy  423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSer 442
            |||   ||| :|| |||:|||   :|||||:|||:|:|
Db    1 TTACCCAAAGGTGCCCGACTTAGCCTGCCAAGTGTCTGTGAAAGGCACAGACACAAACA 60

Qy  443 GlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyr 462
                                                  :||
Db   61 TCAAAGGAAACT--------------------GAAATGTAAAAACAAGTCTCGCTTACTCTAC 102

Qy  463 TyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisIleGlyGluTyrValLeu 482
            ||| |||||| |||  ||||||||| |||   ||: |:  |||   ||:||:|
Db  103 TATGTCAACCTGTTATTAGTTGATCACCGCTCCCTACTTAGACAAGGTGAGTTCATCTTG 162

Qy  483 HisMetTrpGlnLeuSerGlyLysGlyAspGlnLysSerPheAsnAlaAspLysLeu 502
            ||||||||| |||||||||||:|||||||||||||||  |||||||||||||||
Db  163 CACATCTGGAAGATGCCTGAAGAGAGTGAAGACAACAGCAGTGTAAATGCAGATAAGCTT 222

Qy  503 ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuAspAsn 522
            ||||||||||||||||||||||||||||||||||||||||||||
Db  223 ACATCCGCAACCAACCCAGACAAGGAAAACTCAATGGCTGTGTTCATTTCCTGGACACAG 282

Qy  523 TyrCysHisProAlaAlaTyrProLysLeuPheSerGluValTrpGlyProAspTyrArg 542
            ||:|||||||||  :|| |||||||||||||:||||||||||||:|:||||||||
Db  283 TACTGCTACCCTGGCCTCTTCCCAAGAGCAAAGATTCCTGATATTGAAGGCGAAAGA 342

Qy  543 ValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluLeuIleAlaThrAsp 562
            :|| |:||:|||||||||| |||||:|||::|||||||||||||||:||||||||
Db  343 GGGCAGAGAGATGCCAACATTCTACCGCAAACAATTTGAGCAGATTATTGCTACAGAC 402

Qy  563 ProLeuAsnProLeuThrArgAlaGluAspLysLeuLeuTrpHisPheArgTyrGluSer 582
            |||||  ||||||||||:|| |||:||||||:|||||||||:|||||||||||||
Db  403 CCTTTGCACCCGCTCACCTCCGGAGATAAAGAGTTGCTCTGGCACTTCCGGAGGAGTGC 462

Qy  583 LeuLysAspProLysAlaTyrProLysLeuPheSerGluValTrpGlyGlnGlnGlu 602
            ||||||:|||||  ||:|||||||||||||||||||:||||||||||:|||:|||
Db  463 ATGAGGGATCCGAAAGCATACCCGAAGTTTCTTCCTCGTTAAGTGGGGCAACAAGAG 522

Qy  603 IleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeu 622
            ||| ||:|||||||| :|| |||||||:|||||:|||||||||:||:|||||||:|||
Db  523 GCTGTGGCCATAACGCATTATCTTCTGGAAAGGAGACACCATGGGACCCGAAGGCGTGCTT 582

Qy  623 AspValGlyLeuThrMetGlnLeuLeuLeuAspLeuAspCysAsnPheSerAspGluAsnValArgAla 642
            |||||||| ::  ||| |||||||||||||||||||||  ||| :|||:|||||||||| |||:|:||
Db  583 GATGTGGGTTTGGTTTGGTTCTTACAATTACTGGACTGCCACTTCTCTGATGAGAAAACGTGCGCACT 642

Qy  643 IleAlaValGlnLysLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeuGln 662
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Qy  663 LeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuLeuArgPheLeuLeu 682
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Db  703 CTTGTCCAGGCTGTAAAATTGAACCATACCATGCAGCGACCACTTGCAAGGTTCCTTCTG 762

Qy  683 LysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArgSerGlu 702
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Qy  861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
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Db  241 GATCTATGCCTCCTGCCATTGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 300

Qy  881 IleValLysAspAlaThrThrLeuAlaLysIleGlnGlnSerThrValGlyAsnThrGly 900
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Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGlnLys 920
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Db  361 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCCTACTGAAGAAAAG 420

Qy  921 PheGlnAlaAlaAlaGluArgPheValSerCysAlaGlyTyrCysValAlaThrPhe 940
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Db  421 TTTCAGGCAGCAGCTGGAGAGATTTGTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT 480

Qy  941 ValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSer-GluThrGlyAsnIle 960
            ||:||||| ||:|||||||| |||||||||||||||:||||||||    |||||||||:||
Db  481 GTTCTTGGAATAGGCGACAGACCAGACACCAATGACAATATTATGATCACCCGAGACAGGAAACCT 540

Qy  960 uPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle-AsnL 980
             |||||:||||||:|||||:|||||| |||||||||||||||||:|||||||||    |:
Db  541 ATTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTTAATA 600

Qy  980 ys-GluArgValProPheValProThrProAspPheLeuProPheValMetGlyThrSerGly 999
               ||||:||||| ||||||||||||||||:||||||||||||||||:||||||||||||
Db  601 AACGAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTTCTTTGTGATGGAACTTCTGGA 660

Qy 1000 LysLysThrSerLeuHis---PheGlnLysPheGlnAspValCysValValLysAla-TyrLe 1018
            |||||||||||||||:       :||| :|||||:||||||||||:||||||||    :|:
Db  661 ACAGCAAGACAAGCCCAACCCCTCCAGAAATCTCAGGACATCTGTGTTAAGGCTTTATCT 720

Qy 1018 uAla-LeuArgHisHisThrAsnLeuLeuIleLeuLeuPhe 1031
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Db  721 AGCCNTTTCGTCATCACAAAAACTAACTGACATCCTGTTC 761
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RESULT 14
CA471197

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LOCUS       CA471197                 896 bp    mRNA    linear   EST 12-NOV-2002
DEFINITION  AGENCOURT_10698181 NCI_CGAP_ZKid1 Danio rerio cDNA clone
            IMAGE:6791058 5', mRNA sequence.
ACCESSION   CA471197
VERSION     CA471197.1  GI:24927549
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Leonard I. Zon, M.D.
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14294  row: b  column: 17
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
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                     /clone_lib="NCI_CGAP_ZKid1"
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Qy   703  IleAlaGlnSerArgHisTyrGlnGlnArgPheAla-ValIleLeu-GluAlaTyrLeu     721
          ||||||||| ||| ||||||||||||:|::||||||||||||||:|||||||||||
Db   823  AATTGCCCAATCCATGCACTATACGACAGAGGTATGCTTGTAATACTGGGAAGCGTATCTC   881

RESULT 15
BQ232683
LOCUS        BQ232683      7558824 NIH_MGC_92     852 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION   AGENCOURT_7558824 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045373
             5', mRNA sequence.
ACCESSION    BQ232683
VERSION      BQ232683.1    GI:20414083
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 852)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM13289 row: h column: 14
             High quality sequence stop: 632.
             1..852
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:6045373"
             /tissue_type="embryonal carcinoma, cell line"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH_MGC_92"
             /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
             Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
             Average insert size 2.5 kb. Library enriched for
             full-length clones and constructed by Life Technologies.
             Note: this is a NIH_MGC Library."
BASE COUNT   185 a   271 c   250 g   146 t
ORIGIN

Alignment Scores:
Pred. No.:                      1.8e-109          Length:        852
Score:                          1036.50           Matches:       204
Percent Similarity:             85.54%            Conservative:  9
Best Local Similarity:          81.93%            Mismatches:    27
Query Match:                    17.90%            Indels:        9
DB:                             13                Gaps:          2

US-09-974-573-1 (1-1102) x BQ232683 (1-852)

Qy    1  MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg     20
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Db   93  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAGGCGC    152

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle      40
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Db  153  CGGAGGATGAAGCCCGCAGTGCTGCGCCAGCCTGTTCCTCCATGGAGCTCATCCCCATC   212

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis    60
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Db  213  GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGAGCCCGGAAACCGCTGCTGCAC    272

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu    80
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Db   273  GTGGCCGGCCACGGCAACGTCGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  332
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Qy    81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
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Db   333  ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCCGACCATCACTTCCTGCTGCTAT  392

Qy   101  GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGluIleValGlnValThrLeuAsp  120
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Db   393  CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACGAGGTGGTGCAGACTCTGGAC  452

Qy   121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
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Db   453  TGCCTGCGCTACTGGAAGGCCACGCACCGGAGCCCAGGCCAGATCCACCTGGTGCAGCGG  512

Qy   141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
          ||:|| |||||||||||:||:
Db   513  CACCCGGCCCTCCGAGGAGTCCCAGCCTTCCAGCGGCAGCTCAACGCGCTGATTGGCTAT  572

Qy   161  AspValThrArgMetAlaGluValHisAspAspValPheThrArgArgLeu  180
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Db   573  GACGTCACTCGACGTCCAGCAACGTGCACGACGATGAGCTGGAGTTCACGGCCGTGGCTTG  632

Qy   181  ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro  200
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Qy   201  TrpValThrSerLysProLeuProGluTyrLeuLeu--LysLysIleThrAsnAsnCys  219
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Qy   220  ValPheIleValIleHisArgSerThrThrSerGlnThrThrLysValSerAlaAspAsp  239
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Qy   240  ThrProGlyThrIleLeuGlnSerPhe  248
          ::::|||
Db   789  AGGCCAGGAACCATTTAAAGGGCTTTC  815

Search completed: February 15, 2004, 06:38:04
Job time : 5305 secs
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